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(54) Title: HUMAN DNA SEQUENCES

(57) Abstract: Novel human cDNA sequence of a clones, the encoded protein sequence of a clones, antibodies and variants thereof, are provided. The disclosed sequence of a clones find application in a number of ways, including use in profiling assays. In this regard, various assemblages of nucleic acids or proteins are provided that are useful in providing large arrays of human material for implementing large-scale screening strategies. The disclosed sequence of a clones may also be used in formulating medicaments, treating various disorders and in certain diagnostic applications.

## HUMAN DNA SEQUENCES

### Background of the Invention

Current methods for testing pharmacological substances rely  
5 on a three-stage testing approach to drug development. First,  
candidate compounds are typically screened in some sort of *in*  
*vitro* system, like inhibition of cancer cell growth. Candidates  
are then tested in an animal model, as a first approximation of  
systemic effects, including efficacy and toxicity. Compounds  
10 that still show promise after these initial *in vivo* screens,  
finally are tested in humans. Again, human testing typically  
occurs in three phases: toxicity; preliminary efficacy; and  
efficacy. The entire process can take more than a decade and  
cost hundreds of millions of dollars. Aside from the monetary  
15 costs and protracted time scale, moreover, current testing  
regimes waste the lives of countless laboratory animals and  
needlessly endanger the lives of human subjects.

A need exists, therefore, for more sophisticated drug  
screening techniques that can be done rapidly *in vitro*. These  
20 screening techniques ideally will be reflective of systemic  
and/or organ-specific responses, so that they provide a reliable  
indicator of action in a human body. Current techniques,  
however, tend to utilize only a single or limited number of  
markers, thus answering only very simple questions that are of  
25 questionable medical import. For example, a typical *in vitro*  
assay may ask whether a lead compound binds a particular  
receptor, which has been implicated in a certain disorder. It is  
presumed that such binding is indicative of therapeutic  
usefulness, but it does not even purport to address systemic  
30 effects.

Not only are screening techniques for efficacy inadequate,  
the available toxicity screens likewise are inadequate.  
Toxicity, on a first level, is usually measured by animal  
testing. Aside from the complications related to *in vivo* versus  
35 *in vitro* testing, such screens are insufficient because of  
differences in metabolism, uptake, etc., relative to humans.

Thus, improved methods would be not only be *in vitro*-based, they would also be more "human."

With the increasing miniaturization of screening assays and the growing availability of targets for pharmaceutical intervention, there is increasing interest in developing arrays containing large numbers of these targets that can be assayed simultaneously. If such an array contains a large enough population of targets, it can be used to essentially mimic the systemic response. In other words, the array becomes an *in vitro* surrogate for the human body. The more refined the array, the more accurate the predictive capability. In theory, an array could be constructed that can detect all of the known human expression products simultaneously, thereby, providing a very reliable indicator of the human response to a given compound. These arrays offer advantages over the present *in vitro* screening systems in that they can assay large numbers of responses simultaneously. They are superior to animal testing because they are more "human" and, thus, more predictive of human responses.

In order to construct such arrays, however, the field is in need of further human targets. Advantageously, such targets will be provided with additional physiologically relevant information, such as whether the target is expressed in a particular tissue and whether it is related to a known functional class of targets. In this way, the artisan can focus as needed, for example, on tissue-specific effects or target class-specific effects, thereby providing information useful in evaluating efficacy and/or toxicity.

In addition to a need for pharmacological screening targets, there is a need for further pharmacological substances. These substances can be used in the formulation of medicinal compositions and in treating a wide variety of disorders.

The present invention responds to the aforementioned and other needs in the field by providing a population of novel targets useful, *inter alia*, in the profiling and medicinal contexts described above.

### Summary of the Invention

It is an object of the invention, therefore, to provide a set of human cDNA clones. Further to this object, the invention provides sequences of human cDNA clones that were isolated from libraries generated from different human tissues.

5 It is another object of the invention to provide assemblages of targets useful in profiling matrices for screening pharmacological test compounds. According to this object, assemblages comprising different populations of human nucleic acids, proteins and antibodies are provided. In different  
10 embodiments, cDNA library-specific assemblages and target-family-specific targets are provided.

It is a further object of the invention to provide a database of human nucleotide and protein sequences. Further to this object, novel human nucleotide and protein sequences are  
15 provided in electronic form. In one embodiment, one or more of these sequences is provided in a searchable database.

It is still another object of the invention to provide biologically active target molecules useful in treating or detecting human disorders. Further to this object, the invention  
20 provides nucleic acid and protein molecules that have the capacity to affect disease etiology or symptoms or correlate with known disease states. Also further to this object, a database is provided which comprises the disclosed molecules in electronic form.

25

### Detailed Description

The invention results from a need in the art for new human nucleic acids and proteins. This need arises in several contexts. First, there is a need to identify targets for therapeutic intervention. Second, there is a need to identify molecules that  
30 may be adversely affected in a therapeutic context, thereby resulting in toxicity. Knowledge of these molecules will aid in the design of new medicaments with enhanced efficacy and decreased toxicity. Finally, the need encompasses human nucleic acids and proteins that have medicinal applicability in their own right.

35 In view of these needs, the present inventors set out to isolate and sequence human cDNAs from tissue-specific libraries.



In this way, they represent subsets of molecules likely to be targets for therapeutic intervention or for avoiding toxicity. In addition, the inventors divided the molecules into various sub-categories, based on suspected functionality, structural  
5 similarity etc, which are of interest from a pharmacological perspective.

#### GENERAL DESCRIPTION OF THE INVENTIVE MOLECULES

The present invention provides novel polynucleotide molecules that, in some instances, have similarities with known molecules.  
10 The inventive DNAs were cloned from five different human cDNA libraries. In addition to these DNA molecules, the invention provides their protein translations and antibodies derived from them. The inventive DNA and protein sequences are show individually in the Description of the Sequences. The inventive  
15 nucleic acids also include the complements of the DNA sequences provided in the Description of the Sequences as well as their RNA counterparts. Methods of producing the molecules also are provided. Further, the invention provides methods for detecting all or part of the molecules and of detecting polynucleotides  
20 encoding all or part of the molecules.

The inventive molecules derive from five cDNA libraries: human fetal brain; human fetal kidney; human melanoma; human testis; and human amygdala. For convenience, each sequence bears a designation that indicates from which library it is derived. In  
25 particular, these designations are: "hfpbr" for human fetal brain; "hfkcd" for human fetal kidney; "hmel" for human melanoma; "htes" for human testis; and "hamy" for human amygdala. The individual libraries were constructed and screened as described below in the examples.

30 The protein and DNA molecules of the invention are variously described herein as "target" molecules or "inventive" molecules. The sequences and other information pertinent to the nucleic acid and protein molecules of the invention are shown below in the Description of the Sequences.

35

#### Description of the Sequences

#### Key to the Description of the Sequences

The descriptions below provide the coding sequences of the inventive cDNAs, as well as the protein sequences and other useful information, as set out herein.

## 5 Grouping

The clones were assigned to the following sixteen functional and/or tissue-derived groups:

1. Amygdala derived
2. Cell Cycle
3. Cell Structure and Motility
4. Differentiation/Development
5. Intracellular Transport and Trafficking
6. Melanoma derived
7. Metabolism
8. Nucleic Acid Management
9. Signal Transduction
10. Transmembrane Protein
11. Transcription Factors
12. Brain derived
13. Kidney derived
14. Mammary Carcinoma derived
15. Testes derived
16. Uterus derived

## 25 Description of Clone Files

The individual clone files are structured in the same pattern. The Sections are separated by paragraphs.

### 30 1. Clone Name

The clone names are deciphered with reference to the following example:

DKFZphfkd2\_3k1, wherein the code represents:

- producer of library ("DKFZ") (for convenience, this reference may be eliminated)
- a "p" for "plasmid cDNA library" (for convenience, this reference may be eliminated)
- library name (e.g. hfbr = human fetal brain; hfkd = human fetal kidney; hmel = human melanoma; htes = human testis; hamy = human amygdala)
- an underscore ("\_") to separate library information from plate information
- plate number (e.g. "3")
- plate coordinates (letter first; e.g. "k12")

### 45 2. Group

### 3. Introduction

short review of the similarities, function of the protein and possible applications

### 5 4. Short Information

specifications about the cDNA (who sequenced, completeness of the cDNA, similarity, who sequenced, chromosomal localisation, length of cDNA, localisation of poly A tail and polyadenylation signal)

### 10 5. cDNA-Sequence

### 6. BLASTn Results

search results of blasting the cDNA sequence against all public databases

15

### 7. Medline Entries

information about genes/proteins similar to the novel cDNA (if available)

### 20 8. Putative Encoded Protein Information

specifications about the encoded protein (ORF: length and localisation of the reading frame)

### 9. Protein Sequence

25

### 10. BLASTp Results

search results of blasting the protein sequence against all public databases

### 30 11. Pedant Information

output of fully automated annotation: summarises peptide information, homologies, patterns as follows:

#### [[Length]]

35

- length of the protein = number of amino acid residues

#### [[MW]]

- molecular weight of the protein

#### [[pI]]

- isoelectric point

## [HOMOL]

- shows protein with closest similarity to the cDNA-encoded protein

5

## [FUNCAT]

- functional information according to a catalogue developed by Munich Information center for Protein Sequences (MIPS)

## [BLOCKS]

10

- Blocks are multiply aligned ungapped segments corresponding to the most highly conserved regions of proteins. The blocks for the Blocks Database are made automatically by looking for the most highly conserved regions in groups of proteins documented in the Prosite Database. The Prosite pattern for a protein group is not used in any way to make the Blocks Database and the pattern may or may not be contained in one of the blocks representing a group. These blocks are then calibrated against the SWISS-PROT database to obtain a measure of the chance distribution of matches. It is these calibrated blocks that make up the Blocks Database. The WWW versions of the Prosite and SWISS-PROT Databases that are used on this server are located at the ExPASy World Wide Web (WWW) Molecular Biology Server of the Geneva University Hospital and the University of Geneva. World Wide Web URL [http://blocks.fhcrc.org/blocks/about\\_blocks.html/](http://blocks.fhcrc.org/blocks/about_blocks.html/) is the entry point to the database.

15

20

25

- here Blocks segments found in the analysed protein sequences are displayed

30

## [SCOP]

Nearly all proteins have structural similarities with other proteins and, in some of these cases, share a common evolutionary origin. The scop database provides a detailed and comprehensive description of the structural and evolutionary relationships between all proteins whose structure is known, including all entries in Brookhaven National Laboratory's Protein Data Bank (PDB). It is available as a set of tightly linked hypertext documents which make the large database comprehensible and accessible.

35

In addition, the hypertext pages offer a panoply of representations of proteins, including links to PDB entries, sequences, references, images and interactive display systems. World Wide Web URL [http://scop.mrc-](http://scop.mrc-lmb.cam.ac.uk/scop/)

5 [lmb.cam.ac.uk/scop/](http://scop.mrc-lmb.cam.ac.uk/scop/) is the entry point to the database. Existing automatic sequence and structure comparison tools cannot identify all structural and evolutionary relationships between proteins. The scop classification of proteins has been constructed manually by visual inspection and comparison of structures, but with the assistance of  
10 tools to make the task manageable and help provide generality. Proteins are classified to reflect both structural and evolutionary relatedness. Many levels exist in the hierarchy, but the principal levels are family,  
15 superfamily and fold. The exact position of boundaries between these levels are to some degree subjective. Scop evolutionary classification is generally conservative: where any doubt about relatedness exists, we made new divisions at the family and superfamily levels.

20       - - here SCOPE segments found in the analysed protein sequences are displayed  
[EC]

      ENZYMES is a repository of information relative to the nomenclature of enzymes. It is primarily based on the  
25 recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB) and it describes each type of characterized enzyme for which an EC (Enzyme Commission) number has been provided. World Wide Web URL <http://www.expasy.ch/enzyme/> is  
30 the entry point to the database.

      - here EC-number and name of enzymes with similarity to the analysed protein sequences are displayed  
[PIRKW]

      - functional information according to the Protein  
35 Information Resource (PIR) database catalogue developed by Munich Information Center for Protein Sequences (MIPS), the National Biomedical Research Foundation (NBRF) and the International Protein Information Database in Japan (JPIID).  
[SUPFAM]

- information according to the Protein Information Resource (PIR) database catalogue of protein superfamilies developed by Munich Information Center for Protein Sequences (MIPS), the National Biomedical Research Foundation (NBRF) and the International Protein Information Database in Japan (JIPID).

#### [[PROSITE]]

please refer to 12. PROSITE Motifs

#### [[PFAM]]

please refer to 13. PFAM Motifs

#### [[KW]]

- overall 2dimensional folding information
- 3D indicates that the proteins is similar to a protein of which a 3 dimensional structure is known
- overall structural information

#### [[ ]]

The last PEDANT-block depicts information about the folding structure of the protein generated by PREDATOR. PREDATOR is a secondary structure prediction program. It takes as input a single protein sequence to be predicted and can optimally use a set of unaligned sequences as additional information to predict the query sequence. The mean prediction accuracy of PREDATOR is 68% for a single sequence and 75% for a set of related sequences. PREDATOR does not use multiple sequence alignment. Instead, it relies on careful pairwise local alignments of the sequences in the set with the query sequence to be predicted.

World Wide Web URL [http://www.embl-heidelberg.de/argos/predator/predator\\_info.html](http://www.embl-heidelberg.de/argos/predator/predator_info.html) is the entry point to the database.

- H = helix, E = extended or sheet, \_ = coil, T = transmembrane, B = beta

- x indicates a low-complexity region with repeat-like structure which is omitted in all BLAST searches

## 12. PROSITE Motifs

PROSITE is a database of protein families and domains. It consists of biologically significant sites, patterns and profiles that help to reliably identify to which known protein family (if

any) a new sequence belongs. World Wide Web URL  
<http://www.expasy.ch/prosite/> is the entry point to the database.  
A description of the prosite consensus patterns is provided  
herein, after the description of the individual sequences.

5

### 13. PFAM Motifs

PFAM (protein families) is a large collection of multiple  
sequence alignments and hidden Markov models covering many common  
protein domains. World Wide Web URL <http://www.sanger.ac.uk/Pfam/>  
10 is the entry point to the database.

In the charts below, the groups of sequences are listed, and  
the description of the individual clones follows.

## Group Amygdala derived

CloneID	Homology	Function	Group
amy2_12g7	without similarity to known proteins	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	amygdala derived
amy2_12i1	weak similarity to F41E6.3 of <i>Caenorhabditis elegans</i>	No informative BLAST results; No predictive prosite, pfam or SCOP motive	amygdala derived
amy2_13g19	without similarity to known proteins	The novel protein contains a PROSITE ASP_PROTEASE motif and seem to be expressed ubiquitously.	amygdala derived
amy2_16a14	similar to carbonic anhydrase-related proteins	No informative BLAST results; No predictive prosite, pfam or SCOP motive. A similar cDNA encoding a protein of the same length was identified in sheep. This protein shows a strong signal sequence, which indicates that it is a secreted protein. The new protein belongs to a protein family, which was designated carbonic anhydrase-related protein XI (CA-RP XI), encoded by CA11 (human) and CA11 (mouse, rat). Despite potentially inactivating changes in the active-site residues, CA-RP XI is evolving very slowly in mammals, a property indicative of an important function, which has also been observed in the two other "acatalytic" CA isoforms, CA-RP VIII and CA-RP X. No informative BLAST results; No predictive prosite, pfam or SCOP motive	amygdala derived
amy2_24k15	weak similarity to pecanex of <i>Drosophila melanogaster</i> .	Pecanex is a maternal-effect neurogenic gene, involved in differentiation processes in the developing central nervous system. DKFZphamy2_24k15 seems to be expressed ubiquitously. No informative BLAST results; No predictive prosite, pfam or SCOP motive	Amygdala derived
amy2_2a13	without similarity to known proteins	No informative BLAST results; No predictive prosite, pfam or SCOP motive	amygdala derived
amy2_2i17	without similarity to known proteins	Most ESTs are derived from brain and pancreas No informative BLAST results; No predictive prosite, pfam or SCOP motive.	amygdala derived



## Group Brain derived

CloneID	Homology	Function	Group
DKF2ph...			
fbr2_78d1d	weak similarity to a human putative mitogen-activated protein kinase kinase	No informative BLAST results; No predictive prosite, pfam or SCOP motife.	brain derived
fbr2_78e1d	without similarity to known proteins.	The mRNA is differentially polyadenylated. No informative BLAST results; No predictive prosite, pfam or SCOP motife.	brain derived

## Group cell cycle

CloneID	Homology	Function	Group
DXF2ph...			
amy2_121m2	Similarity to human PA26-T2 protein.	PA26-T2 is a p53 responsive gene. The protein is predominantly expressed in brain, breast and kidney and may represent a potential novel regulator of cellular growth. Isoforms are differentially induced by genotoxic stress (UV, gamma-irradiation and cytotoxic drugs) in a p53-dependent manner.	cell cycle
amy2_24b4	Similarity to human STIM1	The stromal interaction molecular 1 gene (STIM1) encodes a type I trans-membrane protein of unknown function, which induces growth arrest and degeneration of the human tumor cell lines G401 and RD but not HBL100 and Calu-6, suggesting a role in the pathogenesis of rhabdomyosarcomas and rhabdoid tumors. There is also strong similarity to a Mus musculus stromal cell protein, which selectively increases interleukin 7-dependent proliferation of pre-B cells. The novel protein contains 1 transmembrane domain.	cell cycle

## Group Cell structure and motility

CloneID	Homology	Function	Group
DKFZph... amy2_121f19	high similarity to a Rat ankyrin binding glycoprotein-1 related mRNA.	Ankyrin binding glycoproteins play a role in neural cell adhesion and in prostate tumor cell transformation. DKFZphamy2_121f19 is expressed in brain, uterus and prostate above average	cell structure and motility
tes3_1bb5	similarity to various tropomyosins.	Tropomyosins play regulatory roles in cellular structure and transport.	cell structure and motility

## Group Differentiation/Development

CloneID	Homology	Function	Group
DK29ph... amy2_1i24	partial similarity to rattus norvegicus Notch2 protein	Notch family molecules are thought to be negative regulators of neuronal differentiation in early brain development. Notch2 is expressed not only by neuronal cells in the embryonic brain, but also by glial cells in the postnatal brain.	differentiat ion/developm ent
amy2_1j19	high similarity to the allograft inflammatory factor-1 of Cyprinus carpio.	Allograft inflammatory factor-1 (AIF-1) is a protein involved in allograft rejection. In experimental autoimmune encephalomyelitis (EAE), neuritis(EAN) and uveitis (EAU) it is produced by macrophages and microglia cells.	differentiat ion/developm ent
amy2_2b19	Originates from TXBP151 mRNA by alternative splicing	It is ubiquitously expressed. The mRNA is also subject to alternative polyadenylation. Overexpression of TXBP151 in NIH3T3 cells causes inhibition of apoptosis induced by tumour necrosis factor (TNF). It binds to A20, which is also an inhibitor of cell death by a yet unknown mechanism.	differentiat ion/developm ent
amy2_7j5	similarity to Tspyl1 testis-specific Y-encoded-like protein of Mus musculus	TSPY genes are arranged in clusters on the Y chromosome of many mammalian species. TSPY is believed to function in early spermatogenesis and is a candidate for GBY, the putative gonadoblastoma-inducing gene on the Y. The TSPY family forms part of a superfamily, TTSN, with autosomal representatives, highly conserved in mammals and beyond.	differentiat ion/developm ent

## Group Intracellular Transport and Trafficking

CloneID	Homology	Function	Group
DKF2ph... amy2_14b5	shows 61% identity to the human TYL protein and 48% identity to the human Tic protein	Both proteins show similarity to Sec7 of <i>Saccharomyces cerevisiae</i> , which takes function in vesicular trafficking. The new protein shows also significant similarity to human ARN03, which is involved in the control of Golgi structure and function. DKF2phamy2_14b5 is predominantly expressed in the CNS and germ cells.	intracellular transport and trafficking
amy2_20b3	high similarity to murine synaptotagmin 3.	The novel protein contains two C2 domains. The C2 domain is thought to be involved in calcium-dependent phospholipid binding. Synaptotagmins are essential for Ca(2+)-regulated exocytosis of neurosecretory vesicles	intracellular transport and trafficking
fkcd2_3k1	very similar to rat testicular dynamin	Dynamin is a microtubule-associated force-producing protein, which is involved in the production of microtubule bundles and which is able to bind and hydrolyze GTP and provides the motor for vesicular transport during endocytosis. The protein is ubiquitously expressed, but in brain and testis above average.	intracellular transport and trafficking
mel2_7g14	Similarity to the dor (deep orange) protein of <i>Drosophila melanogaster</i> .	The novel protein is also similar to the vakuolar membrane protein pep3 of <i>Saccharomyces cerevisiae</i> , which is involved in protein sorting mechanisms. The expression profile is ubiquitous and a role in protein transport/targeting is likely.	intracellular transport and trafficking

## Group Melanoma derived

CloneID	Homology	Function	Group
DKFZpg...			
mel2_12j1	similarity to Integrin I of Saccharomyces cerevisiae	The novel protein contains a leucin zipper. No informative BLAST results; No predictive prosite, pfam or SCOP motife.	melanoma derived
mel2_7k19	without similarity to known proteins	Transcripts can be found in almost any tissue, but are most abundant in kidney and retina. No informative BLAST results; No predictive prosite, pfam or SCOP motife.	melanoma derived

## Group Metabolism

CloneID: DKF2ph...	Homology	Function	Group
amy2_2c22	similarity to the 1-acyl-glycerol-3-phosphate acyltransferase of Zea mais.	It contains one leucine zipper. The protein is believed to play a role in fatty acid metabolism. It is ubiquitous expressed, with a slight predominance in uterus, placenta and foreskin.	metabolism
fbr2_7d121	similarity to beta-aspartate methyltransferases.	The L-isospartyl methyltransferase (Pimt), as an example, is a highly conserved enzyme utilising S-adenosylmethionine (AdoMet) to methylate aspartate residues of proteins damaged by age-related isomerisation and deamidation.	metabolism

## Group Nucleic acid management

CloneID	Homology	Function	Group
any2_1ln4	Similarity to RAD16 of Schizosaccharomyces pombe and YLR363w of Saccharomyces cerevisiae.	The novel protein contains a ATP/GTP-binding site motif A (P-loop). It has similarity to RAD16 acts in a DNA repair pathway for removal of UV-induced DNA damage. YLR363w of Saccharomyces cerevisiae is a recombination repair protein	nucleic acid management
any2_1il	Similarity to the murine hemin-sensitive initiation factor 2.	The hemin-sensitive initiation factor 2 is expressed predominantly in liver, spleen, colon and uterus and contains 2 protein kinase motifs. The mouse homologue inhibits protein synthesis in stress conditions by phosphorylation of eif-2-alpha.	nucleic acid management
any2_2gl2	Similarity to NVL-2 of Rattus norvegicus.	The novel protein contains 3 EF-hand calcium-binding domains. The related human VILIP Ca-dependent protein specifically binds the 3'-untranslated region of the neurotrophin receptor, trkB, an mRNA localized to hippocampal dendrites in an activity-dependent manner. The new protein exhibits elevated expression in brain and testis.	nucleic acid management
fbr2_7ac12	high csimilarity to glutamyl-tRNA (Gln) amidotransferase subunit A of the hyperthermophilic bacterium Aquifex aeolicus.	The novel protein contains one ATP/GTP-binding site motif A (P-loop). This loop interacts with one of the phosphate groups of a A or G nucleotide. It is found in numerous ATP- or GTP-binding proteins, such as ATP synthase alpha and beta subunits, Myosin heavy chains, Kinesin heavy chains and Kinesin-like proteins, dynamins and dynamin-like proteins, several kinases, DNA and RNA helicases, GTP-binding elongation factors and the Ras family of GTP-binding proteins. The protein seems to be expressed ubiquitously.	nucleic acid management
tes3_10ilb	similarity to human ZK1.	The ZK1 gene is one of early response genes by exposure to ionizing radiation, and plays a role in radiation-induced apoptotic cell death on hematopoietic cells. The novel protein contains 18 zinc finger domains, a RGD cell attachment and a ATP GTP A domain.	nucleic acid management
tes3_1la10	Similarity to histone H1 of Drosophila hydei.	Histone H1 variants are known to act as specific regulators of genes via the differential condensation of DNA.	nucleic acid management



## Group Signal transduction

CloneID	Homology	Function	Group
DKF2p... amy2_10h17	weak similarity to murine hac1	The novel protein contains a Zinc finger motif of the C3HC4 type (RING finger). The RING-finger domain is involved in mediating protein-protein interactions. Proteins containing a RING-finger are: mammalian V(D)J recombination activating protein (RAG1), mouse rpt-1, human rfp, human 52 Kd Ro/SS-A protein and others. The family of RING finger proteins contains a number of oncogenes. For example pML, a probable transcription factor, BRCA1, the mammalian cbl- and bmi-1 proto-oncogenes.	signal transduction
amy2_10p7	similarity to Na <sup>+</sup> /Ca <sup>2+</sup> exchange proteins	The Transport of Ca <sup>2+</sup> from the sarcoplasm into the sarcoplasmic reticulum is an essential process in the initiation of muscle relaxation. In addition, the novel protein contains a PROSITE multicopper oxidase signature. Multicopper oxidases are enzymes that possess three spectroscopically different copper centers.	signal transduction
amy2_12d7	a so far unknown alternative spliced form of disks large homolog DLG2.	It seems to be predominantly expressed in the retina, germ cells and brain. It contains a SH3-domain and a guanylate kinase domain. These conserved regions are shared among members of the discs-large family of proteins that include human p55, a membrane protein expressed in erythrocytes, rat PSD-95/SAP90, a synapse protein expressed in brain, Drosophila dig-A, a septate junction protein expressed in various epithelia, and human and mouse ZO-1 and canine ZO-2, two tight junction proteins. The Homologue of Drosophila, dig-A, acts as a tumor suppressor. All members of this family may be involved in signal transduction.	signal transduction
amy2_2f16	Similarity to sodium channel protein beta1 of Rattus norvegicus.	The sodium channel protein beta 1 of Rattus norvegicus is crucial in the assembly, expression, and functional modulation of the heterotrimeric complex of the rat brain sodium channel. The expression of the new protein seems to be restricted to brain, all matching ESTs isolated so far, derive from there.	signal transduction
tes3_11c23	Partial similarity to mouse PC32b	The novel protein contains Ub-repeats. Ub-repeat proteins are known as regulatory elements in a large variety of pathways. The repeats form a propeller like structure, which serves as a platform for protein/protein interaction. The new protein is ubiquitously expressed, indicating that it takes an essential regulatory function in the cell.	signal transduction
tes3_11d21	Contains the full coding sequence of the human Nedd-4-like ubiquitin-protein ligase.	The novel protein contains four Ub domains. The Ub/rsp5/UBP domain has been shown to bind proteins with particular proline-motifs, and thus resembles somewhat SH3 domains. It is frequently associated with other domains typical for proteins in signal transduction processes. There is also a ubiquitin-protein ligase activity reported. The protein is believed to play an important role in protein-degradation pathways	signal transduction
tes3_24f24	Similarity to murine net1a.	The closely related mNET1 activates signalling pathways in addition to those directly controlled by activated RhoA. The novel protein is expressed ubiquitously.	signal transduction
tes3_31j20	contains a Protein phosphatase 2C motif.	The novel protein shares 75% identity with the rat protein phosphatase 2C and is expressed ubiquitously. PP2C is a structurally diversified protein phosphatase family with a wide range of functions in cellular signal transduction. The transcription of the PP2Cdelta gene was activated in response to stress, like alcohol or UV irradiation. PP2C plays a role in cell cycle control.	signal transduction
tes3_5k22	similarity to human paraneoplastic neuronal antigen MA1	Antibodies against MA1 where found in patients with paraneoplastic neurological disorders. The protein is predominantly expressed in testis and brain, but ESTs are also found in liver, lung uterus and kidney	signal transduction

## Group Testis derived

CloneID	Homology	Function	Group
DKFZpg...			
Tes3_10n10	without similarity to known proteins.	The mRNA is differentially polyadenylated and the novel protein is ubiquitously expressed	testis derived
Tes3_11e17	without similarity to known proteins.	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	testis derived
Tes3_12d16	without similarity to known proteins	The EST-distribution signifies an ubiquitous expression pattern.	testis derived
Tes3_14l17	without similarity to known proteins.	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	testis derived
Tes3_15n14	weak similarity to the neurofilament triplet M protein of the rat.	The mRNA is transcribed ubiquitously.	testis derived
Tes3_16p3	without similarity to known proteins	Neurofilaments are the intermediate filaments specific to nervous tissue. They are probably essential to the tensile strength of the neuron, as well as to transport of molecules and organelles within the axon. Until now, ESTs of the novel mRNA could only be isolated from testes, germ cells and uterus.	testis derived
Tes3_17p12	without similarity to known proteins	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	testis derived
Tes3_21k14	without similarity to known proteins	The novel protein is glutamine rich and contains a cell attachment RGD motif. According to the low number of ESTs and their origin the protein seems to be expressed ubiquitously at low levels.	testis derived
Tes3_22i11	Weak similarity to RCC1-like G exchanging factor RL6, UVR8 (UVB-resistance protein) of Arabidopsis thaliana and to the murine retinitis pigmentosa GTPase regulator.	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	testis derived
Tes3_22i24	Similarity to the F-box protein FBL2 of the rat.	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	testis derived
tes3_25g3	Without similarity to known proteins.	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	testis derived
tes3_30p6	without similarity to known proteins.	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	testis derived

## Group Transmembrane proteins

CloneID	Homology	Function	Group
DKFZpg...			
amy2_11d2	Without similarity to known proteins	The novel protein contains 2 transmembrane regions.	transmembrane proteins
amy2_12l017	without similarity to known proteins.	No informative BLAST results; No predictive prosite, pfam or scope motive.	transmembrane proteins
amy2_11l14	Similarity to the human 1(3)mmt protein homolog.	The novel protein contains 1 transmembrane region.	transmembrane proteins
amy2_21c4	without similarity to known proteins	No informative BLAST results; No predictive prosite, pfam or SCOP motive.	transmembrane proteins

fbr2_76d4	without similarity to known proteins.	The novel protein contains 1 transmembrane region and a Cytochrome c family heme-binding site. No Informative BLAST results; No predictive prosite, pfam or SCOP motive.	Transmembrane proteins
tes3_13a17	without similarity to known proteins	The novel protein contains 2 transmembrane regions and one leucine zipper. The protein is ubiquitously expressed with higher abundance in stomach, brain and testis. No Informative BLAST results; No predictive prosite, pfam or SCOP motive.	Transmembrane proteins
tes3_17i21	without similarity to known proteins	The novel protein contains 2 transmembrane regions. ESTs can be found in testis, retina and brain. No Informative BLAST results; No predictive prosite, pfam or SCOP motive.	Transmembrane proteins
tes3_20h12	without similarity to known proteins	The novel protein contains 1 transmembrane region and two leucine zippers. No Informative BLAST results; No predictive prosite, pfam or SCOP motive.	Transmembrane proteins
tes3_7n12	without similarity to known proteins	The novel protein contains 1 transmembrane domain No Informative BLAST results; No predictive prosite, pfam or SCOP motive.	Transmembrane proteins
tes3_9e1b	without similarity to known proteins	The novel protein contains 1 transmembrane region. The only EST described so far is from testis. No Informative BLAST results; No predictive prosite, pfam or SCOP motive.	Transmembrane proteins

## Group Transcription factors

CloneID	Homology	Function	Group
amy2_14m1b DRF2p...	similarity to the homeotic protein emx2 of man, mouse and zebra fish as well as to the gene "empty spiracles" of Drosophila melanogaster.	Homeobox genes are known to play important roles in developmental processes. In zebrafish emx2 mRNAs are found in the dorsal telencephalon, parts of the diencephalon and the otocyst. The human homologue Emx2 appears to be already expressed in 8-5 day embryos. It is also expressed in the presumptive cerebral cortex, olfactory bulbs, in some neuroectodermal areas in embryonic head including olfactory placodes in earlier stages and olfactory epithelia later in development. Mutants of the D. melanogaster gene "empty spiracles" display spiracles devoid of filzkörper, no antenna and an open head.	transcription factors
amy2_1c12	partial identity to I-kappa-B-related protein and to BRCA1.	I-kappa-B-related protein interacts with transcription factors and BRCA1 has a function in DNA damage response. I-kappa-B-alpha mutations contribute to constitutive NF-kappaB activity in cultured and primary HRS (Hodgkin/Reed-Sternberg) cells and are therefore involved in the pathogenesis of Hodgkin's disease (HD) patients	transcription factors
amy2_2f22	similarity to YDL153c of Saccharomyces cerevisia	The novel protein is ubiquitously expressed. YDL153c is involved in transcriptional silencing.	transcription factors
tes3_16n14	similarity to human giantin.	Giantin is discussed as an autoantigen in rheumatoid arthritis. The novel protein contains a leucine zipper and a putative Helix-loop-helix DNA-binding domain. Therefore it might be a novel transcription factor. Most EST hits are from testis and germ cells.	Transcription factors

DKFZphamy2\_10h17

5

group: signal transduction

10 DKFZphamy2\_10h17 encodes a novel 180 amino acid protein which shows weak similarity to murine hac1.

15 The novel protein contains a Zinc finger motif of the C3HC4 type (RING finger). The RING-finger domain is involved in mediating protein-protein interactions. Proteins containing a RING-finger are: mammalian V(D)J recombination activating protein (RAG1), mouse rpt-1, human rfp, human 52 Kd Ro/SS-A protein and others. The family of RING finger proteins contains a number of  
20 oncogenes. For example PML, a probable transcription factor, BRCA1, the mammalian cbl- and bmi-1 proto-oncogenes.

25 The new protein can find application in modulating protein-protein-interaction and in studying the expression profile of amygdala-specific genes.

weak similarity to hac1 (Mus musculus)

Sequenced by LMU

30

Locus: unknown

Insert length: 835 bp

35

Poly A stretch at pos. 751, polyadenylation signal at pos. 729

1 CACAGAGATC ATTGTCAACC AGGCCTGTGG GGGGGACATG CCTGCCTTGG  
51 AAGGGGCACC CCATACCCCG CCACTGCCAC GGCGGCCCCG TAAGGGAAGC  
101 TCGGAGCTGG GCTTTCCCCG CGTGGCCCCA GAGGATGAGG TCATTGTGAA  
40 151 TCAGTACGTG ATTCGGCCTG GCCCCCTCGGC CTCGGCGGCT TCTTCGGCGG  
201 CGGCAGGCGA GCCCCCTGGAG TGCCCCACCT GTGGGCACTC CTACAATGTC  
251 ACCCAGCGGA GGCCCCGCGT GCTGTCCTGC CTGCACTCTG TGTGTGAGCA  
301 GTGCCTGCAG ATTCTCTACG AGTCTGCCCC CAAGTACAAG TTCATCTCCT  
351 GCCCCACCTG CCGCCGTGAG ACTGTGCTCT TCACCGACTA CGGCCTGGCC  
45 401 GCGCTGGCTG TCAACACGTC CATCCTGAGC CGCCTGCCGC CTGAGGCGCT  
451 GACGGCCCCA TCCGGGGGTC AGTGGGGGGC TGAGCCCGAG GGCAGCTGCT  
501 ACCAGACCTT CCGGCAGTAC TGTGGGGCCG CGTGCACTG CCACGTGCGG  
551 AACCCTACTGT CCGCCTGCTC CATCATGTAG TAGCGCCTGC CTGCCCCGCCA  
601 CTGCCCCGCTG AGCCTCGCTC GCTGCTTCTT CAGGGACCCG GCCCTGCCCT  
50 651 GCGGCCCGCT GACCCCTTCTT TCCCCACCAT GGCTTCCGGC CCCACCCCGA  
701 GTGGCATTGT CGCTGCAGCC AACTTTGCCA TTAAAACTCT TTGCCAAAGT  
751 TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA  
801 AAAAAAAAAA AAAAGAAAAA AAAAAAAAAA AAAAG

55

BLAST Results

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No BLAST result

Medline entries

5

No Medline entry

10

Peptide information for frame 2

15 ORF from 38 bp to 577 bp; peptide length: 180  
 Category: similarity to unknown protein  
 Classification: Cellular transport and traffic  
 Prosite motifs: PRENYLATION (177-180)  
 ZINC\_FINGER\_C3HC4 (81-90)

20

1 MPALEGAPHT PPLPRRPRKG SSELGFPRVA PEDEVIVNQY VIRPGPSASA  
 51 ASSAAAGEPL ECPTCGHSYN VTQRRPRVLS CLHSVCEQCL QILYESCPKY  
 101 KFISCPTCRR ETVLFTDYGL AALAVNTSIL SRLPPEALTA PSGGQWGAEP  
 151 EGSCYQTFRQ YCGAACTCHV RNPLSACSIM

25

BLASTP hits

30 No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_10h17, frame 2

No Alert BLASTP hits found

35

Pedant information for DKFZphamy2\_10h17, frame 2

Report for DKFZphamy2\_10h17.2

40

45 [LENGTH] 180  
 [MW] 19400.27  
 [pI] 7.95  
 [HOMOL] TREMBL:AC007727\_7 gene: "F8K7.7"; Arabidopsis  
 thaliana chromosome 1 BAC F8K7 sequence, complete sequence. 3e-06

50 [BLOCKS] BL00839C  
 [BLOCKS] PF01462A  
 [BLOCKS] PR00763H  
 [BLOCKS] BL00518 Zinc finger, C3HC4 type, proteins  
 [PROSITE] PRENYLATION 1  
 [PROSITE] ZINC\_FINGER\_C3HC4 1  
 [PFAM] Zinc finger, C3HC4 type (RING finger)  
 55 [KW] Alpha\_Beta  
 [KW] LOW\_COMPLEXITY 5.56 %

15 Prosite for DKFZphamy2\_10h17.2

20

25 HMM\_NAME Zinc finger, C3HC4 type (RING finger)

35		P C	
	Query	106 PTC	108

DKFZphamy2\_10p7

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5 group: signal transduction

DKFZphamy2\_10p7 encodes a novel 1615 amino acid protein with similarity to Na<sup>+</sup>/Ca<sup>2+</sup> exchange proteins.

10 The Transport of Ca<sup>2+</sup> from the sarcoplasm into the sarcoplasmic reticulum is an essential process in the initiation of muscle relaxation.  
In addition, the novel protein contains a PROSITE multicopper oxidase signature. Multicopper oxidases are enzymes that possess  
15 three spectroscopically different copper centers.

The new protein can find application in modulation of Na<sup>+</sup>/Ca<sup>2+</sup> exchange and voltage-dependend processes.

20 similarity to Na<sup>+</sup>/Ca<sup>2+</sup> exchange proteins

ATG in frame 3 is first in clone.

25 Sequenced by LMU

Locus: unknown

Insert length: 5236 bp

30 Poly A stretch at pos. 5216, no polyadenylation signal found

```

      1 CGGACGCGTG GGC GGACGCG TGGGCCCTGT ATACCTGTGC CACTTTGTGC
      51 CTTAAGGAAC AAGCTTGCTC AGCGTTTTCA TTTTTCAGTG CTTCTGAGGG
35 101 TCCCCAGTGT TTCTGGATGA CATCATGGAT CAGCCCAGCT GTCAACAATT
    151 CAGACTTCTG GACCTACAGG AAAAACATGA CCAGGGTAGC ATCTCTTTTT
    201 AGTGGTCAGG CTGTGGCTGG GAGTGACTAT GAGCCTGTGA CAAGGCAATG
    251 GGCCATAATG CAGGAAGGTG ATGAATTCGC AAATCTCACA GTGTCTATTC
    301 TTCCTGATGA TTTCCCAGAG ATGGATGAGA GTTTTCTAAT TTCTCTCCTT
40 351 GAAGTTCACC TCATGAACAT TTCAGCCAGT TTGAAAAATC AGCCAACCAT
    401 AGGACAGCCA AATATTTCTA CAGTTGTCTAT AGCACTAAAT GGTGATGCCT
    451 TTGGAGTGTT TGTGATCTAC AGTATTAGTC CCAATACTTC CGAAGATGGC
    501 TTATTTGTTG AAGTTCAGGA GCAGCCCCAA ACCTTGGTGG AGCTGATGAT
    551 ACACAGGACA GGGGGCAGCT TAGGTCAAGT GGCAGTCGAA TGGCGTGTTG
45 601 TTGGTGGAAC AGCTACTGAA GGTTTAGATT TTATAGGTGC TGGAGAGATT
    651 CTGACCTTTG CTGAAGGTGA AACCAAAAAG ACAGTCATTT TAACCATCTT
    701 GGATGACTCT GAACCAGAGG ATGACGAAAG TATCATAGTT AGTTTGGTGT
    751 ACACTGAAGG TGGAAGTAGA ATTTTGCCAA GCTCCGACAC TGTTAGAGTG
    801 AACATTTTGG CCAATGACAA TGTGGCAGGA ATTGTTAGCT TTCAGACAGC
50 851 TTCCAGATCT GTCATAGGTC ATGAAGGAGA AATTTTACAA TTCCATGTGA
    901 TAAGAACTTT CCCTGGTCGA GGAAATGTTA CTGTAACTG GAAAATTATT
    951 GGGCAAAATC TAGAACTCAA TTTTGCTAAC TTTAGCGGAC AACTTTTCTT
1001 TCCTGAGGGG TCGTTGAATA CAACATTGTT TGTGCATTTG TTGGATGACA
1051 ACATTCTCTG GGAGAAAGAA GTATACCAAG TCATTCTGTA TGATGTCAGG
55 1101 ACACAAGGAG TTCCACCAGC CGGAATCGCC CTGCTTGATG CTCAAGGATA
    1151 TGCAGCTGTC CTCACAGTAG AAGCCAGTGA TGAACCACAT GGAGTTTAA
    1201 ATTTTGCTCT TTCATCAAGA TTTGTGTTAC TACAAGAGGC TAACATAACA
    1251 ATTCAGCTTT TCATCAACAG AGAATTTGGA TCTCTAGGAG CTATCAATGT

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	1301	CACATATACC	ACGGTTCCTG	GAATGCTGAG	TCTGAAGAAC	CAAACAGTAG
	1351	GAAACCTAGC	AGAGCCAGAA	GTTGATTTTG	TCCCTATCAT	TGGCTTTCTG
	1401	ATTTTAGAAG	AAGGGGAAAC	AGCAGCAGCC	ATCAACATTA	CCATTCTTGA
	1451	GGATGATGTA	CCAGAGCTAG	AAGAATATTT	CCTGGTGAAT	TAACTTACG
5	1501	TTGGACTTAC	CATGGCTGCT	TCAACTTCAT	TTCTCCCAG	ACTAGATTCA
	1551	GAAGGTTTGA	CTGCACAAGT	TATTATTGAT	GCCAATGATG	GGGCCCCGAGG
	1601	TGTAATTGAA	TGGCAACAAA	GCAGGTTTGA	AGTAAATGAA	ACCCATGGAA
	1651	GTTTAAACATT	GGTAGCCCAG	AGGAGCAGAG	AACCTCTTGG	CCATGTTTCC
	1701	TTATTTGTGT	ATGCTCAGAA	TTTGGGAAGCA	CAAGTGGGGC	TGGATTATAT
10	1751	CTTCACCCCA	ATGATTCTTC	ATTTTGCTGA	TGGAGAAAGG	TATAAAAATG
	1801	TCAATATCAT	GATTCTTGAT	GATGACATTC	CAGAAGGAGA	TGAAAAATTT
	1851	CAGCTGATTT	TAACAAATCC	TTCTCCTGGA	CTAGAGCTAG	GGAAAAATAC
	1901	AATAGCCTTA	ATTATTGTCC	TTGCTAATGA	TGACGGCCCT	GGAGTTCTAT
	1951	CATTTAACAA	CAGTGAGCAC	TTTTTCCTAA	GAGAGCCAAC	AGCTCTCTAC
15	2001	GTCCAGGAGA	GTGTTGCAGT	ATTGTACATT	GTTGCGGAAC	CTGCACAAGG
	2051	ATTGTTTGGG	ACAGTGACAG	TTCAGTTCAT	TGTGACAGAA	GTGAATTCCT
	2101	CAAATGAATC	TAAAGATCTG	ACTCCTTCCA	AAGGCTATAT	TGTTTTAGAA
	2151	GAAGGTGTTT	GATTCAAGGC	CCTACAAATA	TCTGCCATAT	TAGACACGGA
	2201	ACCAGAAATG	GATGAGTATT	TTGTTTGCAC	CTTGTTTAAT	CCAACTGGAG
20	2251	GTGCTAGACT	AGGGGTGCAT	GTTCAAACCC	TGATAACAGT	TTTGCAAAAC
	2301	CAGGCCCTT	TGGGGCTATT	CAGTATCTCT	GCAGTTGAAA	ATAGAGCCAC
	2351	CTCCATAGAC	ATCGAAGAAG	CCAATAGGAC	CGTGTATTTA	AATGTATCTC
	2401	GAAC TAATGG	CATTGATTTG	GCTGTGAGTG	TGCAGTGGGA	GACAGTATCT
	2451	GAAACAGCCT	TTGGCATGAG	GGGAATGGAT	GTTGTGTTTT	CCGTATTTCA
25	2501	AAGTTTTTTG	GATGAATCAG	CTTCTGGCTG	GTGTTTCTTT	ACTTTGGAAA
	2551	ATTTAATATA	TGGTATAATG	TAAAGAAAAT	CATCTGTTAC	TGTTTACCGA
	2601	TGGCAGGGGA	TTTTTATTCC	AGTTGAGGAT	TAAATATAG	AAAATCCTAA
	2651	AACTTGTGAG	GCCTTTAATA	TTGGTTTTTC	TCCCTACTTT	GTGATTACTC
30	2701	ATGAAGAAAG	AAATGAAGAA	AAGCCTTCTC	TAAACAGTGT	GTTTACATTC
	2751	ACATCTGGAT	TTAAATTATT	CCTGGTACAA	ACAATCATT	TTCTGGAAAG
	2801	TTCTCAAGTA	AGATATTTTA	CTTCAGACAG	CCAAGATTAT	TTAATCATTG
	2851	CAAGTCAAAG	AGATGATTCC	GAATTAACCT	AGGTCTTCAG	GTGGAATGGA
	2901	GGAAGCTTCG	TGTTGCATCA	AAAACCTCCCT	GTCCGAGGTG	TGCTGACCGT
	2951	GGCCTTGTTT	AACAAGGGAG	GCTCTGTGTT	CTTAGCCATT	TCCCAGGCTA
35	3001	ATGCCAGGCT	AAACTCCCTT	TTATTCAGAT	GGTCTGGCAG	TGGGTTTATT
	3051	AACTTTCAAG	AGGTGCCTGT	CAGTGGGACA	ACAGAAAGTG	AGGCTTTGTC
	3101	TTCAGCCAAT	GATATTTACC	TAATATTTGC	CAAAAATGTC	TTTCTAGGAG
	3151	ATCAGAATTC	AATTGATATT	TTCATCTGGG	AGATGGGACA	GTCTTCCTTC
	3201	AGGTATTTTC	AGTCTGTAGA	TTTTGCTGCT	GTTAACAGAA	TCCACTCTTT
40	3251	CACACCAGCC	TCAGGAATAG	CCCACATACT	TCTTATTGGC	CAAGATATGT
	3301	CTGCTCTTTA	CTGCTGGAAT	TCGGAGCGTA	ATCAATTCTC	TTTTGTTCTG
	3351	GAAGTACCTT	CTGCTTATGA	TGTGGCTTCT	GTTACAGTAA	AGTCCCTTAA
	3401	TTCAAGCAAG	AATTTAATAG	CTCTAGTGGG	AGCTCATTCA	CATATATATG
	3451	AGCTAGCCTA	CATTTCCAGC	CATTCTGACT	TTATTCCTAG	TTCAGGTGAA
45	3501	CTGATATTTG	AACCTGGTGA	GAGAGAAGCT	ACAATAGCAG	TAAATATCCT
	3551	TGATGATACA	GTTCCAGAAA	AAGAAGAATC	CTTCAAAGTT	CAACTTAAAA
	3601	ATCCCAAAGG	AGGAGCAGAG	ATTGGCATT	ATGATTCTGT	AACAATAACC
	3651	ATTCTGTCTA	ATGATGATGC	CTATGGAATT	GTTGCATTTG	CTCAGAATTC
	3701	ATTATATAAG	CAAGTGGAAG	AAATGGAGCA	AGATAGCCTA	GTAACCTTGA
50	3751	ACGTTGAACG	CTTAAAAGGA	ACATATGGCC	GTATAACCAT	AGCATGGGAA
	3801	GCTGATGGAA	GTATTAGTGA	TATATTTCTT	ACCTCAGGAG	TGATTTTATT
	3851	TACTGAAGGC	CAGGTACTGT	CAACAATCAC	TCTAACTATT	CTTGCTGATA
	3901	ATATACCAGA	GTTATCAGAG	GTTGTGATTG	TAACCCTCAC	CCGTATCACC
	3951	ACAGAAGGGG	TTGAGGACTC	ATACAAAGGT	GCTACTATTG	ATCAGGACAG
55	4001	AAGCAAGTCT	GTTATAACAA	CTTTGCCCAA	TGACTCACCT	TTTGCTTGGG
	4051	TGGGCTGGCG	TGCTGCGTCT	GTCTTCATTA	GAGTAGCAGA	GCCTAAAGAA
	4101	AACACCACCA	CTCTTCAGTT	ACAAATAGCT	CGAGATAAAG	GACTACTTGG
	4151	GGATATTGCC	ATTCACTTGA	GAGCTCAACC	CAATTTCTTA	CTGCATGTCG

```

4201 ATAATCAAGC TACTGAGAAT GAAGATTATG TATTGCAAGA AACATAATA
4251 ATAATGAAAG AAAACATAAA AGAAGCTCAT GCCGAAGTTT CCATTTTGCC
4301 GGATGACCTT CCTGAATTGG AGGAAGGATT TATTGTCAC ATCACTGAGG
4351 TGAACCTGGT GAACTCTGAC TTCTCTACAG GACAGCCAAG TGTGCGGAGG
5 4401 CCCGGAATGG AAATAGCTGA GATAATGATA GAAGAAAATG ACGATCCCAG
4451 AGGAATTTTT ATGTTTCATG TTAGTAGAGG CGCTGGGGAA GTTATTACTG
4501 CCTATGAGGT GCCTCCACCC TTGAACGTTT TCAAGTTCC TGTAGTCCGG
4551 CTGGCTGGAA GCTTTGGGGC AGTAAATGTT TATTGGAAAG CATCACCAGA
4601 CAGTGCTGGC CTGGAAGACT TAAACCATC TCATGGGATT CTTGAATTTG
10 4651 CAGATAAACA GGTTACTGCA ATGATAGAAA TCACCATAAT TGATGATGCT
4701 GAATTTGAAT TGACAGAGAC GTTCAATATT TCCTTGATCA GTGTTGCTGG
4751 AGGTGGCAGA CTTGGTGATG ATGTTGTGGT AACTGTTGTT ATTCCACAAA
4801 ATGATTCTCC ATTTGGAGTA TTTGGATTTG AAGAAAAGAC TGTAAGTTAA
4851 ACATATCAGG GGAAAGCCTT GTTTCAGGCT AGCGTTTCAT GTAATTTTGA
15 4901 GTAGAAAGTG TCTCACATTT TTGTTTTGGA AGTCTTGGCC AGGCATGGTG
4951 GCTCATGCCA GTAATCCCAG CACTTTGGGA GGCCGCAGCG GGCAGATCAC
5001 GAGGTGAGGA GATTGACACC ATCCTGGCCA ATATGGTTGA ATTCCCGTCT
5051 CTAAGTAAAG TACAAAAATT AGCTGGGCGT GGTGGCACAT GCCTGTATTC
5101 CCAGATACTT GGGAGGCTGA GGCAGGAGAC TCGCTTGAAC CCAGGAGGCA
20 5151 GAGGTTGCAG TGAGCTGAGA TCACGCCATT GCACTCCAGC CTGGCGACAT
5201 AGAGAGACTC CATCTCAAAA AAAAAAAAAA AAAAAA

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## BLAST Results

25

No BLAST result

30

## Medline entries

No Medline entry

35

## Peptide information for frame 3

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40 ORF from 0 bp to 4847 bp; peptide length: 1616
Category: putative protein
Classification: Cell signaling/communication
Prosites motifs: MULTICOPPER_OXIDASE1 (151-171)

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45

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1 DAWADAWALY TCATLCLKEQ ACSAFSFFSA SEGPQCFWMT SWISPAVNNS
51 DFWTYRKNMT RVALFSGQA VAGSDYEPVT RQWAIMQEGD EFANLTVSIL
101 PDDFPEMDES FLISLLEVHL MNISASLKNQ PTIGQPNIST VVIALNGDAF
151 GVFIYISISP NTSEDGLFVE VQEQPQTLVE LMIHRTGGSL GQVAVEWRVV
50 201 GGTATEGLDF IGAGEILTFA EGETKKTIVL TILDDSEPED DESIIVSLVY
251 TEGGSRI LPS SDTVRVNILA NDNVAGIVSF QASRSVIGH EGEILQFHVI
301 RTFPGRGNVT VNWKIIGQNL ELNFANFSGQ LFFPEGSLNT TLFVHLLDDN
351 IPEEKEVYQV ILYDVRTQGV PPAGIAL LDA QGYAAVL TVE ASDEPHGV LN
401 FALSSRFVLL QEANITIQLF INREFGSLGA INVTYTTVP G MLSLKNQTVG
55 451 NLAEPVDFV PIIGFLILEE GETAAAINIT ILEDDVPELE EYFLVNLT YV
501 GLTMAASTSF PPRLDSEGLT AQVIIDANDG ARGVIEWQQS RFEVNETHGS
551 LTLVAQRSRE PLGHVSLFVY AQNLEAQVGL DYIFTPMILH FADGER YKNV
601 NIMILDDDIP EGDEKFQLIL TNPSGLELG KNTIALIIVL ANDDGPVLS

```

```

5  651 FNNSEHFFLR EPTALYVQES VAVLYIVREP AQGLFGTVTV QFIVTEVNSS
    701 NESKDLTPSK GYIVLEEGVR FKALQISAIL DTEPEMDEYF VCTLFNPTGG
    751 ARLGVHVQTL ITVLQNAAPL GLFSISAVEN RATSIDIEEA NRTVYLVNSR
    801 TNGIDLAVSV QWETVSETAF GMRGMDVVFS VFQSFLESA SGWCFFTLEN
10  851 LIYGIMLRKS SVTVYRWQGI FIPVEDLNIE NPKTCEAFNI GFSPYFVITH
    901 EERNEEKPSL NSVFTFTSGF KLFLVQTIIE LESSQVRYFT SDSQDYLIIA
    951 SQRDDSELTQ VFRWNGGSFV LHQKLPVRGV LTVALFNKGG SVFLAISQAN
   1001 ARLNSLLFRW SGSGFINFQE VPVSGTTEVE ALSSANDIYL IFAKNVFLGD
   1051 QNSIDIFIWE MGQSSFRYFQ SVDFAAVNRI HSFTPASGIA HILLIGQDMS
10  1101 ALYCWNSESN QFSFVLEVPS AYDVASVTVK SLNSSKNLIA LVGAHSHIYE
   1151 LAYISSHSDF IPSSGELIFE PGEREATIAV NILDDTVPEK EESFKVQLKN
   1201 PKGGAEIGIN DSVTITILSN DDAYGIVAFQ QNSLYKQVEE MEQDSLVTLN
   1251 VERLKGTYGR ITIAWEADGS ISDIFPTSGV ILFTEGQVLS TITLTILADN
   1301 IPELSEVVIV TLTRITTEGV EDSYKGATID QDRSKSVITT LPNDSPFGLV
15  1351 GWRAASVFIR VAEPKENTTT LQLQIARDKG LLGDIAIHLR AQPNNFLHVD
   1401 NQATENEDYV LQETIIMKE NIKEAHAQVS ILPDDLPELE EGFIVTITEV
   1451 NLVNSDFSTG QPSVRRPGME IAEIMIEEND DPRGIFMFHV TRGAGEVITA
   1501 YEVPPLNLVL QVPVRLAGS FGAVNVYWKQ SPDSAGLEDF KPSHGILEFA
   1551 DKQVTAMIEI TIIDDAEFEL TETFNISLIS VAGGGRLGDD VVVTVVIPQN
20  1601 DSPFGVFGFE EKTVS

```

## BLASTP hits

25

No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_10p7, frame 3

```

30  TREMBL:AF055084_1 gene: "VLGR1"; product: "very large G-protein
    coupled
    receptor-1"; Homo sapiens very large G-protein coupled receptor-
    1
    (VLGR1) mRNA, complete cds., N = 3, Score = 284, P = 1.2e-33
35

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```

    TREMBL:DMAF9897_1 gene: "Calx"; product: "CALX"; Drosophila
    melanogaster 3Na(+)-1Ca(2+) exchanger (Calx) mRNA, complete cds.,
    N =
    1, Score = 178, P = 3.3e-09
40

```

```

    >TREMBL:AF055084_1 gene: "VLGR1"; product: "very large G-protein
    coupled
    receptor-1"; Homo sapiens very large G-protein coupled
45  receptor-1 (VLGR1)
    mRNA, complete cds.
    Length = 1,967

```

```

50  HSPs:

```

```

    Score = 284 (42.6 bits), Expect = 1.2e-33, Sum P(3) = 1.2e-33
    Identities = 192/738 (26%), Positives = 314/738 (42%)

```

```

    Query:      b7
55  SGQAVAGSDYEPVTRQWAIMQEGDEFANLTVSILPDDFPENDESFLISLLEVHLMNISAS 126
      S + G DY + Q G + + +SI+ D+ E +E +E+
L +

```

Sbjct: 102 SSASPGGVYDI-LHGSTVTFQHGQNLFINISIIDDNESEFEFEP-----  
IEILLTGATGG 155

Query: 127

5 LKNQPTIGQPNISTVVIALNGDAFGVFVIYSISPNTSEDGLFVEVQEQPQTLV-ELMIHR 185  
+G+ +S ++IA + FGV N S+ + +

T++ L++ R

Sbjct: 156 A----VLGRHLVSRIIIAKSDSPFGVIRFL----NQSK----  
ISIANPNSTMILSLVLER 203

10

Query: 186 TGGSLGQVAWEVRVGGTATEGL-----DFIG-AGEILTFAEGETK-  
KTVILTXXXXXXX 238

TGG LG++ V W VG + E L D + F EGE

+T+ILT

15

Sbjct: 204  
TGGLLGEIQVNWETVGPNSQEALLPQNRDIADPVSGLFYFGE GEGGVRTIILTIYPHEEI 263

Query: 239 XXXXXXXXXLVYTEGGSRLPSSDTRVNVILANDNVAGIVSF--  
QTASRSVIGH----EG 292

20

L +G +++ + V + I + G+V F +T S+

EG

Sbjct: 264

EVEETFIKHLHLVKGEAKLDSRAKDVTLTIQEFQDPNGVVQFAPETLSKKTYSSEPLALEG 323

25

Query: 293 EILQFHVIRTFPGR-GNVTNVWIKIIGQ-  
NLELNFANFSGQLFFPEGSLNTTLFVHLLDDN 350

+L +R G G + V W++ + ++ +F + SG +G +

VHLL D

Sbjct: 324

30

PLLITFFVRRVKGTFGEIMVYWELSSSEFDITEDFLSTSGFFTIADGESEASFVHLLPDE 383

Query: 351

IPEEKEVYQVILYDVRTQGVPPAGIALLDAGYAAVLTVEASDEPHGVNLFAL-SSRFVL 409  
+PE +E Y + L V G A LD + +V A+D+PHGV

35

FAL S R +

Sbjct: 384 VPEIEEDYVIQLVSVE-----GGAELDLKSITWFSVYANDDPHGV--  
FALYSDRQSI 434

Query: 410 LQEANI--TIQLFINREFGSLGAINVTYTTVPGMLSLKNQT-  
VGNLAEPEVDFVPIIGFL 466

40

L N+ +IQ+ I R G+ G + V K Q V AE +

L

Sbjct: 435 LIGQNLIRSIQINITRLAGTFGDVAVGLRISSDH---KEQPIVTENAERQ--  
-----L 482

45

Query: 467

ILEEGETA AAINITILEDDVPELEEYFLVNLT YVGLTMAASTSFPPRLDSEGLTAQVIID 526  
++++G T + I L F + L V L P L E

+A V+

50

Sbjct: 483 VVKDGATYKVDVVPKQVFLSLGSNFTLQLVTVMLVGGRFYGMPTILQ-  
EAKSA-VLPV 540

Query: 527 ANDGARGVIEWQQRSEFV-NETHGSLTLVAQRSREPLGHVSLFV---  
YAQNLEAQVGLDY 582

55

+ A + ++ + F++ N T G+ ++ R R G +S+ YA

LE +

Sbjct: 541 SEKAANSQVGFESTAFQLMNITAGTSHVMISR-  
RGTYGALSVAWTTGYAPGLEIPEFIVV 599

Query: 583 -IFTPMI--  
LHFADGERYKKNVNIMILDDDIPEGDEKFQILITNPSPGLELGKNTIALIIV 639  
TP + L F+ GE+ K V + P E F L L+ G

5 + IV  
Sbjct: 600 GNMTPTLGSLSFHGEQRKGVFLWTFPS--  
PGWPEAFVLHLSGVQSSAPGGAQLRSGFIV 657

Query: 640 LANDDGPVLSFN-  
10 NSEHFFLREPTALYVQESVAVLYIVREPAQGLFGTVTVQFIVTEVN 698  
A + GV F+ .S + + E T + ++ V L+ G +  
T  
Sbjct: 658 -AEIEPMGVFQFSTSSRNIIVSED TQM-IRLHVQRLF-----  
GFHSDLIKVSQTTAG 708

15 Query: 699 SSNESKDLTP-SKGYIVLEEGVRFKALQISAILDTEPEMDEYFVCTL-----  
-----FNP 747  
S+ +D P G + ++ +I+ I D E++E+F L  
F+

20 Sbjct: 709  
SAKPLEDFEPVQNGELFFQKFQTEVD FEITIINDQLSEIEEFFYINLTSVEIRGLQKFDV 768

Query: 748 TGGARLG VHVQT-LITVLQNQAPLGLFSISAVENR-ATSIDIE----  
25 EANRTVYLVNVSRT 801  
RL + +IT+L N G+ IS E A ++D E T  
YL+ S+T  
Sbjct: 769 NWSPRNLDFS VAVITILDNDLAGM-  
DISFPETTVAVAVDTTLIPVETESTTYLSTSKT 827

30 Query: 802 NGI 804  
I  
Sbjct: 828 TTI 830

Score = 266 (39.9 bits), Expect = 4.0e-25, Sum P(3) = 4.0e-25  
35 Identities = 175/708 (24%), Positives = 306/708 (43%)

Query: 131  
PTIGQPNISTVVIALNGDAFGVFVIYSISPNTSEDGLFVEVQEQPQTLVELMIHRTGGSL 190  
P IG +I ++I N +A G+ P + EV+E L+ +  
40 + R G+  
Sbjct: 39 PEIGNISIVRIIIMKNDNAEGII---EFDPKYTA---FEVEEDVG-  
LIMIPVVRLHGTY 90

Query: 191 GQVAVEWRVVGGTATEG-  
45 LDFIGAGEILTFAEGETKKT VILTXXXXXXXXXXXXXXXXXXLV 249  
G V ++ +A+ G +D+I G +TF G+ + ++  
L  
Sbjct: 91  
GYVTADFISQSSSASPGGVYILHGSTVTFQHGQNL SFINISIIDDNESEFEEPIELLT 150

50 Query: 250 YTEGGSRILPSSD TVRVNILANDNVAGIVSFQTASRSVIGHEGE--  
ILQFHVIRTFPGRG 307  
GG+ +L R+ I +D+ G++ F S+ I + IL +  
RT G

55 Sbjct: 151 GATGGA-  
VLGRHLVSRIIIAKSDSPFGVIRFLNQSKISIANPNSTMILSLVLERTGGLLG 209

Query: 308 NVTVNWKIIGQN-----LELN--FAN-FSGQLFFPEGSLNT-  
TLFVHLLDDNIPEEKEVY 358

+ VNW+ +G N L N A+ SG +F EG T+ + +

E +E +

5 Sbjct: 210

EIQVNWETVGPNSQEALLPQNRDIADPVSGLFYFGEGEggVRTIILTIYPHEEIEVEETF 269

Query: 359 QVILYDVRTQGVPPAGIALLDAGGYAAVLTVEASDEPHGVNFA---  
LSSRFV---LLQE 412

10 + L+ V+ G A LD++ LT++ +P+GV+ FA LS +

L E

Sbjct: 270 IIKLHLVK-----

GEAKLDSRAKDVTLTIQEFQDPNGVVQFAPETLSKKTYSEPLALE 322

15 Query: 413

ANITIQLFINREFGSLGAINVTYTTVPGMLSLKNQTVGNLAEPEVDFVPIIGFLILEEGE 472  
+ I F+ R G+ G I V + L ++ ++ E DF+

GF + +GE

Sbjct: 323 GPLLITFFVRRVKGTfGEIMVYW-----ELSSEF--DITE---

20 DFLSTSGFFTIADGE 370

Query: 473

TAAAINITILEDDVPELEEYFLVNLTYVGLTMAASTSFPPRLDSEGLTAQVIIDANDGAR 532  
+ A+ ++ +L D+VPE+EE +++ L S LD E

25 + AND

Sbjct: 371 SEASFDVHLLPDEVPEIEEDYVIQLV-----

SVEGGAELDLEKSITWFSVYANDDPH 422

Query: 533 GVIEWQQSRFEV---NETHGSLTLVAQRSREPLGHVS--  
LFVYAQNLEAQVGLDYIFTPM 587

30 + + GV R + S+ + R G V+ L + + + E +

Sbjct: 423

GVFALYSRQSIILIGQNLIRSIQINITRLAGTFGDVAVGLRISSDHKEQPIVTENAERQL 482

35

Query: 588 ILHFADGERYKVNIMILDDDI--PEGDE-KFQLILTNPSPGLELGKNTI--  
-ALIIVLA 641

++ DG YK V+++ + + + G QL+ G G TI

A VL

40 Sbjct: 483 VVK--DGATYK-

VQVPIKNQVFLSLGSNFTLQLVTVMLVGGRFYGMPTILQEAksAVLP 539

Query: 642

NDDGPGVLSFNNSEHFFLREPTALYVQESVAVLYIVREPAQGLFGTVTVQFIV-----TE 696  
+ NS+ F E TA + A' V +G +G ++V +

45

E  
Sbjct: 540 VSEKAA-----NSQVGF--

ESTAFQLMNITAGTSHVMISRRGTYGALSVAWTTGYAPGLE 592

50 Query: 697

VNSSNESKDLTPSKGYIVLEEGVRFKALQISAILDTEPEMDEYFVCTLFNPTGGARLGvH 756  
+ ++TP+ G + G + K + + P E FV L

A G

Sbjct: 593 IPEFIVVGNMTPTLGSLSFHGEQRKGVFLWTF--

55 PSPGWPEAFVLHLSGVQSSAPGGAQ 650

Query: 757 VQTLITVLQNAQPLGLFSISAVENRATSIDIEEANRTVYLNVSRTNGI--  
DLAVSVQWET 814

- +++ V + + P+G+F S +R +I + E + + L+V R G DL  
+ V ++T  
Sbjct: 651 LRSGFIVAEIE-PMGVFQFST-SSR--  
NIIVSED TQMIRLHVQRLFGFHS DL-IKVS YQT 705
- 5 Query: 815 VSETAFGMRGMDVVFS---VFQSF LDE 838  
+ +A + + V + FQ F E  
Sbjct: 706 TAGSAKPLEDFEPVQNGELFFQKFQTE 732
- 10 Score = 246 (36.9 bits), Expect = 4.1e-32, Sum P(3) = 4.1e-32  
Identities = 92/338 (27%), Positives = 157/338 (46%)
- Query: 511 PPRLDSEGLTAQVIIDANDGARGVIEW--  
QQSRFEVNETHGSLTLVAQRSREPLGHVSLF 568  
15 PP + + + ++II ND A G+IE+ + + FEV E G + + R  
G+V+  
Sbjct: 38 PPEIGNISIV-  
RIIIMKNDNAEGIIIEFDPKYTA FEVEEDVGLIMIPVVR LHGT YGYVTAD 96
- 20 Query: 569 VYAQNLEAQVG-  
LDYIFTPMILHFADGERYKVNIMILDDDIPEGDEKFQ LILTNPSPGL 627  
+Q+ A G +DYI + F G+ +NI I+DD+ E +E  
+++LT + G  
Sbjct: 97  
25 FISQSSSASPGGV DYILHGSTVTFQHGQNL SFINISIIDDNESEFEEPIEILLTGATGGA 156
- Query: 628  
ELGKNTIALIIIVLANDDGPVLSFNNSEHFFLREPTALYVQESVAVLYIVREPAQGLFGT 687  
LG++ ++ II+ +D GV+ F N + P S +L +V E  
30 GL G  
Sbjct: 157 VLGRHLVSRIIIAKSDSPFGVIRFLNQSKISIANPN-----  
STMILSLVLERTGGLLGE 210
- Query: 688 VTVQFIVTEVNSSN---ESKDLT-PSKGYIVLEEGVR-  
35 FKALQISAILDTEPEMDEYFV 741  
+ V + NS +++D+ P G EG + + ++ E  
E++E F+  
Sbjct: 211  
IQVNWETVGPNSQEA LLPQNRDIADPVSGLFYFGE GEGGVRTIILTIYPHEEIEVEETFI 270
- 40 Query: 742 CTLFNPTGGARLG VHVQTL-ITVLQNA PLGL--FSISAVENRATSIDIE-  
EANRTVYLN 797  
L G A+L + + +T+ + P G+ F+ + + S + E  
+  
45 Sbjct: 271  
IKLHLVKGEAKLDSRAKDVTLT IQEFGDPNGVVQFAPETLSKKTYSEPLALEGPLLITFF 330
- Query: 798 VSRTNGIDLAVSVQWETVSETAFGMRGMDVVFSVFQSF LDESASGWCFFTL  
848  
50 V R G + V WE SE F + + FL S SG FFT+  
Sbjct: 331 VRRVKGTFGEIMVYWELSS E-----FDITEDFL--STSG--FFT I  
366
- Score = 246 (36.9 bits), Expect = 1.9e-19, Sum P(3) = 1.9e-19  
55 Identities = 87/303 (28%), Positives = 138/303 (45%)
- Query: 1162 PSSGELIFEPGEREA-TIAVNILDDTVPEKEESFKVQLKNPKGGAEIGIN-  
DSVTITILS 1219

P SG F GE TI + I E EE+F ++L KG A++

VT+TI

Sbjct: 236

PVSGLFYFGE GEGVVRTIILTIYPHEEIEVEETFIIKLHLVKGEAKLDSRAKDVTLTIQE 295

5

Query: 1220 NDDAYGIVAFQAQNSL----

YKQVEEME QDSLVTNLVERLKGTYGRITIAWEADGSIS--- 1272

D G+V FA +L Y + +E L+T V R+KGT+G I + WE

Sbjct: 296

10 FGDPNGVVQFAPETLSKKTYSSEPLALEGPLLITFFVRRVKGTGGEIMVYWELSSEFDITE 355

Query: 1273

DIFPTSGVILFTEGQVLSTITLTILADNIPELSEVVIVTLTRITTEGVEDSYKGATIDQD 1332

D TSG +G+ ++ + +L D +PE+ E ++ L ++ EG

15 GA +D +

Sbjct: 356 DFLSTSGFFTIADGESEASFVHLLPDEVPEIEEDYVIQL--VSVEG-----  
-GAELDL 407

Query: 1333

20 RSKSVITTLPNDSFGLVGRASVFIRVAEPKENTTTLLQIARDKGLLGDIHILRAQ 1392

+S + + ND P G+ + I + + ++Q+ I R G

GD+A+ LR

Sbjct: 408 KSITWFSVYANDDPHGVFALYSRQSIILIG--

NLIRSIQINITRLAGTFGDVAVGLRIS 465

25

Query: 1393 PNFLHVDNQ-

ATENEDYVLQETIIMKENIKEAHAEVSIPLDLPLEEFGFIVTITEVN 1451

+ H + TEN E +++K+ V I L F

+ + V

30 Sbjct: 466 SD---HKEQPIVTENA-----

ERQLVVKDGATYKVDVPIKNQVFLSLGSNFTLQLVTVM 517

Query: 1452 LVNSDFSTGQPSV 1464

LV F G P++

35 Sbjct: 518 LVGGRFY-GMPTI 529

Score = 246 (36.9 bits), Expect = 1.9e-19, Sum P(3) = 1.9e-19

Identities = 89/334 (26%), Positives = 150/334 (44%)

40 Query: 1159

DFIPSSGELIFEPGEREATIAVNILDDTVPEKEESFKVQLKNPKGGAEIGINDSVTITIL 1218

D+I + F+ G+ + I ++I+DD E EE ++ L GGA +G +

I I

Sbjct: 110

45 DYILHGSTVTFQHGQNLFINISIIDDNESEFEEPIEILLTGATGGAVLGRHLVSRIIA 169

Query: 1219

SNDDAYGIVAFQAQNSLYKQVEEME QDSLVTNLVERLKGTYGRITIAWEADGSIS----- 1272

+D +G++ F S + +++L +ER G G I + WE G

50 S

Sbjct: 170 KSDSPFGVIRFLNQSKIS-

IANPNSTMILSLVLERTGGLLGEIQVNWETVGPNSQEAALLP 228

Query: 1273 ---DIF-PTSGVILFTEGQV-

55 LSTITLTILADNIPELSEVVIVTLTRITTEGVEDSYKGA 1327

DI P SG+ F EG+ + TI LTI E+ E I+ L + E

DS



Sbjct: 229

QNRDIADPVSGLFYFGE GEGGVRTIILTIYPHEEIEVEETFIKHLHLVKGEAKLDS----- 284

5 Query: 1328 TIDQDRSKSVITTLPN-DSPFGLVGWRAASVFIRV-AEPK--  
ENTTTLQLQIARDKGLLG 1383

R+K V T+ P G+V + ++ + +EP E + +

R KG G

Sbjct: 285 -----

10 RAKDVTLTIQEF GDPNGVVQFAPETLSKKTYS EPLALEGPLLITFFVRRVKGTFG 339

Query: 1384

DIAIHLRAQPNFLLHVDNQATENEDYVLQETIIIMKENIKEAHA EVSILPDDLPELEEGF 1443

+I ++ F + ED++ + + EA +V

+LPD++PE+EE +

15 Sbjct: 340 EIMVYWELSS EFDI-----

TEDFLSTSGFFTIADGESEASFDVHLLPDEVPEIEEDY 391

Query: 1444 IVTITEVNLVNSDFSTGQPSVRRPGMEIAEIMIEENDDPRGIFMFHVTR  
1492

20 Sbjct: 392 VIQLVSVE-----GGAELDLEK---SITWFSVYANDDPHG VFALYS DR  
431

25 Score = 237 (35.6 bits), Expect = 9.4e-34, Sum P(3) = 9.4e-34  
Identities = 101/367 (27%), Positives = 165/367 (44%)

Query: 67

SGQAVAGSDYEPVTRQWAIMQEGDEFANLTVSILPDDFPEMDESFLISLLEVHLMNISAS 126

S + G DY + Q G + + +SI+ D+ E +E +E+

30 L +

Sbjct: 102 SSASPGGV DYI-LHGSTVTFQHGQNL SFINISIIDNESEFE EEP-----  
IEILLTGATGG 155

Query: 127

35 LKNQPTIGQPNISTVVIALNGDAFGVFVIYSISPNTSE DGLFVEVQEQPQTLVELMIHRT 186

+G+ +S ++IA + FGV N S+ +

++ L++ RT

40 Sbjct: 156 A----VLGRHLVSRIIIAKSDSPFGVIRFL----NQSKISI---  
ANPNSTMILSLVLERT 204

Query: 187 GGS LGQVAVEWRVVG GTATEGL-----DFIG-AGEILTFAEGETK-  
KTVILTXXXXXXXXX 239

GG LG++ V W VG + E L D + F EGE +T+ILT

45 Sbjct: 205

GGLLGEIQVNWETVGPNSQEALLPQNRDIADPVSGLFYFGE GEGGVRTIILTIYPHEEIE 264

Query: 240 XXXXXXXX LVYTEGGSRILPSSDTVRVNILANDNVAGIVSF--  
QTASRSVIGH----EGE 293

L +G +++ + V + I + G+V F +T S+

50 EG

Sbjct: 265

VEETFIKHLHLVKGEAKLDSRAKDVTLTIQEF GDPNGVVQFAPETLSKKTYS EPLALEGP 324

55 Query: 294 ILQFHVIRTFPGR-GNVTVNWKIIGQ-  
NLELNFANFSGQLFFPEGSLNTTLFVHLLDDNI 351

+L +R G G + V W++ + ++ +F + SG +G +

VHLL D +

Sbjct: 325

LLITFFVRRVKGTGTFGEIMVYWELSSSEFDITEDFLSTSGFFTIADGESEASFVHLLPDEV 384

Query: 352

5 PEEKEVYQVILYDVRTQGVPPAGIALLDAGYAAVLTVEASDEPHGVLNFAL-SSRFVLL 410  
 PE +E Y + L V G A LD + +V A+D+PHGV FAL

S R +L

Sbjct: 385 PEIEEDYVIQLVSVE-----GGAELDLEKSITWFSVYANDDPHGV--  
 10 FALYSDRQISIL 435

Query: 411 QEANI--TIQLFINREFGSLGAINV 433

N+ +IQ+ I R G+ G + V

Sbjct: 436 IGQNLIRSIQINITRLAGTFGDVAV 460

15 Score = 230 (34.5 bits), Expect = 2.3e-14, Sum P(3) = 2.3e-14  
 Identities = 98/368 (26%), Positives = 164/368 (44%)

Query: 1240 EMEQD-

20 SLVTLNVERLKGTYGRITIAWEADGSISDIFPTSGVILFTEGQVLSTITLILA 1298  
 E+E+D L+ + V RL GTYG +T + + S + P GV G

ST+T

Sbjct: 71 EVEEDVGLIMIPVVRHLHGTYGYVTADFISQSSSAS--P-GGVDYILHG---  
 STVTFQH-G 123

25 Query: 1299 DNIPELSEVVIVTLTRITTEGVEDSYKGATIDQDRSKSVITTL---  
 PNDSPFGLVGWRAA 1355

N+ ++ +I E +E GAT + +++ +

+DSPFG++ +

30 Sbjct: 124 QNLSFINISIIDNESEFEEPIEILLTGATGGAVLGRHLVSRIIIAKSDSPFGVIRFLNQ 183

Query: 1356 SVFIRVAEPKENTTTTLQLQIARDKGLLGDIHLRAQ-  
 PNFLHVDNQATENEDYVLQET 1414

S I +A P +T L L + R GLLG+I ++ PN + Q +

35 D V

Sbjct: 184 SK-ISIANPN-  
 STMILSLVLERTGGLLGEIQVNWETVGPNSQEAALLPQNRDIADPV--SG 239

40 Query: 1415 IIIMKENIKEAHAEV-  
 SILPDDLPELEEGFIVTITEVNLVNSDFSTGQPSVRRPGMEIAE 1473

+ E + +I P + E+EE FI+ +++LV G+ +

++

Sbjct: 240 LFYFGEGEGGVRTIILTIYPHEEIEVEETFII---KLHLVK-----  
 45 GEAKLDSRAKDV- 290

Query: 1474

IMIEENDDPRGIFMFHVTRGAGEVITAYEXXXXXXXXXXXXXXXXXXAGSFGAVNVYWKASPD 1533  
 + I+E DP G+ F + + + G+FG +

VYW+ S +

50 Sbjct: 291 LTIQEFQDPNGVVQFAPETLSKKTYSPLALEGPLLITFFVRRVKGTGTFGEIMVYWELSSSE 350

Query: 1534

55 SAGLEDFKPSHGILEFADKQVTAMIEITIIDDAEFELTETFNISLISVAGGGRLGDDVVV 1593  
 EDF + G AD + A ++ ++ D E+ E + I L+SV GG

L + +

Sbjct: 351 FDITEDFLSTSGFFTIADGESEASFVHLLPDEVPEIEEDYVIQLVSVEGGAELDLEKSI 410

Query: 1594 T-VVIPQNDSPFGVF 1607

T + ND P GVF

Sbjct: 411 TWFSVYANDDPHGVF 425

5

Score = 190 (28.5 bits), Expect = 7.5e-11, Sum P(3) = 7.5e-11  
Identities = 136/591 (23%), Positives = 247/591 (41%)

Query: 67

10 SGQAVAGSDYEPVTRQWAIMQEGDEFANLTVSILPDDFPEMDESFLISLLEVLHLMNISAS 126  
+G A D+EPV Q+ + ++I+ D E++E F I+L V

+ +

Sbjct: 707

AGSAKPLEDFEPVQNGELFFQKFQTEVD FEITIINDQLSEIEEFFYINLTSVEIRGLQKF 766

15

Query: 127 LKN-QPTIGQP-NISTVVIALNGDAFGVFVIY-  
SISPNTSEDGLFVEVQEQPQTLVELMI 183

N P + +++ + I N D G+ + + + + D + V+ +

T L

20 Sbjct: 767

DVNWSPRLNLD FSVAVITILDNDDL AGMDISFPETTVAVAVD TTLPVETESTTY--LST 824

Query: 184 HRTGGSLGQVAVEWRVVGGTATEGLDFIGAGEILTF--  
AEGETKKTVILTXXXXXXXXXX 241

25 +T L V +V T G+ I +++T ++K + T

Sbjct: 825 SKTTTILQPTNVV-AIV--TEATGVSAIPE-  
KLVTLHGTPAVSEKPDVATVTANVSIHGT 880

Query: 242 XXXXXVLVYTEGGSRILPSSD TVRVNILANDNVAGIVSF--  
QTASRSVIGHEGEILQFHV 299

30 +VY E + + +T V I G VS +T E

L F

Sbjct: 881 FSLGPSIVYIEEEMKN-

GTFNATAEVLIRRTGGFTGNVSITVKTFGERCAQMEPNALPF-- 937

35

Query: 300

IRTFPGRGNVTVNWKIIGQNLNLFANFSGQLFFPEGSLNTTLFVHLLDDNIPEEKEVYQ 359  
R G N+T W + E +F + L F +G + V +LDD+

PE +E +

40 Sbjct: 938 -RGIYGISNLT--WAVE----

EEDFEEQTLTLIFLDGERERKVSQILDDDEPEGQEFFY 990

Query: 360 VILYDVRTQGVPPAGIALLDAAQ---GYAA--  
VLTVEASDEPHGVLNLFALSSRFVL-LQEA 413

45 V L + P G +++ + G+AA ++ + SD +G++ F+ S+

L L+E

Sbjct: 991 VFLTN-----

PQGGAQIVEGKDDTGFAAFAMVIITGSDLHNGIIGFSEESQSGLELREG 1044

50 Query: 414 NITIQLFI-----NREFGSLGAI-  
NVTYTTVPGLSLKNQTVGNLAEPEVDFVPIIGFL 466

+ +L + NR F + VT ++ L+ V NL E E+

V G

55 Sbjct: 1045 AVMRRLHLIVTRQPNRAFEDVKVFWRVTLNKT--VVVLQKDG V-NLME-  
ELQSVS--GTT 1098

Query: 467 ILEEGETAAAINITILEDVPELEEYFLVNL--  
TYVGLTMAASTSFPPRLDSEGLTAQVI 524

G+T I+I + + VP++E YF V L G + S F

E +Q +  
 Sbjct: 1099  
 TCTMGQTKCFISIELKPEKVPQVEVYFFVELYEATAGAAINNSARFAQIKILESDESQSL 1158

5 Query: 525 IDANDGARGVIEWQQRSF---EVNETHGS-  
 LTLVAQRSREPLGHVSLFVYAQNLEAQVGL 580  
 + + G+R + +++ +V G+ L + S + L

A G  
 10 Sbjct: 1159  
 VYFSVGSRLAVAHKKATLISLQVARDSGTGLMMSVNFSTQELRSAETIGRTIISPAISGK 1218

Query: 581 DYIFTPMILHFADGERYKNVNIMILDD--  
 DIPEGDEKFQILITNPSPGLELGKNTIALII 638  
 15 D++ T L F G+R +++++ + + ++FQ++L +P G +

K I  
 Sbjct: 1219  
 DFBVITEGTLVFEPGQRSTVLDVILTPETGSLNSFPKRFQIVLFDPKGGARIDKVYGTANI 1278

20 Query: 639 VLAND-DGPGVLSFNENSEH 656  
 L +D D + + H  
 Sbjct: 1279 TLVSDADSQAIWGLADQLH 1297

Score = 188 (28.2 bits), Expect = 1.2e-33, Sum P(3) = 1.2e-33  
 25 Identities = 84/329 (25%), Positives = 146/329 (44%)

Query: 1126 SVTVKSLNS-----  
 SKNLIALVGAHSHIYELAYISSHSDFIIPSSGELIFEPGEREATIAV 1180  
 S+TVK+ N + G + I L + DF + LIF

30 GERE ++V  
 Sbjct: 917 SITVKTFGERCAQMEPNALPFRGIYG-  
 ISNLTWAVEEEDFEEQTLTLIFLDGERERKVS 975

Query: 1181 NILDDTVPEKEESFKVQKPNPKGGAEI--GINDS----VTITILSNDDAY-  
 35 GIVAFQNS 1233  
 ILDD PE +E F V L NP+GGA+I G +D+ + I++ D +

GI+ F++ S  
 Sbjct: 976  
 QILDDDEPEGQEFFYVFLTNPQGGQIVEGKDDTGFAAFAMVIITGSDLHNGIIGFSEES 1035

40 Query: 1234 LYKQVEEMEQDSLVT---LNVERLKG-TYGRITIAWEAD-  
 GSIIDIFPTSGVILFTEGQV 1288  
 + E+ + +++ L V R + + + W + GV

L E Q  
 45 Sbjct: 1036 --  
 QSGLELREGAVMRRLHLIVTRQPNRAFEDVKVFWRVTLNKTVVVLQKDGVNLMEELOS 1093

Query: 1289 LSTITLTILADNIPELS-EVVIVTLTRITTEGVEDSYK---  
 GATIDQDRSKSVITTLPN 1344  
 50 +S T + +S E+ + ++ + Y+ GA I+ +

I L +D  
 Sbjct: 1094  
 VSGTTTCTMGQTKCFISIELKPEKVPQVEVYFFVELYEATAGAAINNSARFAQIKILES 1153

55 Query: 1345 SPFGLVGWRAASVFIRVAEPKENTTTLQIQIARDKG--LLGDIAI---  
 HLRAQPNFLLHV 1399  
 LV + S R+A + T + LQ+ARD G L+ + LR+

+

Sbjct: 1154 ESQSLVYFSVGS---

RLAVAHKKATLISLQVARDSGTGLMMSVNFSTQELRSAETIGRTI 1210

5 Query: 1400 DNQATENEDYVLQETIIIMKENIKEAHAEVSI L P D 1434  
+ A +D+V+ E ++ + + +V + P+

Sbjct: 1211 ISPAISGKDFVITEGTLVFEPGQRSTVLDVILTPE 1245

Score = 186 (27.9 bits), Expect = 2.5e-13, Sum P(3) = 2.5e-13

Identities = 75/242 (30%), Positives = 113/242 (46%)

10

Query: 1206

EIGINDSVTITILSNDDAYGIVAFQAQNSLYKQVEEMEQDSLVTNLNVERLKGTYGRITIAW 1265

EIG V I I+ ND+A GI+ F + Y E E L+ + V RL

GTYG +T +

15

Sbjct: 40 EIGNISIVRIIIMKNDNAEGIIEF--

DPKYTAFEVEEDVGLIMIPVRLHGTGYVTADF 97

Query: 1266 EADGSIS-----

DIFPTSGVILFTEGQVLSTITLTILADNIPELSEVVIVTLTRITTEGV 1320

20

+ S + D + F GQ LS I ++I+ DN E E + +

LT T G

Sbjct: 98

ISQSSSASPGGVDYILHGSTVTFQHGQNLFINISIIDDNESEFEEPIEILLTGAT--G- 154

25

Query: 1321

EDSYKGATIDQDRSKSVITTLPNDSFGLVGWRAASVFIRVAEPKENTTTTLQLQIARDKG 1380

GA + + +I +DSPFG++ + S I +A P +T L

L + R G

30

Sbjct: 155 -----GAVLGRHLVSRIIIA-KSDSPFGVIRFLNQSK-ISIANPN-

STMILSLVLERTGG 206

Query: 1381 LLGDIAIHLRAQ-PNPLLHVDNQATENEDYVLQETIIIMKENIKEAHAEV-  
SILPDDLPE 1438

35

LLG+I ++ PN + Q + D V + E +

+I P + E

Sbjct: 207 LLGEIQVNWETVGPNSQEAALLPQNRDIADPV--

SGLFYFGE GEGGVRTIILTIYPHEEIE 264

Query: 1439 LEEGFIVTI 1447

40

+EE FI+ +

Sbjct: 265 VEETFIIKL 273

Score = 179 (26.9 bits), Expect = 9.4e-34, Sum P(3) = 9.4e-34

Identities = 65/244 (26%), Positives = 114/244 (46%)

45

Query: 581 DYIFTPMILHFADGERYKVNIMILDDDIPEGDEKFLILTNPSPGLEL--  
GKN-----T 633

D+ + L F DGER + V++ ILDDD PEG E F + LTNP G ++

GK+

50

Sbjct: 954

DFEEQTLTLIFLDGERERKVSQILDDDEPEGQEFFYVFLTNPQGGQIVEGKDDTGFAA 1013

Query: 634 IALIIVLANDDGPVLSFNNSEHFFLREPTALYVQESVAVLYIVREPAQG--  
---LFGTV 688

55

A++I+ +D G++ F+ L ++ L + R+P +

+F V

Sbjct: 1014 FAMVIITGSDLHNGIIGFSEESQSGLELREGAVMRR--

LHLIVTRQPNRAFEDVKVFWRV 1071

Query: 689 TVQ--  
 FIVTEVNSSNESKDLTPSKGYIVLEEGVRFKALQISAILDTEPEMDEYFVCTLFN 746  
 T+ +V + + N ++L G G + I + P+++

5 YF L+  
 Sbjct: 1072  
 TLNKTVVVLQKDGVNLMEELOSVSGTTTCTMGQTKCFISIELKPEKVPQVEVYFFVELYE 1131

Query: 747 PTGGARLGVHVQ-  
 10 TLITVLQNAQAPLGLFSISAVENRATSIDIEEANRTVYLNVSRTNGID 805  
 T GA + + I +L++ L S V +R ++ ++A + L  
 V+R +G  
 Sbjct: 1132 ATAGAAINNSARFAQIKILESDESQSLVYFS-VGSRL-AVAHKKAT-  
 LISLQVARDSGTG 1188

15 Query: 806 LAVSVQWET 814  
 L +SV + T  
 Sbjct: 1189 LMMSVNFST 1197

20 Score = 174 (26.1 bits), Expect = 4.1e-32, Sum P(3) = 4.1e-32  
 Identities = 58/200 (29%), Positives = 102/200 (51%)

Query: 1159  
 25 DFIPSSGELIFEPGEREATIAVNILDDTVPEKEESFKVQLKNPKGGAEIGINDSVT-ITI 1217  
 DF+ +SG GE EA+ V++L D VPE EE + +QL + +GGAE+ +  
 S+T ++  
 Sbjct: 356  
 DFLSTSGFFTIADGESEASFVHLLPDEVPEIEEDYVIQLVSVEGGAELDLEKSITWFSV 415

30 Query: 1218 LSNDDAYGIVAFQAQNSLYKQVEEMEQLDSL--  
 VTLNVERLKGTYGRITIAWEADGSISDIF 1275  
 +NDD +G+ A + +Q + Q+ + + +N+ RL GT+G + +  
 SD  
 Sbjct: 416 YANDDPHGVSFALYSD---

35 RQSIILIGQNLIRSIQINITRLAGTFGDVAVGLRIS---SDHK 469

Query: 1276 PTSGVILFTEGQVLSTITLTILADNIPELSEVVI-----  
 VTLTRITTEGVEDSYKGA-TI 1329  
 V E Q++ T D +P ++V + TL +T V

40 + G TI  
 Sbjct: 470  
 EQPIVTENAERQLVVKDGATYKVDVVPKQVFLSLGSNFTLQLVTVMVLVGGRFYGMPTI 529

Query: 1330 DQDRSKSVITTLPNDSPPGLVGWRAAS 1356  
 45 Q+ +KS + + + VG+ + +  
 Sbjct: 530 LQE-AKSAVLVSEKAANSQVGFESTA 555

Score = 145 (21.8 bits), Expect = 4.3e-24, Sum P(3) = 4.3e-24  
 Identities = 104/396 (26%), Positives = 170/396 (42%)

50 Query: 88  
 EGDEFANLTVSILPDDFPEDDESFLISLLEVHLMNISASLKNQPTIGQPNISTVVIALNG 147  
 +G+ A+ V +LPD+ PE++E ++I L+ V A L + +I +  
 + N

55 Sbjct: 368 DGESEASFVHLLPDEVPEIEEDYVIQLVSVEG---GAELDLEKSI-----  
 TWFSVYAND 419

Query: 148

DAFGVFVIYSISPNTSEDLFVEVQEQPQTLVELMIHRTGGSLGQVAVEWRVVGGTATEG 207  
 D GVF +YS D + + + +++ I R G+ G VAV R+

5 Sbjct: 420 DPHGVFALYS-----  
 DRQSIIGQNLIRSIQINITRLAGTFGDVAVGLRISSDHKEQP 472

Query: 208 LDFIGAGEILTFAEGETKKTIVILTXXXXXXXXXXXXXXXXLVYTE-GGSRI-  
 -LPSS-DT 263

10 + A L +G T K ++ LV G R

+P+

Sbjct: 473  
 IVTENAERQLVVKDGATYKVDVPIKNQVFLSLGSNFTLQLVTVMLVGGRFYGMPTILQE 532

15 Query: 264 VRVNIL-ANDNVAGI-VSFQTASRSVIGHEGEILQFHVIRTFPGR-  
 GNVTVNWKI-IGQN 319  
 + +L ++ A V F++ + ++ HV+ + G G ++V

W

20 Sbjct: 533 AKSAVLVPSEKAANSQVGFESTAFQLMNITAGTS--  
 HVMISRRGTYGALSVAWTTGYAPG 590

Query: 320 LEL-----  
 NFANFSGQLFFPEGSLNTTLFVHLLDDNIPEEKEVYQVILYDVRTQGVPP 372

25 LE+ N G L F G +F+ P E + + L  
 V++ P

Sbjct: 591 LEIPEFIVVGNMTPTLGSLSFSGHGEQRKGVFLWTFPS--  
 PGWPEAFVLHLSGVQSSA--P 646

30 Query: 373  
 AGIALLDAAQGYAAVLTVESDEPHGVNLNFASSRFVLLQEANITIQLFINREFG-SLGAI 431  
 G L G+ + A EP GV F+ SSR +++ E I+L + R

FG I

Sbjct: 647 GGAQL--RSGF-----  
 IVAEIEPMGVFQFSTSSRNIIVSEDQMIRLHVQRLFGFHSDLI 699

35 Query: 432 NVTYTTVPGMLS-LKN-QTV--GNLA----EPEVDF-  
 VPIIGFLILEEGETAAAINITIL 482  
 V+Y T G L++ + V G L + EVDF + II L E E

IN+T +

40 Sbjct: 700 KVSQTTAGSAKPLEDFEPVQNGELFFQKFQTEVD FEITIINDQ-  
 LSEIEEFFYINLTSV 758

Query: 483 E 483

E

45 Sbjct: 759 E 759

Score = 142 (21.3 bits), Expect = 5.6e-05, Sum P(3) = 5.6e-05  
 Identities = 54/175 (30%); Positives = 76/175 (43%)

50 Query: 1435  
 DLPELEEGFIVTITEVNLVNSDFSTGQPSVRRPGMEIAEIMIEENDDPRGIFMFHVTRGA 1494  
 DL + G+ TI E N + D QP + I I+I +ND+ GI

F

Sbjct: 16 DLYDFGRGYDFTIQE-NGLQID----QPP-  
 55 EIGNISIVRIIMKNQNAEGIIIEFDPK--- 66

Query: 1495 GEVITAYXXXXXXXXXXXXXXXXAGSFGAVNVYW--  
 KASPD SAGLEDFKPSHGILEFADK 1552

TA+E G++G V + ++S S G D+

+ F

Sbjct: b7 ---

YTAFEVEEDVGLIMIPVVRHLGTYGYVTADFISQSSSASPGGVDYILHGSTVTFQHG 123

5 Query: 1553

QVTAMIEITIIDDAEFELTETFNISLISVAGGGRLGDDVVVTVVIPQNDSPFGVFGF 1609

Q + I I+IIDD E E E I L GG LG +V ++I

++DSPFGV F

10 Sbjct: 124

QNLFSFINISIIDNESEFEEPIEILLTGATGGAVLGRHLVSRIIIAKSDSPFGVIRF 180

Score = 125 (18.8 bits), Expect = 4.0e-25, Sum P(3) = 4.0e-25

Identities = 77/308 (25%), Positives = 134/308 (43%)

15 Query: 1141 LVGAHSHIYELAYISSHS-----DFIP-

SSGELIFEPGEREATIAVNILDDTVPEKEES 1193

L G HS + +++Y ++ DF P +GEL F+ + E + I++D

+ E EE

20 Sbjct: 691

LFGFHSDLIKVSQTTAGSAKPLEDFEPVQNGELFFQKFQTEVD FEITIINDQLSEIEEF 750

Query: 1194 FKVQLKNP--

KGGAEIGINDSVTITILSNDDAYGIVAFQAQNSLYKQVEEMEQDSLVTNLV 1251

F + L + +G + +N S + + D + ++ N

D L +++

Sbjct: 751 FYINLTSVEIRGLQKFDVNWSPRLNL---DFSVAVITILDN-----

DDLGMADI 796

30 Query: 1252

ERLKGTYGRITIAWEADGSISDIFPTSGVILFTEGQVLSTITLTILADNIPELSEVVIVT 1311

++ T+A D ++ + S L T + + + T + + E

+ V +

Sbjct: 797 -----SFPETTVAVAVD TTLIPVETESTTYLSTS-

35 KTTTILQPTNVVAIVTEATGVSAIP 850

Query: 1312

LTRITTEGVEDSYKGATIDQDRSKSVITTLPNDSPPGLVGWRAASVFIRVAEPKENT-TT 1370

+T G T V T N S G + V+I E

40 K T T

Sbjct: 851 EKLVTLHG-----TPAVSEKPDVATVTANVSIHGTFSLGPSIVYIE-

EEMKNGTFNT 901

Query: 1371 LQLQIARDKGLLGDI A IHLRA-----QPNFL-----LHVDNQ--

45 ATENEDYVLQETI 1415

++ I R G G+++I ++ +PN L + N A E

ED+ Q

Sbjct: 902

AEVLIRRTGGFTGNVSITVKTFGERCAQMEPNALPFRGIYGISNLTWAVEEEDFEEQTLT 961

50 Query: 1416 IIMKENIKEAHA EVSILPDDLPELEEGFIVTIT 1448

+I + +E V IL DD PE +E F V +T

Sbjct: 962 LIFLDGERERKVSQILDDDEPEGQEFFYVFLT 994

55 Score = 123 (18.5 bits), Expect = 6.0e-28, Sum P(3) = 6.0e-28

Identities = 91/372 (24%), Positives = 150/372 (40%)



Query: 386 VLTVEASDEPHGVNLFALSSRFVLLQEA--NITI---  
QLFINREFGSLGAINVTYTTV-- 438

V TV A+ HG F+L V ++E N T ++ I R G G

+++T T

5 Sbjct: 868 VATVTANVSIHGT--  
FSLGPSIVYIEEEMKNGTFNTAEVLIRRTGGFTGNVSITVKTFGE 925

Query: 439 -----PGMLSLKN-QTVGNL--  
AEPEVDFVPIIGFLILEEGETAAAINITILEDDVPEL 489

10 P L + + NL A E DF LI +GE +++

IL+DD PE

Sbjct: 926  
RCAQMEPNALPFRGIYGISNLTWAVEEEDFEEQTLTLIFLDGERERKVSQILDDDEPEG 985

15 Query: 490 EEEYFLVNLTYYVGLTMAASTSFPPRLDSEGLTA--QVIIDANDGARGVI---  
EWQQRSEFEV 544

+E+F V LT D G A VII +D G+I E

QS E+

20 Sbjct: 986 QEFFYVFLT----  
NPQGGGAQIVEGKDDTGFAAFAMVIITGSDLHNGIIGFSEESQSGLEL 1041

Query: 545 NE--THGSLTLVAQRS-REPLGHVSLF--  
VYAQNLEAQVGLDYIFTPMILHFADGERYKN 599

E L L+ R V +F V + D + L

25 G  
Sbjct: 1042  
REGAVMRRLHLIVTRQPNRAFEDVKVFWRVTLNKTVVVLQKDGVLNMEELQSVSGTTTCT 1101

30 Query: 600 -----VNIMILDDDIPEGDEKFQILITNPSPGLELGKNT-  
IALIIVLANDDGPVLSF 651

++I + + +P+ + F + L + G + + A I +L

+D+ ++ F

Sbjct: 1102  
MGQTKCFISIELKPEKVPQVEVYFFVELYEATAGAAINNSARFAQIKILESDESQSLVYF 1161

35 Query: 652 NNSEHFFLREPTALYVQESVAVLYIVREPAQGLFGTVTVQFIVTEVNSSNE-  
-SKDLTPS 709

+ + A + L + R+ GL ++V F E+ S+

++P+

40 Sbjct: 1162 SVGSRLAVAHKKATLIS-----LQVARDSGTGML--  
MSVNFSTQELRSAETIGRTIISPA 1214

Query: 710 ---KGYIVLEEGVRFKALQISAILD 731

K +++ E + F+ Q S +LD

45 Sbjct: 1215 ISGKDFVITEGTLVFEPGQRSTVLD 1239

Score = 120 (18.0 bits), Expect = 1.8e-22, Sum P(3) = 1.8e-22  
Identities = 77/316 (24%), Positives = 127/316 (40%)

50 Query: 1255 KGTYGRITIAWE---ADGS-----  
ISDIFPTSGVILFTEGQVLSTITLILADNIPEL 1304

+GTYG +++AW A G + ++ PT G + F+ G+ + L

P

Sbjct: 573  
55 RGTYGALSAVWTTGYAPGLEIPEFIVVGNMTPTLGSLSFSGHGEQRKGVFLWTFPS--PGW 630

Query: 1305  
SEVVIVTLTRITTEGVESYKGATIDQDRSKSVITTLPNDSFGVLVWRAASVFIRVAEP 1364

E ++ L+ GV+ S G Q RS ++ + P G+ + +S  
 I V+E  
 Sbjct: 631 PEAFLHLSS-----GVQSSAPGGA--QLRSGFIVAEI---  
 EPMGVFQFSTSSRNIIIVSE- 679  
 5 Query: 1365 KENTTTTLQLQIARDKGLLGDIHLRAQPNFLLHVDNQATENEDYV-  
 LQETIIIMKENIK 1423  
 +T ++L + R G D+ I + Q A ED+ +Q  
 + ++  
 10 Sbjct: 680 --DTQMIRLHVQRLFGFHSDL-IKVSQTTA-----  
 GSAKPLEDFEPVQNGELFFQKFQT 731  
 Query: 1424 EAHA EVSILPDDLPELEEGFIVTITEVNLVN-  
 SDFSTGQPSVRRPGMEIAEIMIEENDDP 1482  
 15 E E++I+ D L E+EE F + +T V + F +A I  
 I +NDD  
 Sbjct: 732  
 EVDFEITIIINDQLSEIEEFFYINLTSVEIRGLQKFDVNWSPRLNLD FSVAVITILDNDL 791  
 20 Query: 1483 RGI-FMFHVTRGAGEVITAY---  
 EXXXXXXXXXXXXXXXXXXAGSFGAVNVYWKASPD SAGLE 1538  
 G+ F T A V T E V +  
 +A+ SA E  
 Sbjct: 792  
 25 AGMDISFPETTVAVAVDTTLIPVETESTTYLSTSKTTTILQPTNVVAIVTEATGVSAIPE 851  
 Query: 1539 DFKPSHGILEFADKQVTAMIEITIIDDAEFEL 1570  
 HG ++K A + + F L  
 Sbjct: 852 KLVTLHGTPAVSEKPDVATVTANVSIHGTFSL 883  
 30 Score = 113 (17.0 bits), Expect = 9.4e-34, Sum P(3) = 9.4e-34  
 Identities = 28/87 (32%), Positives = 50/87 (57%)  
 Query: 1156 SHSDFIPSSGELIFEPGEREATIAVNILDDT--  
 35 VPEKEESFKVQLKNPKGGAEIG-INDS 1212  
 S DF+ + G L+FEPG+R + V + +T + + F++ L +PKGGA  
 I + +  
 Sbjct: 1216  
 SGKDFVITEGTLVFEPGQSTVLVDVILTPETGSLNSFPKRQIVLFDPKGGARIDKVYGT 1275  
 40 Query: 1213 VTITILSNDDAYGIVAFQAQNSLYKQVEE 1240  
 IT++S+ D+ I A + L++ V +  
 Sbjct: 1276 ANITLVSDADSQAIWGLA-DQLHQPVND 1302  
 45 Score = 93 (14.0 bits), Expect = 4.1e-32, Sum P(3) = 4.1e-32  
 Identities = 57/222 (25%), Positives = 90/222 (40%)  
 Query: 1404 TENEDYVL--QETIIIMKENIKEAHAE---VSILPDDLPEL-----  
 EEGFIVTITEVN 1451  
 50 TE+ Y+ + T I+ N+ E VS +P+ L L E+  
 + T+T  
 Sbjct: 816  
 TESTTYLSTSKTTTILQPTNVVAIVTEATGVSAIPEKLVTLHGTPAVSEKPDVATVTANV 875  
 55 Query: 1452 LVNSDFSTGQPSVRRPGMEIAEIMIEENDDPRGIFMFHVTRGAGEV-  
 ITAYXXXXXXXXX 1510  
 ++ FS G PS+ + I E M + + + G V IT

-46-

Sbjct: 936 PFRGIYGISNLTWAVEEEDF--EEQTLT-----  
LIFLDGERERKVSQILDDDEPEGQEF 988

5 Query: 740 FVCTLFNPTGGARL-----  
GVHVQTLITVLQNAQPLGLFSISAVENRATSIDIEEAN- 791  
F L NP GGA++ G ++ + + G+ S E +

+++ E

Sbjct: 989 FYVFLTNPQGGAQIVEGKDDTGFAAFAMVIITGSDLHNGIIGFS--  
EESQSGLELREGAV 1046

10

Query: 792 -RTVYLVNSRT-NGIDLAVSVQWE-TVSETAF-----  
GMRGMDVVFVSFQSFLEDESASGW 843

R ++L V+R N V V W T+++T G+ M+ + SV +

Sbjct: 1047

15 MRRRLHLIVTRQPNRAFEDVKVFWRVTLNKTVVVLQKDGVLNMEELQSVSGTTTCTMGQTK 1106

Query: 844 CFFTLE 849

CF ++E

Sbjct: 1107 CFISIE 1112

20

Score = 91 (13.7 bits), Expect = 6.6e-32, Sum P(3) = 6.6e-32  
Identities = 49/153 (32%), Positives = 70/153 (45%)

Query: 1466

25 RPGMEIAEIMIEENDDPRGIFMFHVTRGAGEVITAYXXXXXXXXXXXXXXXXXAGSFGAVN 1525

R G +AEI +P G+F F + + +I + +

+ +

Sbjct: 652 RSGFIVAEI-----EPMGVFQFSTS--

SRNIIVSEDTQMIRLHVQRLFGFHSQ---LIK 700

30

Query: 1526 VYWKASPDASAG-LEDFKP-

SHGILEFADKQVTAMIEITIIDDAEFELTETFNISLISVAG 1583

V ++ + SA LEDF+P +G L F Q EITII+D E+ E F

I+L SV

35 Sbjct: 701

VSYQTTAGSAKPLEDFEPVQNGELFFQKFQTEVD FEITIIINDQLSEIEEFFYINLTSVEI 760

Query: 1584 GG-----RLGDDVVVTVV-IPQNDSPFGV-FGFEEKTVS 1615

G RL D V V+ I ND G+ F E TV+

40 Sbjct: 761 RGLQKFDVNWSRNLNDFSAVITILDNDLAGMDISFPETTVA 804

Score = 65 (9.8 bits), Expect = 8.8e-29, Sum P(3) = 8.8e-29  
Identities = 26/99 (26%), Positives = 50/99 (50%)

45 Query: 1232 NSLYKQVEEMEQLSLVTLNVERLKGTYGRITIAWEADGS----ISDIF--  
PTSGVILFTE 1285

NS K+ + + D +++++ GT IT+ +AD ++D P

+ IL

Sbjct: 1250 NSFPKRFQIVLFDPKGGARIDKVYGT-

50 ANITLVSDADSQAIWGLADQLHQPVNDDIL--- 1305

Query: 1286 GQVLSTITLTILADNIPELSEVVIVTLTRITTEGVEDSYKGAT 1328

+VL TI++ + +N E ++ + +ITTEG ++ A+

Sbjct: 1306 NRVLHTISMKVATENTDEQLSAMMHLIEKITTEGKIQAFSVAS 1348

55

Score = 48 (7.2 bits), Expect = 1.9e-27, Sum P(3) = 1.9e-27  
Identities = 23/115 (20%), Positives = 44/115 (38%)

Query: 1499 TAYEXXXXXXXXXXXXXXXXXXAGSFGAVNVYWKAS-----  
 PDSAGLEDFKPSHGILEFAD 1551

TA++

G++GA++V W

P+ + + P+

G L F+

5 Sbjct: 554

TAFQLMNITAGTSHVMISRRGTYGALSVAWTTGYAPGLEIPEFIVVGNMPTLGSLSFSH 613

Query: 1552 KQVTAMIEITIIDDAEFELTETFNISLI--

SVAGGGRLGDDVVVTVVIPQNDSPFGVFGF 1609

10 + + + + ++S + S GG +L +V +

P GVF F

Sbjct: 614 GEQRKGVLWTFPSPGWPEAFVLHLSGVQSSAPGGAQLRSGFIVAEI-----

EPMGVFQF 668

15

Pedant information for DKFZphamy2\_10p7, frame 3

Report for DKFZphamy2\_10p7.3

20

[LENGTH] 1615

[MW] 177600.58

[pI] 4.37

25 [HOMOL] TREMBL:AF055084\_1 gene: "VLGR1"; product: "very  
 large G-protein coupled receptor-1"; Homo sapiens very large G-  
 protein coupled receptor-1 (VLGR1) mRNA, complete cds. 5e-24

[BLOCKS] BP01493A

[BLOCKS] BL00713B Sodium:dicarboxylate symporter family proteins

30

[BLOCKS] PR01003A

[BLOCKS] PR00412C

[BLOCKS] BL00824E

[PIRKW] heart 1e-08

35 [PIRKW] ion transport 1e-08

[PIRKW] transmembrane protein 3e-08

[PIRKW] phosphoprotein 2e-08

[PIRKW] membrane protein 1e-08

[PROSITE] MULTICOPPER\_OXIDASE1 1

40 [KW] All\_Beta

[KW] LOW\_COMPLEXITY 2.60 %

45 SEQ DAWADAWALYTCATLCLKEQACSAFSFFSASEGPQCFWMTSWISPAVNNSDFWYRK NMT  
 SEG .....xxxxxxxxxxxxx.....  
 PRD ccchhhhhhhhhchhhhhhhhhhhheeeeeecccccceeeeeecccccccccceeeccce

50 SEQ RVASLFSGQAVAGSDYEPVTRQWAIMQEGDEFANLTVSILPDDFPEMDESFLISLLEVHL  
 SEG .....  
 PRD eeeeeccccccccccccceeeceeeeeecccccceeeeeecccccccchhhhhhhhhhhhhhh

55 SEQ MNISASLKNQPTIGQPNISTVVIALNGDAFGVFVIYSISPNTSEDGLFVEVQEQPQTLVE  
 SEG .....  
 PRD hccccccccccccccccceeeeeecccccceeeeeecccccccccceeeeeecccccce

SEQ LMIHRTGGSLGQVAVEWRVVGGTATEGLDFIGAGEILTFAEGETKKTVILTILDDSEPED  
 SEG .....xxxxxxxxxx  
 PRD eeeeeccccccccceeeeeecccccccccccccceeeeeecccccceeeeeeccccccc

5 SEQ DESIIVSLVYTEGGSRILPSSD TVRVN ILANDNVAGIVSFQTASRSVIGHEGEILQFHVI  
SEG xxxxxxxx.....  
PRD ccc

10 SEQ RTFPGRGVNTVNWKIIGQNL ELNFANFSGQLFFPEGSLNTTLFVHLLDDNIPEEKEVYQV  
SEG .....  
PRD ecc

15 SEQ ILYDVRTQGVPPAGIALLD AQGYAAVL TVEASDEPHGV LNFALSSRFVLLQ EANITIQLF  
SEG .....  
PRD eccccccccccchhhhhhhhhcc

20 SEQ INREFGSLGAINVTYTTVP GMLSLKNQTVGNLAEPEVDFVPIIGFLILEEGETAAAINIT  
SEG .....  
PRD ccc

25 SEQ ILEDDVPELEEYFLVNL TYVGLTMAASTSFPPRLDSEGLTAQVIIDANDGARGVIEWQQS  
SEG .....  
PRD eccccchhhhhhheeeeeeecc

30 SEQ RFEVNETHGSLTLVAQRSREPLGHVSLFVYAQNL EAQVGLDYIFTMILHFADGERYKNV  
SEG .....  
PRD eeeeecc

35 SEQ NIMILDDDIPEGDEKFQLIL TNPSGLELGKNTIALIIVLANDDGPVLSFNNSEHFFLR  
SEG .....  
PRD eeeeecc

40 SEQ EPTALYVQESVAVLYIVREPAQGLFGTVTVQFIVTEVNSSNESKDLTPSKGYIVLEEGVR  
SEG .....  
PRD cccccceccchhhhhhhhhcc

45 SEQ FKALQISAILDTEPEMDEYFVCTLFNPTGGARLG VHVQTLITVLQNA PLGLFSISAVEN  
SEG .....  
PRD eeeeeeeccccchhhhhhhhheeeeeccccccccceehhhhhhhhhhhhhcccccccccech

50 SEQ RATSIDIEEANRTVYLVNVSRTNGIDLAVSVQWETVSETAFGMRGMDVVSFVQSF LDESA  
SEG .....  
PRD hhhhhccccccccccccccccccccchhhhhhheeeeecccccccccccccccccccccccc

55 SEQ SGWCFFTL ENLIYGIMLRKSSVTYRWQGIFIPVEDLNIENPKTCEAFNIGFSPYFVITH  
SEG .....  
PRD ccccccecc

60 SEQ EERNEEKPSLNSVFTFTSGFKLFLVQTIIILESSQVRYFTSDSQDYLI IASQRDDSEL TQ  
SEG .....  
PRD hhhhhcc

65 SEQ VFRWNGGSFVLHQLPVRGVLTV ALFNKGGSVFLAISQANARLNSLLFRWSGSGFINFQE  
SEG .....  
PRD eeeeecc

70 SEQ VPVSGTTEVEALSSANDIYLIFAKNVFLGDQNSIDIFIWEMGQSSFRYFQSVDFAAVNRI  
SEG .....  
PRD ecc

75 SEQ HSFTPASGIAHILLIGQDMSALYCWN SERNQFSFVLEVPSAYDVASVTVKSLNSSKNLIA

```

SEG .....
PRD eeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeee

5  SEQ LVGAHSHIYELAYISSHSD FIPSSGELIFEPGEREATIAVNILDDTVPEKEESFKVQLKN
   SEG .....
   PRD eeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeec

10  SEQ PKGGAEIGINDSVTITILSNDDAYGIVAFQAQNSLYKQVEEMEQLDSLVTLNVERLKGTYGR
   SEG .....
   PRD cccccceeeeeeeeeeeeeeeeeccccchhhhhhhccchhhhhhhhhhhhhhhhhhhhhccccceee

15  SEQ ITIAWEADGSISDIFPTSGVILFTEGQVLSTITLTILADNIPELSEVVIVTLTRITTEGV
   SEG .....
   PRD eeeeeeeeeccccceeeeeeeeeccccceeeeeccccceeeeeeeeeeeeeeeeeeeeeceeee

20  SEQ EDSYKGATIDQDRSKSVITTLPNDSFGLVGWRAASVFIRVAEPKENTTTLQLQIARDKG
   SEG .....
   PRD cceeeeeeeeeccccceeeeeeeeeccccceeeeehhhhhhheeeeeccccccccceeeeecccccc

25  SEQ LLGDIAIHLRAQPNFLLHVDNQATENEDYVLQETIIIMKENIKEAHAEVSIPLPDDLPELE
   SEG .....
   PRD cccccceeeeeccccceeeeeccccccccceeeeeeeeeeeeeccccchhhhhheeeeecccccccccc

30  SEQ EGFIVTITEVNLVNSDFSTGQPSVRRPGMEIAEIMIEENDDPRGIFMFHVTRGAGEVITA
   SEG .....
   PRD cceeeeeeeeeeeeeccccccccccccccccchhhhhhhhhccccceeeeeeeeeccccceeeee

35  SEQ YEVPPLNLVLQVPVRLAGSFGAVNVYWKASPD SAGLEDFKPSHGILEFADKQVTAMIEI
   SEG ..xxxxxxxxxxxxxxxx.....
   PRD eeeeeccccceeeeeeeeeccccceeeeeeeeeccccccccccccccccceeeeeccccceeece

   SEQ TIIDDAEFELTETFNISLISVAGGRLGDDVVVTVVIPQNDSPFGVFGFEKTVS
   SEG .....
   PRD eeecchhhhhhhhhcceeceeeeeccccccccceeeeeeeeeccccccccceeeeecccccc

```

## Prosites for DKFZphamy2\_10p7.3

40 PS00079 151->172 MULTICOPPER\_OXIDASE1 PD0C00076

(No Pfam data available for DKFZphamy2\_10p7.3)

DKFZphamy2\_11d2

-----

5 group: transmembrane protein

DKFZphamy2\_11d2 encodes a novel 552 amino acid protein without similarity to known proteins.

10 The novel protein contains 2 transmembrane regions.  
No informative Blast results; no predictive prosite, pfam or scope motife.

15 The new protein can find application in studying the expression profile of amygdala-specific genes and as a new marker for amygdala cells.

unknown protein

20

Pedant: TRANSMEMBRANE 2

Sequenced by EMBL

25 Locus: /map="16p13.3"

Insert length: 2939 bp

Poly A stretch at pos. 2920, polyadenylation signal at pos. 2869

30

1 GGC GGG GTG AGG CCG CGG GCG CAG GTT CCA CCT GGG CTT GCG AAG GCACA  
51 GATT CCCC GT CCAC AGCT CA CGAC CAG ATG CACC AGC AGG AGT CCAC ATC  
101 GAG GAC GTT C TCC GGG CACT CCC ACG ACCA GTG ACC AGGA GTT AAA CTTT  
151 GGG ATG TGCC CGT GAT GTT G GACC ACA AGG ACT TAG AGGC CGA AAT CCAC  
35 201 CCT TGA AAA ATGA AGA AAG AAA ATC GCAG GAAA ATCT GG GAA ATCC ATC  
251 AAAAA ATG AG GATA AC GTGA AAAG CG CGCC TCC ACAG TCC CGG CTCT CCC  
301 GGT GCC GAGC GCG GCG GTT TTT CTT TCA TGT TTT CTCT G CCT TTT TGT G  
351 GTG TTC GTCG TCT CAT TCGT CAT CCC GTGT CCAG ACC GGC CGG CGT CACA  
401 GCG AAT GTGG AGG ATA GACT ACAG TG CCGC TGT TAT CTAT GACT TTT CTGG  
40 451 CTG TGG ATGA TATA AAC GGG GAC AGG ATCC AAG ATG TTCT TTT CTT TAT  
501 AAAAA CACCA ACAG CAG CAA CAAT TT CAGC CGAT CCT GTG TGG ACG AAGG  
551 CTT TT CCTCT CCCT GCA CCT TTG CAG CTGC TGT GT CGGG G GCG AAC GCG CA  
601 GCAC GCTCT GGG AGA GAC CT GTG GCG CCA AG ACG TGG CCG CT CGT GGAG TGT  
651 GCT GTG CCCC AGCCA AGAG G CAG TGAG GCA CTT CTG CCT GCAT CCT GGT  
45 701 GGG CAG ACC AGTT CTTT CA TTG CAG TCA CTT GTT CACA GGG GAA ACCC  
751 TGT GGA ACCA CAG CAG CAG TTC AGC GGG AAT GCG TCC AT CCT GAG CCG CT  
801 CTG CTG CAGG TGC CTG ATGT GGC CGG CGAT GGG GCG CAG ACCT GCT GGT  
851 TCT ACC CAG GAG CGG GAG AGG TTAG TGG CCAC CTCT AC TCC GGC AGCA  
901 CCG GGC ACCA GATT GGC CTC AGAG GCAG CC TTGG TGT GGA CGG GGA AGT  
50 951 GGCT TCCT CC TTC ACGT CAC CAG GAC AGGT GCG CACT ACA TCCT CTTT CC  
1001 CTG CGC AAGC TCC CTCT GCG GCT GCT CTGT GAAG GGT CTC TAC GAG AAGG  
1051 TGAC CGG GAG CGG CGG CCG TTCA AGAG TG ACC CGC ACTG GGAG AGCATG  
1101 CTCA ATGCCA CCAC CCG CAG GAT GCTT TCC CAC AGCT CTG GAG CAG TCG  
1151 CTAC CTG ATG CAT GTCCC AG GGA AC GCG CG TGC AGAT GTG CTT CTT GTTG  
55 1201 GCT CAG AGGC CTT CGT GCTG CTGG AC GGGC AGG AGCT GAC GCCT CGCT GG  
1251 ACAC CCA AGG CAG CCC ATGT CCT GAG AAAA CCC ATCT TC GCG CTAC AA  
1301 ACC AGA CACC TTGG CTGT AG CCG TTG AAAA CGG AACT GGC ACC GAC AGAC  
1351 AGAT CCT GTT TCT GGA CCTT GGC ACT GGA GCGT CCT GTG TAG CCT AGCC



```

1401 CTCCCGAGCC TCCCTGGGGG TCCACTGTCC GCCAGCCTGC CGACCGCAGA
1451 CCACCGCTCA GCCTTCTTCT TCTGGGGCCT CCACGAGCTG GGGAGCACCA
1501 GCGAGACGGA GACCGGGGAG GCGCGGCACA GCCTGTACAT GTTCCACCCC
1551 ACCCTGCCGC GCGTGCTGCT GGAGCTGGCC AATGTCTCTA CCCACATTGT
5 1601 CGCCTTTGAC GCCGTCTGTG TTGAGCCAAG CCGCCACGCC GCCTACATCC
1651 TTCTGACAGG CCGGCAGAC TCAGAGGCAC CCGGCCTGGT CTCTGTGATC
1701 AAGCACAAGG TCGGGGACCT TGTCCCAAGC AGCAGGGTGG TCCGCCTGGG
1751 TGAGGGTGGG CCAGACAGTG ACCAAGCCAT CAGGGACCGG TTCTCCCGGC
1801 TCGGGTACCA GAGTGAGGCG TAGAGGCACG CCAGCCAGAG CCTGTGGAGA
10 1851 GACTCCGCCT GCTGACACTA AACGTCTTGG GAAGTGGGCC CTTCCCTGGG
1901 TCTCTGCACT GACTCCCCCA CTCCTGACCC TGGTGATGGT CGCCACTGGG
1951 CAGCAGCAGC CTTACCAGTC CTCCATGATC ACACCCAGGG ACCTGCATGG
2001 GTGAGGGGAC ACCCTGGGCC TCTCTCCCGC CCAGCATCCT CCCTGAGTCC
2051 CCACACAGGG CTTCACTCTG CACCCACCA GGGTCCCGCT CACACCAGGC
15 2101 AGCCTTCATA GTGGTCTCCC TGGCCACCTT GGGCAGAGCT GGGTCATGCA
2151 GCACCCCATC CTTACCCGGT GCCCTCTCCT TGCCAGCTTC TCCCCAGGCC
2201 AGAGCGGCCA TCGCGTAGAA AGAACCAGGG TGTCCCCGGG ACAGGCCGTC
2251 CCCCACCCCA TCCTGTAGAG TCCATTCCCC TTTTCCCTCC TGTGCTCTGT
2301 CCCCCAAGGA GTCATGGAAC TCAGGGTACT GGGCCTCAAC GGGAACCTGA
20 2351 GACAGCTTCC AGCTTCGCAG CCCTTCCCGG AGCTACAGGG GGATCCTCTA
2401 GCATGGGGGG TGTGACTTGG TTCCTTTGAC CAGGTCCTGT GAGGAAGCCT
2451 GGAGCAAGGG TCTCCCCAG CAGGATGGGT GGGGCCTGCT CTGGAGCTGA
2501 GCCCGTGGCC GCTCACAGGT GTCCTTAGTG GTGTTGCAGC TGTCTACTGG
2551 CTGCATGTGC TGTGAATATC CCAAGGAAC GGCTGTGGAA TGCCTGTTTG
25 2601 GGTCACTCTG TGCCCTCTCA GTAGACACTG GAGCTGCTCT GTCCCTGAAG
2651 AGGCCCCGTG CCCCAGGCAT GGCAAGCGCC TGCCCTCTCC CTTCCGGTGC
2701 TCACACGCCC ACGCCGTGCC ACCCGATGCA GGACTCACCT CTGTGCCTTG
2751 CTGCTCCTGA GGCCCAAGGG CAGCCATGGT GCTCTGTACT GCTCGGGCCG
2801 CCCAGGTCAC AGAGCCTGAG CTTGCTAGCC AAAGCAGCCT GATGACCCAC
30 2851 CCACCAAGGA AGAAAGCAGA ATAAACATTT TTGCACTGCC TGA AAAAACC
2901 CGGTGGTCAG GCGTGAGCCT AAAAAAAAAA AAAAAAAAAA

```

## BLAST Results

35

No BLAST result

40

## Medline entries

No Medline entry

45

## Peptide information for frame 2

```

50 ORF from 2555 bp to 2839 bp; peptide length: 95
   Category: questionable ORF
   Classification: unclassified

```

```

55 1 MCCEYPKELA VECVFGSVCA LSVDTGAALS LKRPRAPGMA SACLSPSGAH
   51 TPTPCHPMQD SPLCLAPEA QGQPWCSVLL GPPRSQSLSF VAKAA

```

## BLASTP hits

No BLASTP hits available

5 Alert BLASTP hits for DKFZphamy2\_11d2, frame 2

TREMBL:MMIGCF\_2 Mouse ig gamma2a-b(c57b1/b allele) c gene and  
secreted

10 tail., N = 1, Score = 73, P = 0.1

>TREMBL:MMIGCF\_2 Mouse ig gamma2a-b(c57b1/b allele) c gene and  
secreted

15 tail.

Length = 334

HSPs:

Score = 73 (11.0 bits), Expect = 1.1e-01, P = 1.0e-01

20 Identities = 16/49 (32%), Positives = 27/49 (55%)

Query: 44 LSPSGAHTPTPCHPMQDSPLCLAAPEAQGGQWCSVLLGPPRSQSLSFVA 92  
+ P T PC P+++ P C AAP+ G P SV + PP+ + + ++Sbjct: 96 IEPRVPITQNPCPPLKECPPC-AAPDLLGGP--SVFIFPPKIKDVLMIS  
25 141

## Peptide information for frame 3

30 -----

ORF from 165 bp to 1820 bp; peptide length: 552

Category: putative protein

Classification: Transmembrane proteins unclassified

35

1 MLDHKDLEAE IHPLKNEERK SQENLGNPSK NEDNVKSAPP QSRLSRCRAA  
 51 AFFLSLFLCL FVVVFVVSFVI PCPDRPASQR MWRIDYSAAV IYDFLAVDDI  
 101 NGDRIQDVLF LYKNTNSSNN FSRSCVDEGF SSPCTFAAAV SGANGSTLWE  
 151 RPVAQDVALV ECAVPQPRGS EAPSACILVG RPSSFIAVNL FTGETLWNHS  
 40 201 SSFSGNASIL SPLQVPDQD GDGAPDLLVL TQEREEVSGH LYSGSTGHQI  
 251 GLRGS LGVDG ESGFLLHVTR TGAHYILFPC ASSLCGCSVK GLYEKVTGSG  
 301 GPFKS DPHWE SMLNATTRM LSHSSGAVRY LMHVPGNAGA DVLLVGSEAF  
 351 VLLDGQELTP RWTPKAAHVL RKPIFGRYKP DTLAVAVENG TGTDRQILFL  
 401 DLGTGAVLCS LALPSLPGGP LSASLPTADH RSAFFFWGLH ELGSTSETET  
 45 451 GEARHSLYMF HPTLPRVLE LANVSTHIVA FDAVLFEPSR HAAYILLTGP  
 501 ADSEAPGLVS VIKHKVRDLV PSSRVVRLGE GGPDSDAQAIR DRFSRLRYQS  
 551 EA

50

## BLASTP hits

No BLASTP hits available

55 Alert BLASTP hits for DKFZphamy2\_11d2, frame 3

No Alert BLASTP hits found

## Pedant information for DKFZphamy2\_11d2, frame 2

## Report for DKFZphamy2\_11d2.2

5

[LENGTH] 95  
 [MW] 9757.38  
 [pI] 6.68  
 10 [BLOCKS] PRO0521E  
 [KW] Alpha\_Beta

15 SEQ MCCEYPKELAVECVFGSVCALSVDTGAALSLKRPRAPGMASACLSPSGAHTPTPCHPMQD  
 PRD cccchhhhhhhhhccceeeeeeeccccchhhhhcccccccccccccccccccccccccccccc

SEQ SPLCLAAPEAQGPWC SVLLGPPRSQSLSFVAKAA  
 PRD cccccccccccccceeeccccccccchhhhhhccc

20

(No Prosite data available for DKFZphamy2\_11d2.2)

(No Pfam data available for DKFZphamy2\_11d2.2)

25

## Pedant information for DKFZphamy2\_11d2, frame 3

## Report for DKFZphamy2\_11d2.3

30

[LENGTH] 552  
 [MW] 59659.68  
 [pI] 5.84  
 35 [BLOCKS] PRO0211G  
 [BLOCKS] BL00288C Tissue inhibitors of metalloproteinases  
 proteins  
 [BLOCKS] PRO0436A  
 [KW] TRANSMEMBRANE 2  
 40 [KW] LOW\_COMPLEXITY 8.15 %

45 SEQ MLDHKDLEAEIHPLKNEERKSQENLGNPSKNEQNVKSAPPQSRLSRCRAAAFFLSLFLCL  
 SEG .....xxxxxxxxxxxx  
 PRD ccchhhhhhhhhcc  
 MEM .....MMMMMMM

50 SEQ FVVVFVVSFVIPCPDRPASQRMWRIDYSAAVIYD FLAVDDINGDRIQDVLFYKNTNSSNN  
 SEG xxxxxxxxxxxx.....  
 PRD hhhhhhhhhccccccccccccchhhhhhhchhhhhhhhhccccccccchhhhhhhcccccccccc  
 MEM MMMMMMMMMM.....

55 SEQ FSRSCVDEGFSSPCTFAAAVSGANGSTLWERPVAQDVALVECAVPQPRGSEAPSACILVG  
 SEG .....  
 PRD cchhhhhhhccccccccccccceeeec  
 MEM .....

SEQ RPSSFIAVNLFTGETLWNHSSSFSGNASILSPLLQVPDVG DGAPDLLVLTQERE EVSGH

35

(No Pfam data available for DKFZphamy2\_11d2.3)

DKFZphamy2\_11n4

-----

5 group: nucleic acid management

DKFZphamy2\_11n4 encodes a novel 1091 amino acid protein with similarity to RAD18 of *Schizosaccharomyces pombe* and YLR383w of *Saccharomyces cerevisiae*.

10

The novel protein contains a ATP/GTP-binding site motif A (P-loop). It has similarity to RAD18 acts in a DNA repair pathway for removal of UV-induced DNA damage. YLR383w of *Saccharomyces cerevisiae* is a recombination repair protein.

15

The new protein can find application in modulation of DNA-repair and as a new tool for manipulation of nucleic acids.

similarity to RAD18 (*Schizosaccharomyces pombe*)

20

comment on P53692:

FUNCTION: ACTS IN A DNA REPAIR PATHWAY FOR REMOVAL OF UV-INDUCED DNA DAMAGE THAT IS DISTINCT FROM CLASSICAL NUCLEOTIDE EXCISION REPAIR AND IN REPAIR OF IONIZING RADIATION DAMAGE.

25

Sequenced by EMBL

Locus: /map="2"

30

Insert length: 3679 bp

Poly A stretch at pos. 3646, polyadenylation signal at pos. 3620

35

```

1  ACCGCGGTGG GCGCCGGGGC TCCCGGGAAT CTACCTTCTC CTGCGGCCGG
51 CACGCGGTTC CCAGGGGGCC AGCGGCGGTC AGCCGAGGTC GAGACGCCCC
101 CAGGGTGGCC TTAGCGGCCG GTCGTACCAC GGCAGCCCCG CCGATCAGGT
151 TCCTTTGGGA GACTTCGACT TGTTGGCGAA ATGAACCGGA GAAGAATCCC
201 AATTGGGAAT TGCGGAAAAC AGGACTCTAG GGTAGAGAAA GGTGTAGAA
251 CCAATAGGGT TTGAGACCTG ATGGCCAAAA GAAAGGAAGA AAATTTTTC
40 301 TCTCCTAAAA ATGCCAAAAG GCCAAGACAA GAAGAATTGG AGGATTTTGA
351 TAAAGATGGT GACGAAGACG AATGTAAAGG TACTACTTTG ACTGCAGCAG
401 AAGTTGGAAT AATTGAGAGT ATTCACTAA AAAACTTCAT GTGTCAATTCA
451 ATGCTTGGAC CTTTAAAGTT TGGTTCTAAT GTCAACTTTG TTGTTGGCAA
501 CAATGGAAGT GGGAAAGAGTG CAGTACTCAC AGCTCTCATA GTCGGTCTTG
45 551 GTGGAAGAGC AGTTGCTACT AATAGAGGAT CCTCTTTAAA AGGTTTTGTG
601 AAAGATGGAC AGAACTCTGC AGATATCTCA ATAACATTGA GGAACAGAGG
651 AGATGATGCC TTTAAAGCCA GTGTGTATGG TAACTCTATA CTTATACAGC
701 AACACATCAG CATAGATGGA AGTCGATCTT ATAAACTTAA AAGTGCAACA
751 GGCTCCGTGG TTTCCACGAG GAAAGAAGAG CTGATTGCAA TTCTTGATCA
50 801 TTTTAACATC CAGGTGGATA ATCCAGTTTC TGTTTTAACA CAAGAAATGA
851 GCAAGCAGTT CTTACAGTCT AAAAATGAAG GAGACAAATA CAAATTCCTC
901 ATGAAAGCAA CGCAACTTGA ACAGATGAAG GAAGATTATT CATACATTAT
951 GGAAACGAAA GAAAGAACAA AGGAGCAGAT ACATCAAGGA GAAGAGCGGC
1001 TTA CTGAACT AAAGCGCCAG TGTGTAGAGA AAGAGGAACG TTTTCAAAGT
55 1051 ATTGCTGGTT TAAGTACAAT GAAGACTAAT TTAGAGTCCT TGAAACATGA
1101 AATGGCTTGG GCAGTGGTCA ATGAAATTGA AAAACAATTG AATGCCATCA
1151 GAGATAATAT CAAAATTGGA GAAGATCGTG CTGCTAGACT TGACAGGAAA
1201 ATGGAAGAAC AGCAGGTCAG ACTTAATGAG GCAGAACAAA AGTACAAGGA

```

1251	TATTCAAGAC	AAACTAGAAA	AGATTAGTGA	AGAGACAAAT	GCACGAGCAC
1301	CAGAATGTAT	GGCATTGAAA	GCAGATGTTG	TTGCTAAGAA	AAGGGCCTAT
1351	AATGAAGCTG	AGGTTTTATA	TAACCGATCC	TTAAACGAAT	ATAAAGCATT
1401	AAAGAAAAGAT	GATGAGCAGC	TTTGTAAACG	AATTGAAGAG	CTGAAAAAAA
5 1451	GTACTGACCA	ATCTTTGGAA	CCTGAACGGT	TGGAAAGACA	AAAAAAAAATA
1501	TCTTGGTTAA	AAGAGAGAGT	AAAGGCCCTT	CAAAATCAAG	AAAATTTCAGT
1551	CAATCAAGAG	ATCGAACAGT	TTCAGCAAGC	CATAGAAAAG	GACAAAGAAG
1601	AACATGGCAA	AATTAAGAGA	GAAGAATTAG	ATGTGAAGCA	TGCACTGAGC
1651	TACAATCAGA	GGCAACTGAA	AGAATTGAAA	GATAGTAAAA	CTGATCGACT
10 1701	CAAAAGATTT	GGCCCTAATG	TTCCAGCTCT	TCTTGAAGCC	ATAGATGATG
1751	CTTATAGACA	AGGACATTTT	ACCTATAAAC	CTGTAGGCCC	TTTAGGAGCT
1801	TGCATTTCATC	TTCGGGACCC	AGAACTTGCT	TTGGCTATTG	AATCTTGCTT
1851	AAAAGGGCTT	CTGCAGGCCT	ATTGTTGCCA	TAATCATGCT	GATGAAAGGG
1901	TCCTTCAGGC	ACTCATGAAA	AGGTTTTATT	TACCAGGGAC	CTCACGGCCA
15 1951	CCGATAATAG	TTTCTGAGTT	TCGGAATGAG	ATATATGATG	TAAGACACAG
2001	AGCTGCTTAT	CATCCAGACT	TTCCAACAGT	TCTGACAGCT	TTAGAAATAG
2051	ATAATGCGGT	TGTGGCAAAAT	AGCCTAATTG	ACATGAGAGG	CATAGAGACA
2101	GTGCTACTAA	TCAAAAATAA	TTCTGTAGCT	CGTGCAGTAA	TGCAGTCCCA
2151	AAAGCCACCC	AAAAATTGTA	GAGAAGCTTT	TACTGCTGAT	GGTGATCAAG
20 2201	TTTTTGCAGG	ACGTTATTAT	TCATCTGAAA	ATACAAGACC	TAAGTTCCTA
2251	AGCAGAGATG	TGGATTCTGA	AATAAGTGAC	TTGGAGAATG	AGGTTGAAAA
2301	TAAGACGGCC	CAGATATTAA	ATCTTCAGCA	ACATTTATCT	GCCCTTGAAA
2351	AAGATATTAA	ACACAATGAG	GAACCTCTTA	AAAGGTGCCA	ACTACATTAT
2401	AAAGAACTAA	AGATGAAAAAT	AAGAAAAAAT	ATTTCTGAAA	TTCGGGAACT
25 2451	TGAGAACATA	GAAGAACACC	AGTCTGTAGA	TATTGCAACT	TTGGAAGATG
2501	AAGCTCAGGA	AAATAAAAAGC	AAAATGAAAA	TGGTTGAGGA	ACATATGGAG
2551	CAACAAAAAG	AAAATATGGA	GCATCTTAAA	AGTCTGAAAA	TAGAAGCAGA
2601	AAATAAGTAT	GATGCAATTA	AATTCAAAAT	TAATCAACTA	TCGGAGCTAG
2651	CAGACCCACT	TAAGGATGAA	TTAAACCTTG	CTGATTCTGA	AGTGGATAAC
30 2701	CAAAAACGAG	GGAAACGACA	TTATGAAGAA	AAACAAAAAG	AACACTTGGA
2751	TACCTTAAAT	AAAAAGAAAC	GAGAACTGGA	TATGAAAGAG	AAAGAACTAG
2801	AGGAGAAAAT	GTCACAAGCA	AGACAAATCT	GCCCAGAGCG	TATAGAAGTA
2851	GAAAAATCTG	CATCAATTCT	GGACAAAGAA	ATTAATCGAT	TAAGGCAGAA
2901	GATACAGGCA	GAACATGCTA	GTCATGGAGA	TCGAGAGGAA	ATAATGAGGC
35 2951	AGTACCAAGA	AGCAAGAGAG	ACCTATCTTG	ATCTGGATAG	TAAAGTGAGG
3001	ACTTTAAAAA	AGTTTATTAA	ATTACTGGGA	GAAATCATGG	AGCACAGATT
3051	CAAGACATAT	CAACAATTTA	GAAGGTGTTT	GACTTTACGA	TGCAAAATTAT
3101	ACTTTGACAA	CTTACTATCT	CAGCGGGCCT	ATTGTGGAAA	AATGAATTTT
3151	GACCACAAGA	ATGAAACTCT	AAGTATATCA	GTTCAAGCCTG	GAGAAGGAAA
40 3201	TAAAGCTGCT	TTCAATGACA	TGAGAGCCTT	GTCTGGAGGT	GAACGTTCTT
3251	TCTCCACAGT	GTGTTTTATT	CTTTCCTGT	GGTCCATCGC	AGAATCTCCT
3301	TTGAGATGCC	TGGATGAATT	TGATGTCTAC	ATGGATATGG	TTAATAGGAG
3351	AATTGCCATG	GACTTGATAC	TGAAGATGGC	AGATTCCCAG	CGTTTTAGAC
3401	AGTTTATCTT	GCTCACACCT	CAAAGCATGA	GTTCACTTCC	ATCCAGTAAA
45 3451	CTGATAAGAA	TTCTCCGAAT	GTCTGATCCT	GAAAGAGGAC	AAACTACATT
3501	GCCTTTCAGA	CCTGTGACTC	AAGAAGAAGA	TGATGACCAA	AGGTGATTTG
3551	TAACTTAACA	TGCCTTGTCC	TGATGTTGAA	GGATTTGTGA	AGGGAAAAAA
3601	AATTCTGGAC	TCTTTGATAT	AATAAAATGA	GACTGGAGGC	ATTCTGAAAA
3651	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA		

## BLAST Results

-----

55 No BLAST result

Medline entries

96069417:

5 Lehmann AR, Walicka M, Griffiths DJ, Murray JM, Watts FZ,  
 McCready S,  
 Carr AM.: The rad18 gene of Schizosaccharomyces pombe defines a  
 new subgroup of the SMC superfamily involved in DNA  
 repair. Mol Cell Biol 1995 Dec;15(12):7067-80

10 99380167:

15 Mengiste T, Revenkova E, Bechtold N, Paszkowski J.: An SMC-like  
 protein  
 is required for efficient homologous  
 recombination in Arabidopsis. EMBO J 1999 Aug 16;18(16):4505-12

20 Peptide information for frame 1  
 -----

ORF from 271 bp to 3543 bp; peptide length: 1091

Category: similarity to known protein

Classification: Nucleic acid management

25 Prosite motifs: RGD (126-128)

ATP\_GTP\_A (76-83)

30	1	MAKRKEENFS	SPKNAKRPRQ	EELEDFDKDG	DEDECKGTTL	TAAEVGIIES
	51	IHLKNFMCHS	MLGPFKFGSN	VNFVVGNGGS	GKSAVLTALI	VGLGGRAVAT
	101	NRGSSLKGFV	KDGQNSADIS	ITLRNRGDDA	FKASVYGNSI	LIQQHISIDG
	151	SRSYKLKSAT	GSVVSTRKEE	LIAILDHFNI	QVDNPVSVLT	QEMSKQFLQS
	201	KNEGDKYKFF	MKATQLEQMK	EDYSYIMETK	ERTKEQIHQG	EERLTELEKRQ
	251	CVEKEERFQS	IAGLSTMKTN	LESLKHEMAW	AVVNEIEKQL	NAIRDNIKIG
35	301	EDRAARLDRK	MEEQQVRLNE	AEQKYKDIQD	KLEKISEETN	ARAPECMALK
	351	ADVVAKKRAY	NEAEVLYNRS	LNEYKALKKD	DEQLCKRIEE	LKKSTDQSLE
	401	PERLERQKKI	SWLKERVKAF	QNGENSVNQE	IEQFQQAIEK	DKEEHGKIKR
	451	EELDVKHALS	YNQRQLKELK	DSKTDRCLKRF	GNVPALLEA	IDDAYRQGHF
	501	TYKPVGPLGA	CIHLRDPELA	LAIESCLKGL	LQAYCCHNHA	DERVLQALMK
40	551	RFYLPGTSRP	PIIVSEFRNE	IYDVRHRAAY	HPDFPTVLTA	LEIDNAVVAN
	601	SLIDMRGIET	VLLIKNNSVA	RAVMQSQKPP	KNCREAFTAD	GDQVFAGRYY
	651	SSENTRPKFL	SRDQDSEISD	LENEVENKTA	QILNLQQHLS	ALEKDIKHNE
	701	ELLKRCQLHY	KELKMKIRKN	ISEIRELENI	EEHQSVDIAT	LEDEAQENKS
	751	KMKMVEEHME	QQKENMEHLK	SLKIEAENKY	DAIKFKINQL	SELADPLKDE
45	801	LNLADSEVDN	QKRGKRHYEE	KQKEHLDTLN	KKKRELDMEKE	KELEEKMSQA
	851	RQICPERIEV	EKSASILDKE	INRLRQKIQA	EHASHGDREE	IMRQYQEAARE
	901	TYLDLDSKVR	TLKKFIKLLG	EIMEHRFKTY	QQFRRCLTLR	CKLYFDNLLS
	951	QRAYCGKMN	DKNETLSIS	VQPGEGNKAA	FNDMRALSGG	ERSFSTVCFI
	1001	LSLWSIAESP	FRCLDEFDVY	MDMVNRRIAM	DLILKMADSQ	RFRQFILLTP
50	1051	QSMSSLPSSK	LIRILRMSDP	ERGQTTLPFR	PVTQEEDDDDQ	R

BLASTP hits

55

No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_11n4, frame 1

SWISSPROT:RA18\_SCHPO DNA REPAIR PROTEIN RAD18., N = 1, Score = 1021, P = 5.2e-103

5

PIR:S51470 hypothetical protein YLR383w - yeast (Saccharomyces cerevisiae), N = 1, Score = 823, P = 5e-82

10 >SWISSPROT:RA18\_SCHPO DNA REPAIR PROTEIN RAD18.  
Length = 1,140

## HSPs:

15 Score = 1021 (153.2 bits), Expect = 5.2e-103, P = 5.2e-103  
Identities = 315/1091 (28%), Positives = 540/1091 (49%)

Query: 2 AKRKEENFSSPKNAKRPRQEELED--DKDGDDEDECKGTTLTAAE----  
VGIIIESIHLKN 55

20 A R ++N ++ + +E ++DG+ D T T +

VG+IE IHL N

Sbjct: 45

ASRNQDNRPERQSRLEQSSSLIEQVRGNEDGENDVLNQTRETNNSFQNRVGVIECIHLVN 104

25 Query: 56  
FMCHSMLGPXXXXXXXXXXXXXXXXXXXXAVLTALIVGLGGRVATNRGSSLKGFVKDGQN 115  
FMCH L A+LT L + LG +A TNR ++K

VK G+N

Sbjct: 105 FMCHDSL-

30 KINFGPRINFGVHNGSGKSAILTGLTICLGAKASNTNRAPNMKSLVKQGKN 163

Query: 116  
SADISITLRNRGDDAFKASVYGNISILIQQHISIDGSRYSYKLKSATGSVVSTRKEELIAIL 175  
A IS+T+ NRG +A++ +YG SI I++ I +GS Y+L+S

35 G+V+ST+++EL I

Sbjct: 164

YARISVTISNRGFAYQPEIYGKSITIERTIRREGSSEYRLRSFNGTVISTKRDELNDNIC 223

Query: 176  
40 DHFNIQVDNPVSVLTQEMSKQFLQSKNEGDKYKFFMKATQLEQMKEDYSYIMETKERTKE 235  
DH +Q+DNP+++LTQ+ ++QFL + + +KY+ FMK QL+Q++E+YS I

++ TK

Sbjct: 224

DHMGLQIDNPMNILTQDTARQFLGNSSPKEYQLFMKGIQLKQLEENYSYLIEQSLINTKN 283

45

Query: 236  
QIHQGEERLTTELKRQCVKEERFQSIAGLSTMKTNLESLKHEMAWAVVNEIEKQLNAIRD 295  
+ + ++ L ++ E + ++ + LE K EM WA V

E+EK+L

50 Sbjct: 284

VLGNKKTGVSYLAKKEEYKLLWEQSRATENLHNLLEQKKGEMVWAQVVEVEKEL----- 338

Query: 296 NIKIGEDRAARLDRKMEEQQVRLNEAEQKYKDIQDKLEKISEETNARAP-  
ECMALKADV 354

55 + E + K+ E + L DI K+ EE RA E

K+

Sbjct: 339 --LLAEKEFQHAEVKLSEAKENLESIVTNQSDIDGKISS-  
KEEVIGRAKGETDTTKSKFE 395



Query: 355  
AKKRAYNEAEVLYNRSLENEYKALKKKDDDEQLCKRIEELKKSTDQSLERLERQKKISWLK 414  
+ ++ Y +N+ K+D + I K D E ER

5 ++ +  
Sbjct: 396 DIVKTFDG----YRSEMNDVDIQRDIQN---  
SINAAKSCLDVYREQLNTERARENNLGG 448

Query: 415 ERVKAFQNNQENSVDNQEIEQF-QQAIEKDKE-----EHG----  
10 KIKREELDVKHALS 460  
+++ N+ N++ +EI +Q +E + + E G + ++  
+ + +S  
Sbjct: 449  
SQIEKRANESNNLQREIADLSEQIVELESKRNDLHSALLEMGGNLTSLLTKKDSIANKIS 508

15 Query: 461  
YNQRQLKELKDSKTDRLKRFGNVPALLEAIDDAYRQGHFTYKPVGPLGACIHLRDPELA 520  
LK L+D + D++ FG N+P LL+ I R+ F + P GP+G +  
+++ +  
20 Sbjct: 509 DQSEHLKVLEDVQRDKVSAFGKNMPQLLKLIT---  
RETRFQHPKGPMPGKMYMTVKEQKWH 565

Query: 521  
25 LAIESCLKGLLQAYCCHNHADERVLQALMKRFYLPGTSRPPIIVSEFRNEIYDVRHRAAY 580  
L IE L ++ + +H D+ +L+ LM++ T ++V +  
YD ++  
Sbjct: 566 LIIERILGNVINGFIVRSHHDQLILKELMRQSNCHAT-----VVVGK-----  
YDPFDYSSG 616

30 Query: 581 HPD--  
FPTVLTALEIDNAVANSIDMRGIETVLLIKNNSVARAVMQSQKPPKNCREAFT 638  
PD +PTVL ++ D+ V ++LI+ GIE +LLI++ A A M+ +  
N + +  
Sbjct: 617 EPDSQYPTVLKIIKFDDDEVLHTLINHLGIEKMLLIEDRREAEAYMK--  
35 RGIANVTQCYA 674

Query: 639 ADG-DQVFAGRYSSSENTR--PKFLSRDQDSEI---  
SDLENEVENKTAQILNLQQLHSAL 692  
D ++ + R S++ + K + I S E E K L

40 Q + ++  
Sbjct: 675  
LDPRNRGYGFRIVSTQRSSGISKVTPWNRPPRIGFSSSTSIEAEKKILDDLKKQYNFASN 734

Query: 693 E-KDIKHNEELLKRCQLHYKELKMKIRKNIS-EIRELENIEEHQ-SV-D---  
45 IATLEDEA 745  
+ + K + KR + E I+K I + RE+ ++E + SV D  
I TLE  
Sbjct: 735  
QLNEAKIEQAKFKRDEQLLVEKIEGICKRILLKRREVNSLESQELSVLDTEKIQTLERRI 794

50 Query: 746 QENKSKMKMVEEHMEQQKENMEH-  
LKSLKIEAENKYDAIKFKINQLSELADPLKDELN-L 803  
E + +++ ++ K N EH ++ + + + KI ++  
L+ EL+ L

55 Sbjct: 795 SETEKELESYAGQLQDAK-  
NEEHRIRDNRPRVIEEIRIYREKIQTETQRLSSLQTELSRL 853

Query: 804

ADSEVDNQRGKRHYEEKQKEHLDTLNXXXXXXXXXXXXXXXXXXXXXQARQICPERIEVEKS 863  
D + +++ +RH + + + L ++A C

ER+ V+ S

5 Sbjct: 854 RDEKRNSEVDIERH-RQTVESCTNILREKEAKKVQCAQVVADYTAKANTRC-  
ERVPVQLS 911

Query: 864 ASILDKEINRLRQKIQAESHASHG-

DREEIMRQYQEAARETYLDLDSKVRTLKKFIKLLGEI 922

10 + LD EI RL+ +I G E+ Y A+E + V L +

++ L E

Sbjct: 912

PAELDNEIERLQMQIAEWRNRTGVSVEQAAEDYLNAGEKHDQAKVLVARLTQLLQALEET 971

15 Query: 923

MEHRFKTYQQRFRCLTLRCKLYFDNLLSQRAYCGKMNFDHKNETLSISVQPGEGNKA-AF 981

+ R + + +FR+ +TLR K F+ LSQR + GK+ H+ E L V P

N A A

Sbjct: 972

20 LRRRNEMWTFRKLITLRTKELFELYLSQRNFTGKLVIKHQEEFLEPRVYPANRNLATAH 1031

Query: 982 N-----

DMRALSGGERSFSTVCFILSLWSIAESPFRCLEFDVYMDMVNRRIAMDIL 1034

N ++ LSGGE+SF+T+C +LS+W P RCLDEFDV+MD VNR

25 +++ +++

Sbjct: 1032

NRHEKSKVSQGLSGGEKSFATICMLLSIWEAMSCPLRCLDEFDVMDAVNRLVSIKMMV 1091

Query: 1035 KMADSQRFRQFILLTPQSMSSLPSSKLIRILRMSDPERGQTTLP 1078

30 A +QFI +TPQ M + K + + R+SDP + LP

Sbjct: 1092 DSAKDSSDKQFIFITPQDMGQIGLDKDVVVFRLSDPVVSSSALP 1135

Pedant information for DKFZphamy2\_11n4, frame 1

35 -----

## Report for DKFZphamy2\_11n4.1

40 [LENGTH] 1091

[MW] 126326.13

[pI] 6.57

[HOMOL] SWISSPROT:RA18\_SCHPO DNA REPAIR PROTEIN RAD18. 1e-109

45 [FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YLR383w] 1e-88

[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL058w] 3e-16

50 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YDL058w] 3e-16

[FUNCAT] 09.13 biogenesis of chromosome structure [S. cerevisiae, YLR086w] 2e-14

[FUNCAT] 1 genome replication, transcription, recombination and repair [M. jannaschii, MJ1643] 3e-14

55 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YIL149c] 1e-12

[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YDR356w] 8e-12

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 55
- [FUNCAT] 09.10 nuclear biogenesis [S. cerevisiae, YDR356w] 8e-12  
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YFL008w] 3e-11  
 [FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision repair) [S. cerevisiae, YKR095w] 2e-09  
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YOR216c] 5e-09  
 [FUNCAT] 03.25 cytokinesis [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 8e-08  
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 8e-08  
 [FUNCAT] 08.22 cytoskeleton-dependent transport [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 8e-08  
 [FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation, palmitoylation, farnesylation and processing) [S. cerevisiae, YKL201c] 2e-07  
 [FUNCAT] 03.13 meiosis [S. cerevisiae, YDR285w] 4e-07  
 [FUNCAT] 30.13 organization of chromosome structure [S. cerevisiae, YDR285w] 4e-07  
 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YJR134c] 7e-07  
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YPR141c] 7e-07  
 [FUNCAT] 30.05 organization of centrosome [S. cerevisiae, YPR141c] 7e-07  
 [FUNCAT] 11.01 stress response [S. cerevisiae, YPR141c] 7e-07  
 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YPR141c] 7e-07  
 [FUNCAT] r general function prediction [H. influenzae, HI0756] 1e-06  
 [FUNCAT] 10.05.99 other pheromone response activities [S. cerevisiae, YHR158c] 2e-06  
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YAL035w] 3e-04  
 [FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YER008c] 4e-04  
 [FUNCAT] 08.16 extracellular transport [S. cerevisiae, YER008c] 4e-04  
 [FUNCAT] 09.04 biogenesis of cytoskeleton [S. cerevisiae, YKL179c] 7e-04  
 [FUNCAT] 03.22.01 cell cycle check point proteins [S. cerevisiae, YGL086w] 7e-04  
 [FUNCAT] 08.01 nuclear transport [S. cerevisiae, YDL207w] 0.001  
 [FUNCAT] 04.07 rna transport [S. cerevisiae, YDL207w] 0.001  
 [BLOCKS] BL00326C Tropomyosins proteins  
 [BLOCKS] PR010048  
 [BLOCKS] BL00121A Colipase proteins  
 [BLOCKS] PF00580A  
 [SCOP] d2tmab\_1.105.4.1.1 Tropomyosin [rabbit (Oryctolagus cuniculus)] 3e-06  
 [EC] 3.6.1.32 Myosin ATPase 9e-20  
 [PIRKW] phosphotransferase 9e-16  
 [PIRKW] nucleus 2e-10  
 [PIRKW] blocked amino end 2e-07  
 [PIRKW] citrulline 2e-10  
 [PIRKW] tandem repeat 9e-20  
 [PIRKW] heterodimer 3e-11

	[[PIRKW]]	endocytosis 2e-13
	[[PIRKW]]	heart 9e-20
	[[PIRKW]]	polymorphism 1e-10
	[[PIRKW]]	serine/threonine-specific protein kinase 9e-16
5	[[PIRKW]]	transmembrane protein 8e-15
	[[PIRKW]]	zinc finger 2e-13
	[[PIRKW]]	metal binding 2e-13
	[[PIRKW]]	DNA binding 2e-06
	[[PIRKW]]	muscle contraction 9e-20
10	[[PIRKW]]	acetylated amino end 3e-13
	[[PIRKW]]	actin binding 9e-20
	[[PIRKW]]	mitosis 8e-10
	[[PIRKW]]	microtubule binding 3e-09
	[[PIRKW]]	chromosomal protein 3e-11
15	[[PIRKW]]	ATP 9e-20
	[[PIRKW]]	receptor 2e-06
	[[PIRKW]]	thick filament 9e-20
	[[PIRKW]]	phosphoprotein 2e-14
	[[PIRKW]]	glycoprotein 1e-10
20	[[PIRKW]]	skeletal muscle 1e-18
	[[PIRKW]]	calcium binding 2e-10
	[[PIRKW]]	alternative splicing 3e-12
	[[PIRKW]]	DNA condensation 3e-11
	[[PIRKW]]	P-loop 9e-20
25	[[PIRKW]]	coiled coil 9e-20
	[[PIRKW]]	heptad repeat 1e-10
	[[PIRKW]]	methylated amino acid 9e-20
	[[PIRKW]]	basement membrane 1e-10
	[[PIRKW]]	immunoglobulin receptor 4e-09
30	[[PIRKW]]	peripheral membrane protein 2e-13
	[[PIRKW]]	cardiac muscle 9e-20
	[[PIRKW]]	extracellular matrix 1e-10
	[[PIRKW]]	hydrolase 9e-20
	[[PIRKW]]	microtubule 2e-10
35	[[PIRKW]]	muscle 2e-14
	[[PIRKW]]	membrane protein 1e-10
	[[PIRKW]]	EF hand 2e-10
	[[PIRKW]]	cell division 8e-10
	[[PIRKW]]	cytoskeleton 1e-13
40	[[PIRKW]]	hair 2e-10
	[[PIRKW]]	calmodulin binding 2e-13
	[[PIRKW]]	Golgi apparatus 6e-08
	[[PIRKW]]	smooth muscle 2e-07
	[[SUPFAM]]	conserved hypothetical P115 protein 4e-26
45	[[SUPFAM]]	myosin heavy chain 9e-20
	[[SUPFAM]]	unassigned Ser/Thr or Tyr-specific protein kinases 9e-16
	[[SUPFAM]]	centromere protein E 3e-09
	[[SUPFAM]]	calmodulin repeat homology 2e-10
50	[[SUPFAM]]	alpha-actinin actin-binding domain homology 7e-07
	[[SUPFAM]]	myosin motor domain homology 9e-20
	[[SUPFAM]]	tropomyosin 5e-08
	[[SUPFAM]]	plectin 7e-07
	[[SUPFAM]]	pleckstrin repeat homology 3e-09
55	[[SUPFAM]]	trichohyalin 2e-10
	[[SUPFAM]]	hypothetical protein MJ1322 2e-06
	[[SUPFAM]]	ribosomal protein S10 homology 7e-07
	[[SUPFAM]]	protein kinase C zinc-binding repeat homology 3e-09

-64-

-65-

SEG .....  
 PRD hhhhhhhhhhhhhhhhhhhhhhhceeeeecccccccccccccccccccccccccccccccccccc  
 COILS .....  
 .....

5

SEQ PVTQEEDDDQR  
 SEG .....  
 PRD chhhhhhccc  
 COILS .....

10

Prosites for DKFZphamy2\_11n4.1

15	PS00016	126->129	RGD	PD0C00016
	PS00017	76->84	ATP_GTP_A	PD0C00017

20

(No Pfam data available for DKFZphamy2\_11n4.1)

DKFZphamy2\_121f19

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5 group: cell structure and motility

DKFZphamy2\_121f19 encodes a novel 251 amino acid protein with high similarity to a Rat ankyrin binding glycoprotein-1 related mRNA.

10 Ankyrin binding glycoproteins play a role in neural cell adhesion and in prosate tumor cell transformation. DKFZphamy2\_121f19.p3 is expressed in brain, uterus and prostate above average.

15 The new protein can find application modulation of cyto skeleton-membrane interactions.

20 similarity to ankyrin binding glycoprotein-1 related mRNA (Rattus norvegicus)

Sequenced by DKFZ

Locus: /map="1"

25 Insert length: 1498 bp

Poly A stretch at pos. 1479, polyadenylation signal at pos. 1460

```

30      1 CGGCACCTTC GCCGGCGCCC TCGCCCACCC CAGCCCCGCC CCAGAAGGAG
      51 CAGCCCCCCG CGGAGACCCC TACAGACGCT GCTGTCTTGA CCTCACCCCC
     101 AGCCCCCTGCT CCCCCGGTGA CCCCTAGCAA ACCAATGGCC GGCACCACAG
     151 ACCGAGAAGA AGCCACTCGG CTCTTGGCTG AGAAGCGGCG CCAGGCCCGG
     201 GAGCAGCGGG AGCGCGAGGA GCAGGAGCGG AGGCTGCAGG CAGAAAGGGA
35     251 CAAGCGAATG CGAGAGGAGC AGCTGGCACG GGAGGCCGAG GCCCGGGCGG
     301 AGCGGGAGGC GGAGGCCCGG AGGCGGGAGG AGCAGGAGGC ACGAGAGAAG
     351 GCGCAGGCCG AGCAGGAGGA GCAGGAGCGG CTGCAGAAGC AGAAAGAGGA
     401 GGCCGAAGCT CGGTCGCGGG AAGAGGCGGA GCGGCAGCGT CTGGAGCGGG
     451 AAAAGCACTT CCAGCAGCAG GAGCAAGAGC GGCAAGAGCG CAGAAAGCGT
40     501 CTGGAGGAGA TCATGAAGAG GACTCGGAAG TCAGAAAGTTT CTGAAACCAA
     551 GAAGCAGGAC AGCAAGGAGG CCAACGCCAA CGGTTCCAGC CCAGAGCCTG
     601 TGAAGCTGT GGAGGCTCGG TCCCCAGGGC TGCAGAAGGA GGCTGTGCAG
     651 AAAGAGGAGC CCATCCCACA GGAGCCTCAG TGGAGTCTCC CAAGCAAGGA
     701 GTTGCCAGCG TCCCTGGTGA ATGGCCTGCA GCCTCTCCCA GCACACCGA
45     751 AGAATGGCTT CTCCACCAAC GGACCCTCTG GGGACAAGAG TCTGAGCCGA
     801 ACACCAGAGA CACTCCTGCC CTTTGCAGAG GCAGAAGCCT TCCTCAAGAA
     851 AGCTGTGGTG CAGTCCCCGC AGGTACAGAG AGTCCTTTAA GAGGGTTTGC
     901 CTTGGATCCG GGCACAGTTG TGAGGGCTCC TCTGCATCAC CTACCAGGAT
     951 GTCTGGAGGA GAAAAAGACA GAACAAAGAT GGAAGTGGCC TGGGCCCTG
50    1001 GGGGTGGGTC CTCTCTGTTG TTTTAAATCT GCACCTTATA GACTGATGTC
     1051 TCTTTGGCCG GAGCCAGATC TGCCCCCTAG TGCATTCTGT TGCTCGCACG
     1101 CGCAGACATC CCTTCTCCCC CATAACACA TATACTCA CAGCCTCTCT
     1151 GGCCTCTTCC CTTGGGGAGG GGCCACCTGT AGTATTTGCC TTGATTTGGT
     1201 GGGGTACAGT GGATGTGAAT ACTGTAAATA GCTTGTGCTC AGACTCCTCT
55    1251 GCGTGGAGAG GGTGGGTGCA GGAGGCAGAC CCTCCCCCA AAGCCCCCTG
     1301 GGGAGATCTT CCTCTCTCTA TTTAACTGTA ACTGAGGGGG ATCCCAGGTC
     1351 TGGGGATGGG GGACACCTTG GGCCACAGGA TACTGGTTGC TTCAGGGGTA
     1401 CCCATGCCCC CTGCCCTCGC CTGGAATCAG TGTTACTGCA TCTGATTAAG

```



1451 TGTCTCCAGA AATAAAGAAT AATTCTGCCA AAAAAAAAAA AAAAAAAAAA

# BLAST Results

5

No BLAST result

10

## Medline entries

No Medline entry

15

## Peptide information for frame 3

20 ORF from 135 bp to 887 bp; peptide length: 251

Category: putative protein

Classification: Cell signaling/communication

25 1 MAGTTDREEA TRLLAEKRRQ AREQREREEQ ERRLQAERDK RMREEQLARE  
 51 AEARAEREAE ARRREEQEAR EKAQAEQEEQ ERLQKQKEEA EARSREEAER  
 101 QRLEREKHFQ QQEQRQERR KRLEEIMKRT RKSEVSETKK QDSKEANANG  
 151 SSPEPVKAVE ARSPGLQKEA VQKEEPIQE PQWSLPSKEL PASLVNGLQP  
 201 LPAHQENGFS TNGPSGDKSL SRTPETLLPF AEAEAFLLKA VVQSPQVTEV  
 251 L

30

## BLASTP hits

35 No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_121f19, frame 3

No Alert BLASTP hits found

40

Pedant information for DKFZphamy2\_121f19, frame 3

## Report for DKFZphamy2\_121f19.3

45

50 [LENGTH] 295  
 [MW] 33517.96  
 [pI] 5.61  
 [HOMOL] TREMBLNEW:AB033013\_1 gene: "KIAA1187"; product:  
 "KIAA1187 protein"; Homo sapiens mRNA for KIAA1187 protein,  
 partial cds. 1e-64  
 [BLOCKS] PF01140  
 [BLOCKS] BL004120 Neuromodulin (GAP-43) proteins  
 55 [BLOCKS] BL00826C  
 [BLOCKS] BL00422C Granins proteins  
 [BLOCKS] PR00167C  
 [BLOCKS] PF00992A

40 (No Prosite data available for DKFZphamy2\_121f19.3)  
(No Pfam data available for DKFZphamy2\_121f19.3)

DKFZphamy2\_121m2

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5 group: cell cycle

DKFZphamy2\_121m2 encodes a novel 480 amino acid protein with similarity to human PA2b-T2 protein.

10 PA2b-T2 is a p53 responsive gene. The protein is predominantly expressed in brain, breast and kidney and may represent a potential novel regulator of cellular growth. Isoforms are differentially induced by genotoxic stress (UV, gamma-irradiation and cytotoxic drugs) in a p53-dependent manner.

15 The new protein can find application in modulating cell division and apoptosis pathways.

20 similarity to PA2b nuclear protein isoforms (Homo sapiens)  
probably differential polyadenylation

Sequenced by DKFZ

25 Locus: unknown

Insert length: 3327 bp

30 Poly A stretch at pos. 3306, polyadenylation signal at pos. 3279

```

      1 TCCAGCACCA AAGCGGCCGT TCTCGGATTC CGGAGCGTTC TGGAGCCCCG
      51 AGAGACGCCC CGGGGTTCTA GAAGCTCCCC GGCGGCGCCC AGTCCCGGCT
     101 TCATTGCGGC GTCCCTCCGA AACCCACTCG GGTGCACGGG TCGTCGGCGA
     35 151 GCCGCGACCG GGTCCGTGGCG CGCACCATGA TCGTGGCGGA CTCCGAGTGC
      201 CGCGCAGAGC TCAAGGACTA CCTGCGGTTC GCCCCGGGCG GCGTCGGCGA
      251 CTCGGGCCCC GGAGAGGAGC AGAGGGAGAG CCGGGCTCGG CGAGGCCCTC
      301 GAGGGCCAG CGCCTTCATC CCGTGGAGG AGGTCCTTCG GGAGGGGGCT
      351 GAGAGCCTCG AGCAGCACCT GGGGCTGGAG GCACTGATGT CCTCTGGGCG
     40 401 AGTAGACAAC CTGGCAGTGG TGATGGGCCT GCACCCTGAC TACTTTACCA
      451 GCTTCTGGCG CCTGCACTAC CTGCTGCTGC ACACGGATGG TCCCTTGGCC
      501 AGCTCCTGGC GCCACTACAT TGCCATCATG GCTGCCGCCC GCCATCAGTG
      551 TTCTTACCTG GTAGGCTCCC ACATGGCCGA GTTTCTGCAG ACTGGTGGTG
      601 ACCCTGAGTG GCTGCTGGGC CTCCACCGGG CCCCCGAGAA GCTGCGCAAA
     45 651 CTCAGCGAGA TCAACAAGTT GCTGGCGCAT CGGCCATGGC TCATCACCAA
      701 GGAACACATC CAGGCCTTGC TGAAGACCGG CGAGCACACT TGGTCCCTGG
      751 CCGAGCTCAT TCAGGCTCTG GTCTGTCTCA CCCACTGCCA CTCGCTCTCC
      801 TCCTTCGTGT TTGGCTGTGG CATCCTCCCT GAGGGGGATG CAGATGGCAG
      851 CCCTGCCCCC CAGGCACCTA CACCCCTAG TGAACAGAGC AGCCCCCAA
     50 901 GCAGGGACCC GTTGAACAAC TCTGGGGGCT TTGAGTCTGC CCGCGACGTG
      951 GAGGCGCTGA TGGAGCGCAT GCAGCAGCTG CAGGAGAGCC TGCTGCGGGA
     1001 TGAGGGGACG TCCCAGGAGG AGATGGAGAG CCGCTTTGAG CTGGAGAAGT
     1051 CAGAGAGCCT GCTGGTGACC CCCTCAGCTG ACATCCTGGA GCCCTCTCCA
     1101 CACCCAGACA TGCTGTGCTT TGTGGAAGAC CCTACTTTCG GATATGAGGA
     55 1151 CTTCACCTCG AGAGGGGCTC AGGCACCCCC TACCTTCCGG GCCCAGGATT
     1201 ATACCTGGGA AGACCATGGC TACTCGCTGA TCCAGCGGCT TTACCCTGAG
     1251 GGTGGGCAGC TGCTGGATGA GAAGTTCCAG GCAGCCTATA GCCTCACCTA
     1301 CAATACCATC GCCATGCACA GTGGTGTGGA CACCTCCGTG CTCCGCAGGG

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1351 CCATCTGGAA CTATATCCAC TGCCTCTTTG GCATCAGATA TGATGACTAT  
 1401 GATTATGGGG AGGTGAACCA GCTCCTGGAG CGGAACCTCA AGGTCTATAT  
 1451 CAAGACAGTG GCCTGCTACC CAGAGAAGAC CACCCGAAGA ATGTACAACC  
 1501 TCTTCTGGAG GCACTTCCGC CACTCAGAGA AGGTCCACGT GAACTTGCTG  
 5 1551 CTCCTGGAGG CGCGCATGCA AGCCGCTCTG CTGTACGCCC TCCGTGCCAT  
 1601 CACCCGCTAC ATGACCTGAC TCCTGAGCAG GACCTGGGCC CGGTTCAGCT  
 1651 CCCCACAAGG ACTTCTCTGT CTGGAGACAG CCCAGACCC TTTTGTGTCC  
 1701 CATGCCCACC CTCCCCACGC TGCAGTGGGC TTGTGTGTGA TGTGCAGTCC  
 1751 CGAAGCCACA CCCTCCCTTT TCCTCACTGG AATGGACAGT TCATTGCACT  
 10 1801 GACTCTGGGA TCTCAGCCCT GCTCCTGGGA GCTGGAAGAG CACTTGAGAG  
 1851 TCCTAAGGGA CCACACCCTT CCTCCTTCCC CTGCCCACAG AGGCAGAGGG  
 1901 CACAGGAAAG AAGCCGGGCC AAGCTCGGAA TTAATGTGCC ACAAGTGTG  
 1951 TGGCCTTCCCT GAACTGGGAA GTCCCTGGCT GGCCCCGGG GGAGAGGGGC  
 2001 AAATGCCTCC GGGACTGACA CTCCAGGCAG CTTTGCCTTC TCTCCCCTGT  
 15 2051 CATTTCCAGA TTTTATTACC TCCTACTTGC CATTACCCA TCAATGTGAA  
 2101 AGTCAGGGTC ACAGCTGGTC TGTGTGTCCA GTTCCCTAAA AGCCTGTTCT  
 2151 GTTGGGCAGC CTGAGGCTGT TGCCCGAATC CTAGTTCAGT TTTTGTACTT  
 2201 CCTTTGCCCT TTTTCCCTTT TCTCCATGCT TAATGGTGTG AGGCGTCAGG  
 2251 AGAGAGGCCA AGTACATAAA AAAAAAAAAA AGCAGATTAT CTCTAGAGAG  
 20 2301 TTTGAGCCTT TGCTGGTCAC ATTGCCTTCT GAAGAGGAGG GAGTATTAGA  
 2351 TTATAAATCC TCTTTATTTT GGTCCTTTAT GCTTGAGGTT CCAACCTGGA  
 2401 GCCACAGTGT GTGAGAGGAG GAGGAGAGGG AGAATTCTGT TCTCCCAGAG  
 2451 CTGCACCTGC CTCGCAGAGG CCAGCACCCC ACTCTCCTGC CTCCAGTGGC  
 2501 CCTGCCGCAG ATGTCTCCCA AAAAGTTGAG CCTTTCTAGA TGGCTTAGGT  
 25 2551 GGCACCATGG CTCAGCAGGA GGGGCGGGAG GCACCAGGGT TCTTGTGTTG  
 2601 ACCCTGCCCC TGGGCCATGG CCAGGTGACC ATGGCTACAT TGCCAAACCT  
 2651 CTGACTGCCA CAGCTGCAGA CTGAGAGGGT GGGTCTGAGT CCCCACAATG  
 2701 TCTGAAGCTG CCCCTGGGAT TCTCAGGCCA ACCTGCCAAC AGCAAGCGGA  
 2751 TTTTCTTGCA AGATCAGGGA CCCCATTTCT GCAGCCAGTG TCTCCTGGGT  
 30 2801 GCCTTCTGAG GACTCCCACC CCCATCCAG TATCTCATCT GTCCCCCTCTC  
 2851 CTGGGGCTTA AGTGGGTTGC TTCCAGGCAG AAGCAGCCAA GGACCGATTG  
 2901 CAGGCACCTT CTGTAGCAAA TGA CTGTGAA TTACGACTTC TCTTGCCCTT  
 2951 CTTCTAGCAG TCTGTGCCTC CTCTCTGACC AGTTTGGAGG GCACTGAAGA  
 3001 AAGGCAAGGG CCGTGCTGCT GCTGGGCGGG GCAGGAGAGG AGCCTGGCCA  
 35 3051 GTGTGCCACA TTAAATACCC GTGCAGGCGC GGAGAAGCAA CCGGCACCCC  
 3101 CTTCCGGCCT GAAAGCCCTC CTGCAAGAA GGTGTGCAGG AGAGAAGAGG  
 3151 CCCCGGCATG GGGATCTGGG TTCTAGAGGG CATGTGATGA CTGTAAATGT  
 3201 TCACTGGGTG GGTAGGGAGT GGTATCCAGT GTTCAAGTGC AGAAATCTTT  
 3251 GGCTTTGCTA CCAGTTCCAT ATGATGAGAA ATAAACGTTC GCTGAGGTTT  
 40 3301 TGTTTCATAA AAAAAAAAAA AAAAAA

## BLAST Results

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No BLAST result

## Medline entries

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95024170:

Buckbinder L., Talbott R., Seizinger B.R., Kley N.; Gene regulation by

55 temperature-sensitive p53 mutants: identification of p53 response genes. Proc. Natl. Acad. Sci. U.S.A. 91(22):10640-10644(1994).

9124117:

Velasco-Miguel S, Buckbinder L, Jean P, Gelbert L, Talbott R, Laidlaw

J, Seizinger B, Kley N.; PA26, a novel target of the p53 tumor suppressor and member of the GADD

5 family of DNA damage and growth arrest inducible genes. *Oncogene* 1999

Jan 7;18(1):127-37

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# Peptide information for frame 3

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15 ORF from 177 bp to 1616 bp; peptide length: 480

Category: strong similarity to known protein

Classification: Cell division

20 1 MIVADSECRA ELKDYLRFAP GGVGDSPGGE EQRESRARRG PRGPSAFIPV  
51 EEVLREGAES LEQHLGLEAL MSSGRVDNLA VVMGLHPDYF TSFWRLLHYLL  
101 LHTDGPLASS WRHYIAIMAA ARHQCSYLVG SHMAEFLQTG GDPEWLLGLH  
151 RAPEKLRKLS EINKLLAHRP WLITKEHIQA LLKTGEHTWS LAELIQALVL  
201 LTHCHSLSSF VFGCGILPEG DADGSPAPQA PTPPSEQSSP PSRDPLNNSG  
251 GFESARDVEA LMERMQQLQE SLLRDEGTSQ EEMESRFELE KSESLLVTPS  
25 301 ADILEPSPHP DMLCFVEDPT FGYEDFTRRG AQAPPTFRAQ DYTWEDHGYS  
351 LIQRLYPEGG QLLDEKFQAA YSLTYNTIAM HSGVDTSVLR RAIWNYIHCV  
401 FGIRYDDYDY GEVNQLLERN LKVYIKTVAC YPEKTTRRMV NLFWRHFRHS  
451 EKVHVNLLLL EARMQAALLY ALRAITRYMT

30

# BLASTP hits

No BLASTP hits available

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Alert BLASTP hits for DKFZphamy2\_121m2, frame 3

TREMBL:AF033120\_1 gene: "PA26"; product: "p53 regulated PA26-T2 nuclear

40 protein"; Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26)

mRNA, complete cds., N = 1, Score = 1377, P = 9.7e-141

45 TREMBL:AF033122\_1 gene: "PA26"; product: "non-p53 regulated PA26-T1 nuclear protein";

Homo sapiens non-p53 regulated PA26-T1 nuclear protein (PA26) mRNA, complete cds., N = 1, Score = 1363, P = 3e-139

50 TREMBL:AF033121\_1 gene: "PA26"; product: "p53 regulated PA26-T3 nuclear protein";

Homo sapiens p53 regulated PA26-T3 nuclear protein (PA26)

mRNA, complete cds., N = 1, Score = 1307, P = 2.5e-133

55

>TREMBL:AF033120\_1 gene: "PA26"; product: "p53 regulated PA26-T2 nuclear

protein"; Homo sapiens p53 regulated PA26-T2 nuclear  
 protein (PA26) mRNA,  
 complete cds.  
 Length = 492

5

HSPs:

Score = 1377 (206.6 bits), Expect = 9.7e-141, P = 9.7e-141  
 Identities = 277/471 (58%), Positives = 334/471 (70%)

10

Query: 22 GVGDSPGEEQRESRARRGPR---GPSAFIPVEEVVLRGAESLEQH-  
 LGLEALMSSGRV 76

G G G +Q E R PR GPS FIP +E+L+ G+E + H L

++ + GR+

15

Sbjct: 22  
 GCKQCGGGRDQDEELGIRIPRPLGQGPSRFIPEKEILQVGSEDAQMHALFADSFAALGRL 81

Query: 77  
 DNLAIVVMGLHPDYFTSFWRHLHYLLHTDGPLASSWRHYIAIMAAARHQCSYLVGSHMAEF 136

20

DN+ +VM HP Y SF + + LL DGPL +RHYI

IMAAARHQCSYLV H+ +F

Sbjct: 82  
 DNITLVMVFHPQYLESFLKTQHYLLQMDGPLPLHYRHYIGIMAAARHQCSYLVNLHVND 141

25

Query: 137  
 LQTGGDPEWLLGLHRAPEKLRKLSEINKLLAHRPWLTKEHIQALLKTGEHTWSLAELIQ 196

L GGD+WL GL AP+KL+ L E+NK+LAHRPWLTKEHI+ LLK

EH+WSLAEL+

Sbjct: 142

30

LHVGGDPKWLNGLENAPQKLQNLGELNKVLAHRPWLTKEHIEGLLKAEHSWSLAELVH 201

Query: 197 ALVLLTHCHSLSSSFVFGCGILPEGDADGXXXXXXXXXX-----  
 XXXXXXXXRDPLNNS 249

A+VLLTH HSL+SF FGCGI PE DG

35

P+N++

Sbjct: 202

AVVLLTHYHSLASFTFGCGISPEIHCDDGGHTFRPPSVSNYCICDITNGNHSVDMPVNSA 261

Query: 250 GGF---ESARDVEALMERMQQLQESLLRDEG-  
 TSQEE MESRFELEKSESLLVTPSADILE 305

40

+S +VEALME+M+QLQE RDE SQEEM SRFE+EK ES+ V

S+D E

Sbjct: 262 ENVSVSDSFFEVEALMEKMRQLQEC--

RDEEEASQEE MASRFEIEKRESMFVF-SSDDEE 318

45

Query: 306  
 PSPHPDMLCFVEDPTFGYEDFTRRGAQAPPTFRAQDYTWEDHGYSLIQRLYPEGGQLLDE 365

+P + ED ++GY+DF+R G P TFR QDY WEDHGYSL+

RLYP+ GQL+DE

50

Sbjct: 319 VTPARAVSRHFEDTSYGYKDFSRHGMHVP-  
 TFRVQDYCWEDHGYSLVNRLYPDVGQLIDE 377

Query: 366  
 KFQAAAYSLTYNTIAMHSGVDTSVLRRRAIWNYIHCVFIRYDDYDYGEVNQLLERNLKVYI 425

55

KF AY+LTYNT+AMH

VDTS+LRRRAIWNYIHC+FGIRYDDYDYGE+NQLL+R+ KVYI

Sbjct: 378

KFHIAYNLTYNTMAMHKD VDTSM LRRRAIWNYIHC MFGIRYDDYDYGEINQLLDRSFKVYI 437

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## Report for DKFZphamy2\_121m2.3

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(No Prosite data available for DKFZphamy2\_121m2.3)

(No Pfam data available for DKFZphamy2\_121m2.3)

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5 group: transmembrane protein

DKFZphamy2\_121017 encodes a novel 212 amino acid protein without similarity to known proteins.

10 The novel protein contains 1 transmembrane region.  
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

15 The new protein can find application in studying the expression profile of amygdala-specific genes and as a new marker for amygdala cells.

unknown protein

20 Pedant: TRANSMEMBRANE 1

Sequenced by DKFZ

25 Locus: /map="18b.b cR from top of Chr22 linkage group"

Insert length: 2690 bp

Poly A stretch at pos. 2661, polyadenylation signal at pos. 2634

30  
1 TGCTGGGAAA AGTGA CTGCG ATTCTGAAGA ACCGCTGCCT TGCAAGGTCA  
51 AGGACATTCA GTGGTTGCTG GGGTCCGCAG ACTACTGCCA CCCACTCACC  
101 ATCAACTCTG TTAGCCCAAT TGCCCTGCTG AACAACTGCC TGAATACAGG  
151 CTTTAGGTTT CCCTGGACTC CAGCCAAGGC TGTTTCAGGTG GGACCATGGT  
35 201 GCTCTTTAAG CGTGATCGGA GGAAGACAC ACAGCAGGGC CACCATTCCA  
251 TGAATGGGAG GTGTACAGAT CACTTTCTCT TTGTGCTCAG TTCTCTTCTG  
301 TCTCCAGCAG CTATATTGGT AAGACTAGTA CCTGCCAGGG AGAGGTGCCC  
351 CCAAGTGAAG GGGTACAGTG GCACCTGGGA AAAGGCACCT GGAAGGTTTC  
401 CATGTGGCCC AGCCAGCAT GGAAGCAGGG TGGGAACCTC GCTGTGTGCG  
40 451 CAGCCCTCAC TCTACTCAAG TGGCTTTTTC AGAGCCCTGC CATGTCTGTG  
501 TCAGGCCTGT GCTGCTTCAC ACCCTACAGC TGCCTGGGAA AGGCCGGCCA  
551 CGCTCCCTGT CCACACACTC CCTGTCCACA CACTCCCTGT CCACA ACTGC  
601 AGCCGGGCCC TCTGCCTATG GGCACCCAAT CCAAGCAGCT GCTCCACCTT  
651 TGTTTGGCAT GGTGATTTGT GTTTTTTCTC TTGGTGCTTA TGTGTGTGGG  
45 701 CTTGGGACGA GTGCTGGTAT GCACTTAGGA CCTTCTTGAT AGCTCCCTGC  
751 ACTTTGGAAC ACGGAGCAGA TGAGAGAGGG TCAGGGGCTT GCCCTCCACC  
801 TTGGACTTGG AAGAAGCCCA CATTGGAGAG GTGAGGACCC CATGGTGGCT  
851 CTAGTGGAAG ATACGTTAGT CTCCAGCTAA GGAGGATGAG GCGCAGCCCC  
901 AGAGGGAGAC CTCAGTGATA GGGGATCAGG CTACGAAAGT GGGGGAAGGG  
50 951 AGATGCTTTG TACATATTTT GGGGTTATAA TTTCTCTAAA TTTTAGGAGA  
1001 ACGGGTATTG ATTGATAAAA GGGACAGGCA GTAGTGTTCA ACAGTGCATG  
1051 TGAAGGAAAG TTCTGTTTTT CATGGTTTTG ACATTCTTTG GACTGTATTG  
1101 TGA CTGCTGT CTGGTCCACA TGGTACCCTT TTGGTAAGTA GGCTTCAGTG  
1151 CATACCAGGG TATCACTGGA GATGGGAGTT AGTGAAGGGG TGACTCCCTG  
55 1201 GCCTAGTATA GTGTGACCCT GGGACA ACTT AATGTCTTAA AGCATTTTGG  
1251 TGACTTCTAG GGAATAGCAA AGACCTATTT CATTGTCCCC AGGTAAAGTAT  
1301 GTGATGAGCA ATGAGGAGGA GTGGAAAACA AAACCCAGAA AGTGCGGCAG  
1351 GACCAGCCTG ACGCACACGC TCCTGTTGTC ATGGCAGACA GCCGCCTTGG

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1401 GTGGGCACCA CCCTGGCAGT TCCAGCCTGT AGGGGAGTGA AGGGACATGG
1451 CTGAGCTGGG CATGTGCTGA GGTTGACTTA GGGAAACAAGC CCTGGGATTG
1501 GACAAAAGGG CCCATGCTGC AGCCACTGAC TGGGGGCAGA GCTCTGGGTG
1551 GAAGAGGGAA GAGATCCTAA TGGAGGCGCC TCCATCTGCA ACCACAGTTG
5 1601 TAAGGCTCAT GGCACCTCTG CTTGGAAAGC ACTGGTTTAG GGAATTAGAG
1651 AGGTAGGCAC AAGGTGGGTC TCCTGGGTAA GGGAAAGCAAG AGCAGACTGT
1701 TGGGCCAACA GGAGAAGCTC CCCAGAGTAG GGGAGAAGGT TGGGGTGTAG
1751 GGCCTTCCAC GTGGAACAGA CAGCCCCTGT GTCTCTGTCT CTTGGGGACC
1801 TGAGTTTGGG TGGGGTGGCA GTTGGCACAG CGCAGATGCG GTAGAGATGG
10 1851 GAGGAAACCC AGCTCCTCAC TTCCGTGTGC CTCATGCCTT TGCATACACA
1901 AGCACCAAAC CTACTAGGTC TTCTCATTAC CCATGTAAAC CACATGTTAG
1951 ATAAATTTTT GCAAGTAGAG GAAAGAAGGA AATAAAACAT CACATTTTGG
2001 TGTCTCTCAG GCTTTCCCCC CCAACTATGG TTTCTTTGCT TTTTGTTTTA
2051 ACATAGTTTT GTTGCTGTCT TCTGTAATGA TACAGTTTTG TGCAGCTGTT
15 2101 TTCACTTAGC ATATCGTGGG CATCTCCCCT TATGATTACT AAATATTTTA
2151 TTTTGGAGTG GCTGTGTACT CTCCCATTGA CTAGATGGAC CATTGTGCCA
2201 GTTGCCAATC ACTAATGCTG TTAATACTT TTCAGTTATA AATTGATGAA
2251 TATCTTTGTG CACAGGCTGT TTCCCAATGT CAAGTTATTA GGGTAGACTC
2301 CAGGAGGTGG GATTCTTCAA CTAAAGAATA TGAAAACCTT TGAGGCTTTT
20 2351 ACTACATATT GACAAAATGG TTTCCGGAAA TATTTGTATC CCCTTACACT
2401 GCCACCAGCA AGGATAAACA TGTCCATCTT GCCCGTATTG GGAATTATCA
2451 TCTGGCTAAA TATTTGCTAA TTTGATAATG AAAAAATAGC ATCGTGTTC
2501 AGTTGGCATT TCACTGACTT CTAGCACGGT TGAACATCTT TCATGTGGAG
2551 CGATTGTATT TCCTCCTTTG TGGATTGTCA GTGTCCTTTG CTCTATCTTC
25 2601 TGGGGTCAGA TAAATTTGTA TGAGCTCGGT ATATATTAAA GATATTAACC
2651 TGGTGTGTGT CAAAAA AAAA AAAAAA AAAAAA

```

## BLAST Results

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Entry HS1033E15 from database EMBL:

Human DNA sequence from clone 1033E15 on chromosome 22q13.1-13.2.  
Contains part of a novel gene, ESTs and a GSS.

35 Score = 5919, P = 5.1e-262, identities = 1187/1195

Entry HSN128A12 from database EMBL:

Human DNA sequence from cosmid N128A12 on chromosome 22q12-qter  
contains ESTs, CpG island.

40 Score = 5038, P = 0.0e+00, identities = 1014/1019

Entry HS690346 from database EMBL:

human STS WI-14034.

Score = 1800, P = 1.4e-76, identities = 392/417

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## Medline entries

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No Medline entry

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## Peptide information for frame 1

ORF from 196 bp to 831 bp; peptide length: 212

Category: putative protein  
Classification: no clue

5 1 MVLFKRDRRE DTQQGHSMN GRCTDHFLFV LSSLLSPAAT LVRLVPARER  
51 CPQVKGYSGT WEKAPGRFPC GPAQHGSRVG TLLCRQPSLY SSGFLRALPC  
101 LCQACAASHPTAAWERPATL PVHTLPVHTL PVHNCSRALC LWAPNPSSCS  
151 TFVWHGDLCF FSWCLCVWAW DECWYALRTF LIAPCTLEHG ADERGSACP  
201 PPWTWKKPTL ER

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## BLASTP hits

No BLASTP hits available

15

Alert BLASTP hits for DKFZphamy2\_121017, frame 1

No Alert BLASTP hits found

20

Pedant information for DKFZphamy2\_121017, frame 1

## Report for DKFZphamy2\_121017.1

25

[[LENGTH]] 212  
[[MW]] 23727.55  
[[pI]] 8.73  
[[KW]] TRANSMEMBRANE 1

30

SEQ MVLFKRDRREDTQQGHSMNGRCTDHFLFVLSSLLSPAAILVRLVPARERCPQVKGYSGT  
PRD ccchhhhhccccccccccccccccccccchhhhhhhhccccceeecccccccccccccccccc  
MEM .....MMMMMMMMMMMMMMMM.....

35

SEQ WEKAPGRFPCGPAQHGSRVGTLLCRQPSLYSSGFLRALPCLCQACAASHPTAAWERPATL  
PRD cchhhhhhcccccccccccccc  
MEM .....cc

40

SEQ PVHTLPVHTLPVHNCSRALCLWAPNPSSCSTFVWHGDLFFSWCLCVWAWDECWYALRTF  
PRD ccc  
MEM .....cc

45

SEQ LIAPCTLEHGADERGSACPPPWTKKPTLER  
PRD eeeeecccccccccccccccccccccccccccccccccccccc  
MEM .....cc

50

(No Prosite data available for DKFZphamy2\_121017.1)

(No Pfam data available for DKFZphamy2\_121017.1)

DKFZphamy2\_12d7

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5 group: signal transduction

DKFZphamy2\_12d7 encodes a novel 552 amino acid protein, which is a so far unknown alternative spliced form of disks large homolog DLG2.

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It seems to be predominantly expressed in the retina, germ cells and brain. It contains a SH3-domain and a guanylate kinase domain. These conserved regions are shared among members of the discs-large family of proteins that include human p55, a membrane protein expressed in erythrocytes, rat PSD-95/SAP90, a synapse protein expressed in brain, Drosophila dIg-A, a septate junction protein expressed in various epithelia, and human and mouse ZO-1 and canine ZO-2, two tight junction proteins. The Homologue of Drosophila, dIg-A, acts as a tumor suppressor. All members of

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The new protein can find application in modulating/blocking intracellular signal transduction pathways.

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similarity to disks large homolog DLG2 (Homo sapiens)

alternative splicing: see DLG2  
complete cds.

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frame shift: around position 1437 one C too many

Sequenced by EMBL

35

Locus: /map="338-b cR from top of Chr17 linkage group"

Insert length: 4220 bp

Poly A stretch at pos. 4180, polyadenylation signal at pos. 4165

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1 CCCGGCTGCG CTGGAGCCGC CCGGAGCTAG GGGCTTCCCG GGGCGCAGGA
51 GAGACGTTTC AGAGCCCTTG CCTCCTTCAC CATGCCGTTT GCCGCCACCA
101 ACTCTGAAAC TGCCATGCAG CAAGTCCTGG ACAACTTGGG ATCCCTCCCC
151 AGTGCCACGG GGGCTGCAGA GCTGGACCTG ATCTTCCTTC GAGGCATTAT
201 GGAAAGTCCC ATAGTAAGAT CCCTGGCCAA GGCCCATGAG AGGCTGGAGG
251 AGACGAAGCT GGAGGCCGTG AGAGACAACA ACCTGGAGCT GGTGCAGGAG
301 ATCCTGCGGG ACCTGGCGCA GCTGGCTGAG CAGAGCAGCA CAGCCGCCGA
351 GCTGGCCAC ATCCTCCAGG AGCCCCACTT CCAGTCCCTC CTGGAGACGC
401 ACGACTCTGT GGCCTCAAAG ACCTATGAGA CACCACCCCC CAGCCCTGGC
451 CTGGACCCTA CGTTCAGCAA CCAGCCTGTA CCTCCCGATG CTGTGCGCAT
501 GGTGGGCATC CGCAAGACAG CCGGAGAACA TCTGGGTGTA ACGTTCGCGG
551 TGGAGGGCGG CGAGCTGGTG ATCGCGCGCA TTCTGCATGG GGGCATGGTG
601 GCTCAGCAAG GCCTGCTGCA TGTGGGTGAC ATCATCAAGG AGGTGAACGG
651 GCAGCCAGTG GGCAGTGACC CCCGCGCACT GCAGGAGCTC CTGCGCAATG
701 CCAGTGGCAG TGTCATCCTC AAGATCCTGC CCAGCTACCA GGAGCCCCAT
751 CTGCCCCGCC AGGTATTTGT GAAATGTCAC TTTGACTATG ACCCGGCCCCG
801 AGACAGCCTC ATCCCCTGCA AGGAAGCAGG CCTGCGCTTC AACGCCGGGG
851 ACTTGCTCCA GATCGTAAAC CAGGATGATG CCAACTGGTG GCAGGCATGC
901 CATGTCGAAG GGGGCAGTGC TGGGCTCATT CCCAGCCAGC TGCTGGAGGA

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	951	GAAGCGGAAA	GCATTTGTCA	AGAGGGACCT	GGAGCTGACA	CCAAACTCAG
	1001	GGACCCCTATG	CGGCAGCCTT	TCAGGAAAGA	AAAAGAAGCG	AATGATGTAT
	1051	TTGACCACCA	AGAATGCAGA	GTTTGACCGT	CATGAGCTGC	TCATTTATGA
	1101	GGAGGTGGCC	CGCATGCCCC	CGTTCCGCCG	GAAAACCCTG	GTACTGATTG
5	1151	GGGCTCAGGG	CGTGGGACGG	CGCAGCCTGA	AGAACAAGCT	CATCATGTGG
	1201	GATCCAGATC	GCTATGGCAC	CACGGTGCCC	TACACCTCCC	GGCGGCCGAA
	1251	AGACTCAGAG	CGGGAAGGTC	AGGGTTACAG	CTTTGTGTCC	CGTGGGGAGA
	1301	TGGAGGCTGA	CGTCCGTGCT	GGGCGCTACC	TGGAGCATGG	CGAATACGAG
	1351	GGCAACCTGT	ATGGCACACG	TATTGACTCC	ATCCGGGGCG	TGGTCGCTGC
10	1401	TGGGAAGGTG	TGCGTGCTGG	ATGTCAACCC	CCAGGCCGGT	GAAGGTGCTA
	1451	CGAACGGCCG	AGTTTGTCCC	TTACGTGGTG	TTCATCGAGG	CCCCAGACTT
	1501	CGAGACCCTG	CGGGCCATGA	ACAGGGCTGC	GCTGGAGAGT	GGAATATCCA
	1551	CCAAGCAGCT	CACGGAGGCG	GACCTGAGAC	GGACAGTGGA	GGAGAGCAGC
	1601	CGCATCCAGC	GGGGCTACGG	GCACTACTTT	GACCTCTGCC	TGGTCAATAG
15	1651	CAACCTGGAG	AGGACCTTCC	GCGAGCTCCA	GACAGCCATG	GAGAAGCTAC
	1701	GGACAGAGCC	CCAGTGGGTG	CCTGTCAGCT	GGGTGTACTG	AGCCTGTTCA
	1751	CCTGGTCCTT	GGCTCACTCT	GTGTTGAAAC	CCAGAACCTG	AATCCATCCC
	1801	CCTCCTGACC	TGTGACCCCC	TGCCACAATC	CTTAGCCCCC	ATATCTGGCT
	1851	GTCTTTGGGT	AACAGCTCCC	AGCAGGCCCT	AAGTCTGGCT	TCAGCACAGA
20	1901	GGCGTGCCT	GCCAGGGAGG	TGGGCATTCA	TGGGGTACCT	TGTGCCCAGG
	1951	TGCTGCCCCA	TCCTGATGCC	CATTGGTCAC	CAGATATCTC	TGAGGGCCAA
	2001	GCTATGCCCC	GGAATGTGTC	AGAGTCACCT	CCATAATGGT	CAGTACAGAG
	2051	AAGAGAAAAG	CTGCTTTGGG	ACCACATGGT	CAGTAGGCAC	ACTGCCCCCTG
	2101	CCACCCCTCC	CCAGTCACCA	GTTCTCCTCT	GGACTGGCCA	CACCCACCCC
25	2151	ATTCTGAGAC	TCCTCCCACC	TCTCACCCCT	GTGTGCGAGG	AACAGGCCTT
	2201	GGGCTGTTTC	CGTGTGACCA	GGGGAATGTG	TGGCCCCGCTG	GCAGCCAGGC
	2251	AGGCCCCGGG	GGTGGTGCCA	GCCTGGTGCC	ATCTTGAAGG	CTGGAGGAGT
	2301	CAGAGTGAGA	GCCAGTGGCC	ACAGCTGCAG	AGCACTGCAG	CTCCCAGCTC
	2351	CTTTGGAAAG	GGACAGGGTC	GCAGGGCAGA	TGCTGCTCGG	TCCTTCCCTC
30	2401	ATCCACAGCT	TCTCACTGCC	GAAGTTTCTC	CAGATTTCTC	CAATGTGTCC
	2451	TGACAGGTCA	GCCCTGCTCC	CCACAGGGCC	AGGCTGGCAG	GGGCCATTGG
	2501	GCTCAGCCCA	GGTAGGGGCA	GGATGGAGGG	CTGAGCCCTG	TGACAACCTG
	2551	CTGTTACCAA	CTGAAGAGCC	CCAAGCTCTC	CATGGCCCCA	AGCAGGCACA
	2601	GGTCTGAGCT	CTATGTCTCT	GACCTTGGTC	CATTTGGTTT	TCTGTCTAGC
35	2651	CAGGTCCAGG	TAGCCCACTT	GCATCAGGGC	TGCTGGGTTG	GAGGGGCTAA
	2701	GGAGGAGTGC	AGAGGGGACC	TTGGGAGCCT	GGGCTTGAAG	GACAGTTGCC
	2751	CTCCAGGAGG	TTCTTCACAC	ACAACCTCAG	AGGCGCCATT	TACACTGTAG
	2801	TCTGTACAAC	CTGTGGTTCC	ACGTGCATGT	TCGGCACCTG	TCTGTGCTCT
	2851	TGGCACCAGG	TTGTGTGTGT	GTGCGTGTGC	ACGTGCGTGT	GTGTGTGTGT
40	2901	GTGTCAAGTT	TAGTTTGGGG	AGGAAGCAAA	GGGTTTTGTT	TTGGAGGTCA
	2951	CTCTTTGGGG	CCCCTTTCTG	GGGGTTCCCC	ATCAGCCCTC	ATTTCTTATA
	3001	ATACCTTGAT	CCCAGACTCC	AAAGCCCTGG	TCCTTTCCTG	ATGTCTCCTC
	3051	CCTTGTCTTA	TTGTCCCCCT	ACCCTAAATG	CCCCCTGCC	ATAACTTGGG
	3101	GAGGGCAGTT	TTGTAAAATA	GGAGACTCCC	TTTAAGAAAG	AATGCTGTCC
45	3151	TAGATGTACT	TGGGCATCTC	ATCCTTCATT	ATTCTCTGCA	TTCCTTCCGG
	3201	GGGGAGCCTG	TCCTCAGAGG	GGACAACCTG	TGACACCCTG	AGTCCAAACC
	3251	CTTGTGCCTC	CCAGTTCTTC	CAAGTGTCTA	ACTAGTCTTC	GCTGCAGCGT
	3301	CAGCCAAAGC	TGGCCCCCTGA	ACCACTGTGT	GCCCATTTC	TAGGGAAAGG
	3351	GAAGGAGAAT	AAACAGAATA	TTTATTACAA	ATGTTAGAAT	ATATTTCTTA
50	3401	TACTAGGAAT	CTCATTTGCA	TTTGCATAGA	CTATACACAT	GGGGTGGAAA
	3451	GGCCAGGCCCT	GCCCCCATCT	CGTTGGTGTG	GCTCTGCGTA	TACTACACAC
	3501	TCATTCTCCT	GCTCCTCTTT	TCCCTTAGTC	AGTGTCCCTT	CATCCTGATT
	3551	CAGCTCTGCC	TTGCATCACC	CTCAGCCTAA	GGGAGTGGGA	AGGAAATGGG
	3601	GTGTTTTCTT	GCTGACCTGA	GGCTATAGGG	TCACTTGCCA	TTTCTTACCT
55	3651	TCTCTGGGGG	ATTTGAGGGT	AGAGGCAGGG	GAAGATCTGT	TGTTGCAGTT
	3701	GCTTCTGCCC	CCTTGATCCA	AATGACCATC	ATCTCTGATG	GAGATGGGTT
	3751	GGGTACCTGG	CCTTCATGGC	ACCTTCACTG	CTAGGGATGC	TCAAGGGGCA
	3801	GGCCTGGGGC	CCTTCCCTCC	TGTCTCTTCT	CGGTCTTTCC	TCTCTGAGCA

3851 GCCTCCTACC TCCCCTGCCT GAGCCCTCAC TCCACAGCCC TCCCAGGTAC  
 3901 CTAGCAGAGG CTGTCTAGTCC TTGGCTCACC TGGAACAGGG CTGGGGCTGG  
 3951 GTTGGAAACAG GTGTGTGCCC CCACCACAGC TCTATGACTC TGTTCCTCCT  
 4001 CCTGCCATT GTGGACTCTT GTATTGAGG GACCTCAAGA GAGTGAGGAC  
 5 4051 CCTACCATCC ACTGTCCATA TTCAGTCCCA GCCCAGTGC GCTTCCTCTG  
 4101 TTCCCTCCCT CAGCCATCCA ATTCTTGAGT TTTCTCACTG ATTGGTTTTC  
 4151 TTTCTTTTTC CTTGGATTAA ATGTGAAAGC AAAGAAAAAA AAAAAAAAAA  
 4201 AAAAAAAAAA AAAAAAAAAA

10

## BLAST Results

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No BLAST result

15

## Medline entries

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20 96070428:  
 Mazoyer S, Gayther SA, Nagai MA, Smith SA, Dunning A, van  
 Rensburg EJ,  
 Albertsen H, White R,  
 Ponder BA.; A gene (DLG2) located at 17q12-q21 encodes a new  
 25 homologue  
 of  
 the Drosophila tumor suppressor dIg-A. Genomics 1995 Jul  
 1;28(1):25-31

30

## Peptide information for frame 1

-----

35

ORF from 82 bp to 1437 bp; peptide length: 452  
 Category: strong similarity to known protein  
 Classification: Cell signaling/communication  
 Prosite motifs: GUANYLATE\_KINASE\_1 (385-402)

40

1 MPVAATNSET AMQQLVDNLG SLPSATGAAE LDLIFLRGIM ESPIVRSLAK  
 51 AHERLEETKL EAVRDNNLEL VQEILRDLAQ LAEQSSTAAE LAHILQEPHF  
 101 QSLLETHDSV ASKTYETPPP SPGLDPTFSN QPVPPDAVRM VGIRKTAGEH  
 45 151 LGVTFRVEGG ELVIARILHG GMVAQQGLLH VGDIIKEVNG QPVGSDPRAL  
 201 QELLRNASGS VILKILPSYQ EPHLPRQVFV KCHFDDYDPAR DSLIPCKEAG  
 251 LRFNAGDLLQ IVNQDDANWQ QACHVEGGSA GLIPSQLEE KRKAFVKRDL  
 301 ELTPNSGTLC GSLSGKKKKR MMYLTTKNAE FDRHELLIYE EVARMPFFRR  
 351 KTLVLIGAQG VGRSLKKNKL IMWDPDRYGT TVPYTSRRPK DSEREGQGYG  
 50 401 FVSRGEMEAD VRAGRYLEHG EYEGNLYGTR IDSIRGVVAA GKVCVLDVNP  
 451 QA

55

## BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_12d7, frame 1

No Alert BLASTP hits found

5

Peptide information for frame 2

ORF from 1439 bp to 1738 bp; peptide length: 100  
 10 Category: strong similarity to known protein  
 Classification: Cell signaling/communication  
 Prosite motifs: LEUCINE\_ZIPPER (66-87)

15 1 VKVLRTAEFV PYVVFIEAPD FETLRAMNRA ALESGISTKQ LTEADLRRTV  
 51 EESSRIQRGY GHYFDLCLVN SNLERTFREL QTAMEKLRTE PQWVPVSWVY

20

BLASTP hits

No BLASTP hits available

25

Alert BLASTP hits for DKFZphamy2\_12d7, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphamy2\_12d7, frame 1

30

Report for DKFZphamy2\_12d7.1

35 [LENGTH] 516  
 [MW] 56458.36  
 [pI] 6.21  
 [HOMOL] PIR:A57653 disks large homolog DLG2 - human 0.0  
 [FUNCAT] 01.03.99 other nucleotide-metabolism activities [S.  
 cerevisiae, YDR454c] 7e-15  
 40 [FUNCAT] f nucleotide metabolism and transport [H. influenzae,  
 HI1743] 3e-07  
 [BLOCKS] PR00834F  
 [BLOCKS] BL00856C  
 [BLOCKS] BL00856B Guanylate kinase proteins  
 45 [BLOCKS] BL00856A Guanylate kinase proteins  
 [SCOP] dlgy\_ 3.29.1.1.1 Guanylate kinase [baker's  
 yeast (Saccharomyce 8e-45  
 [SCOP] dlkwab\_ 2.26.1.1.2 Cask/Lin-2 [Human (Homo  
 sapiens) 4e-34  
 50 [EC] 2.7.4.8 Guanylate kinase 8e-17  
 [PIRKW] blocked amino end 8e-17  
 [PIRKW] phosphotransferase 8e-17  
 [PIRKW] monomer 8e-17  
 [PIRKW] duplication 5e-29  
 55 [PIRKW] signal transduction 3e-24  
 [PIRKW] alternative splicing 5e-29  
 [PIRKW] P-loop 8e-17  
 [PIRKW] acetylated amino end 1e-16

[PIRKW] membrane protein 9e-74  
 [PIRKW] magnesium 8e-17  
 [PIRKW] ATP 8e-17  
 [SUPFAM] SH3 homology 9e-74  
 5 [SUPFAM] discs-large tumor suppressor 3e-24  
 [SUPFAM] unassigned Ser/Thr or Tyr-specific protein kinases 5e-11  
 [SUPFAM] protein kinase homology 5e-11  
 [SUPFAM] GLGF domain homology 9e-74  
 10 [SUPFAM] guanylate kinase 8e-17  
 [SUPFAM] guanylate kinase homology 9e-74  
 [PROSITE] GUANYLATE\_KINASE\_1 1  
 [PFAM] Src homology domain 3  
 [KW] Irregular  
 15 [KW] 3D

SEQ MPVAATNSETAMQAVLDNLGSLPSATGAAELDLIFLRGIMESPIVRSLAKAHERLEETKL  
 20 lgky- .....  
 SEQ EAVRDNNLELVQELRLDLAQLAEQSSTAAELAHILQEPHFQSLLETHDSVASKTYETPPP  
 25 lgky- .....  
 SEQ SPGLDPTFSNQPVPPDAVRMVGIRKTAGEHLGVTFRVEGGELVIARILHGGMVAQAGLLH  
 30 lgky- .....  
 SEQ VGDIIEKVNQGPVGS DPRALQELLRNASGSVILKILPSYQEPHLPRQVFVKCHFDDYD PAR  
 35 lgky- .....  
 SEQ DSLIPCKEAGLRFNAGDLLQIVNQDDANWUQACHVEGGSAGLIPSQILLEEKRAKAFVKRDL  
 40 lgky- .....CCEEEECTTT  
 SEQ ELTPNSGTLGSLSGKKKKRMMYLTTKNAEFDRHELLIYEEVARMPFRRKTLVLIGAQG  
 45 lgky- TCHHHHHHHHHHHHTTTTEEECCCEEECCCTTTTTTTTTTTEECCHHHHHHHHHHCCEEEEEE  
 SEQ EYEGNLYGTRIDSIRGVVAAGKVCVLDVNPQAGEGATNGRVCPLRGVHRGPRLRDPAGHE  
 50 lgky- EETTEEEEEHHHHHHHHHHHCCEEEECCHH.....  
 SEQ QGCAGEWNIHQAAHGGGPETDSGGEQPHPAGLRALL  
 55 lgky- .....

55 Prosite for DKFZphamy2\_12d7.1

PS00856

385-&gt;403

GUANYLATE\_KINASE\_1

PD0C00670



## Pfam for DKFZphamy2\_12d7.1

5

HMM\_NAME Src homology domain 3

HMM

\*pyVIALYDYqAqd.....pDELSFKEGDIIiIIIEdsDD.WWrgRnnn

10

+V+ +DY++ + + L F GD ++I++++D+ WW +

Query

228

VFVKCHFDDYDPARDSLIPCKEAGLRFNAGDLLQIVNQDDANWWQACHVE 276

HMM

TNGQEGWIPSNYVEPi\*

15

++ G+IPS +E+

Query

277 GG-SAGLIPSQILLEEK 291

20

Pedant information for DKFZphamy2\_12d7, frame 2

-----

## Report for DKFZphamy2\_12d7.2

25

[LENGTH] 175

[MW] 19721.90

[pI] 9.69

[HOMOL] PIR:A57653 disks large homolog DLG2 - human 7e-53

30

[PIRKW] membrane protein 1e-13

[SUPFAM] SH3 homology 1e-13

[SUPFAM] GLGF domain homology 1e-13

[SUPFAM] guanylate kinase homology 1e-13

[PROSITE] LEUCINE\_ZIPPER 1

35

[KW] Alpha\_Beta

SEQ MAPRCPTPPGGRKTQSGKVRVTALCPVGRWRLTSVLGATWSMANTRATCMHVLTTPSGAW

PRD ccc

40

SEQ SLLGRACWMSTPRPVKVLRTAEFVPYVVFIEAPDFETLRAMNRAALESgistKQLTEAD

PRD ccc

SEQ LRRTVEESSRIQRGYGHYFDLCLVNSNLERTFRELQTAMEKLRTEPQWVPVSWVY

45

PRD hhh

## Prosite for DKFZphamy2\_12d7.2

50

PS00029

141-&gt;163

LEUCINE\_ZIPPER

PD0C00029

(No Pfam data available for DKFZphamy2\_12d7.2)

55

5 group: amygdala derived

DKFZphamy2\_12g7 encodes a novel 254 amino acid protein without similarity to known proteins.

10 No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of amygdala-specific genes.

15

putative protein

Sequenced by EMBL

20

Locus: unknown

Insert length: 1257 bp

No poly A stretch found, no polyadenylation signal found

25

```

1 CTCCAAGACT TCCTTGCTGT GAGGCTCGTG TGGACCCAG AGCATGCACA
51 GGCTGTTTAC TCCACAGAGT GGCTTTGAGA ATCAGATGAG ACTGTGCTGG
101 CGAAGGCCCT GTGGGAATGA GGAACGCTGT AGTGTGCTGT GGTCCCTGTT
151 TCTGCCCCCA GGAAAGCAGC TGTGTGAGGA GGAGCGCCGG GCCATGCAGG
201 CTGCCCTGGA CTCCGTCTGT TGCCACACGC CCTCAACAA CCTTGCTTTT
251 TCCCGGAAGG GCAGCGCGCT CACCTTCAGT GTGGCCTTCC AGGCTCTGAG
301 GACGGGGGCTC TTCGAGCTAA GCCAGCACAT GAAACTGAAG CTGCAGTTCA
351 CCGCCAGCGT GTCCACCTT CCACCCGAGG CCCGGCCCCCT CTCCCGCAAG
401 AGCAGCCCCA GAAGCCCTGC TGTCCGGGAC TTGGTGGAGA GGCATCAGGC
451 TAGCCTGGGC CGCTCCAGT CCTTCTCCCA CCAGCAGCCT TCCCGAAGCC
501 ACCTCATGAG GTCGGGCAGT GTGATGGAGC GCAGAGCATC ACGCCCCCTG
551 TGGCCTCTCC TGTGCGCCGC CCCCTCTACC TGCCCCCGGA CAAGGCTGTG
601 TTGTCTCTGG ACAAGATTGC CAAGCGCGAG TGCAAGGTCC TGGTGGTGGG
40 651 ACCCGTCAAG TAGCACCCTG CCAGCTCTGT TCCCTCTTAC ACTCCAGAGA
701 CCCAACGCCC CCAGAGGGTA TCCTTGCTCC CGGGCTGTGC CTCCCCTGGG
751 ATGCCTCCCA GACGGGGGTG AAGAGGCCTG GCAGAGCTGC CTGTCTTGTG
801 TCTGCTGATG AGGGATGGGG GAAGAAGCTG TGAAGTGGGC GGGCATGGCT
851 GGGACTAAGC CACCAGTATT CCCCAGCTT CCTGTGGGGG GGGCTGGCCC
45 901 ACCCTAGGC CAGGGCAAGG GTTCCCAGAG CTCCCTTGTC CCCGGCCCTT
951 TACCCTGGTT CTGAGTTTAC AAAGTCTCTT CCTCATTCCC GTTGAGTTCT
1001 TTCCCACCTC TGACATTCCC TCCCTCCCTC CCGCAGGCTG AGATTAGAGG
1051 GTGGTGATGG CTAAGGGCCC CTGACAGTGA CCTTCCTGTC TCAGGGGTTG
1101 GGGACAGGGC CAGGTAGCCT CCTGCCCTT ATGTTTACGT TTGCAGCCTG
50 1151 AAGCACTTTA ATTTTTTTTT TTTTGGTCT GTCCCTGTAA CTAATTTTCC
1201 AACTATTGCT TCCAAGTAA ATAAGACTAT TAAATGCCTG TTCAGAGGGA
1251 AAAAAAA
```

55

#### BLAST Results

-----

No BLAST result

\_\_\_\_\_

No Medline entry

Peptide information for frame 2

Category: putative protein

Classification: no clue

```

20      1 MHRLFTPQSG FENQMLRCWR RPCGNEERCS VCWSLFLPPG KQLCEEERRA
      51 MQAALDSVVC HTPLNNLGFS RKGSALTFSV AFQALRTGLF ELSQHMKLKL
     101 QFTASVSHPP PEARPLSRKS SPRSPAVRDL VERHQASLGR SQSFSSHQQPS
     151 RSHLMRSGSV MERRASRPLW PLLLAAPSTC PRTRLCCLWT RLPSASARSW
     201 WWNPSSSTVP ALFPLTLQRP NAPRGYPCSR AVPPLGCLPD GGEEAWQSCL
     251 SCVC

```

## BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_12g7, frame 2

No Alert BLASTP hits found

35 Pedant information for DKFZphamy2\_12g7, frame 2  
-----

Report for DKFZphamy2\_12g7.2

```

40  [LENGTH]    254
    [MW]        28479.91
    [pI]        10.00
    [BLOCKS]    BL01013C Oxysterol-binding protein family proteins
    [KW]        Alpha_Beta
45  [KW]        LOW COMPLEXITY          4.72 %

```

[illegible]

SEQ PRTRLCCLWTRLPSASARSWWWNPSSSTVPALFPLTLQRPNAPRGYPCSRVPPLGCLPD  
SEG .....  
PRD ccc

5

SEQ GGEEAWQSLSCVC  
SEG .....  
PRD cchhhhhhhhhccc

10

(No Prosite data available for DKFZphamy2\_12g7.2)

(No Pfam data available for DKFZphamy2\_12g7.2)

DKFZphamy2\_12i1

-----

5 group: amygdala derived

DKFZphamy2\_12i1 encodes a novel 283 amino acid protein with weak similarity to F41Eb.3 of *Caenorhabditis elegans*.

10 No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of amygdala-specific genes.

15

putative protein

Sequenced by EMBL

20

Locus: /map="3"

Insert length: 2528 bp

Poly A stretch at pos. 2515, polyadenylation signal at pos. 2491

25

1 ATATAGTTGG ATCAAACAAA AACAACACAA TTTGTCCCGA TAATTATCAA  
51 ACAGCACAGC TACTTGCCCTT AATTTTAGAG TTACTCACAT TTTGTGTGGA  
101 ACATCACACA TATCACATAA AAAACTATAT TATGAACAAG GACTTGCTAA  
151 GAAGAGTCTT GGTCTTGATG AATTCAAAGC ACACTTTCTT GGCCTTGTGT  
201 GCCCTTCGCT TTATGAGGCG GATAATTGGA CTFAAGATG AATTTTATAA  
251 TCGTTACATC ACCAAGGGAA ATCTTTTGA GCCAGTTATA AATGCACTTC  
301 TGGATAATGG AACTCGGTAT AATCTGTTGA ATTCAAGCTGT TATTGAGTTG  
351 TTTGAATTTA TAAGAGTGGA AGATATCAAG TCTCTTACTG CCCATATAGT  
401 TGAAAACTTT TATAAAGCAC TTGAATCGAT TGAATATGTT CAGACATTCA  
451 AAGGATTGAA GACTAAATAT GAGCAAGAAA AAGACAGACA AAATCAGAAA  
501 CTGAACAGTG TACCATCTAT ATTGCGTAGT AACAGATTTC GCAGAGATGC  
551 AAAAGCCTTG GAAGAGGATG AAGAAATGTG GTTTAATGAA GATGAAGAAG  
601 AGGAAGGAAA AGCAGTTGTG GCACCAAGTGG AAAAACCTAA GCCAGAAGAT  
40 651 GATTTTCCAG ATAATTATGA AAAGTTTATG GAGACTAAAA AAGCAAAAAGA  
701 AAGTGAAGAC AAGGAAAACC TTCCCAAAAG GACATCTCCT GGTGGCTTCA  
751 AATTTACTTT CTCCCCTCTT GCCAGTGCTG CTAATGGAAC AAACAGTAAA  
801 TCTGTAGTGG CTCAGATACC ACCAGCAACT TCTAATGGAT CCTCTTCCAA  
851 AACCACAAAC TTGCCTACGT CAGTAACAGC CACCAAGGGA AGTTTGTTG  
45 901 GCTTAGTGGA TTATCCAGAT GATGAAGAGG AAGATGAAGA AGAAGAATCG  
951 TCCCCCAGGA AAAGACCTCG TCTTGGCTCA TAAAATATTT ATTAGGGGAC  
1001 CCTCAACATG TGGTCTTACA ATGCTGCAAC TGTTCAAGTGA GCTGAAAATC  
1051 TGAATCAGAA AGCTTTCTCA ATTGAACCTA TAAAATATAC AAGGAGTAGC  
1101 AAAAGACAGT ATATCAGCTA AGAGAGTTTA GTTCTAATAA AAATCAGGCT  
50 1151 TCCCAGGAAC TTGATTGCTT GCTAGTAATT AAGGGGTTTG CCTTTTAGGC  
1201 TGTCAAAACA AACATTAGTA ACCAGAACCT GGGAGATAGC TTCTCAGCAA  
1251 GGAAAAGTCA CAGGTTTGGG GACGGTTTAG GGGAGGGGAA AAGGTTGATA  
1301 TAATAATGCA GGGTTGCTCC TCGGGGTGTC GATCTAGAAA CAATTTTACA  
1351 GAACTTCAGT TGTAACACTCA ATAACATTAC TTGTATAATG GTGCTGGCCA  
55 1401 TGTTGTTGTT TTAATCAGTT GCCTCTTTTT AAAAGAAATT TTTATGGAAA  
1451 ACACATTCAA CTATCATTA AAAAAATGAAG TTAAGCTGTT GGGACCATTT  
1501 CTTTAAGATT TAACAAAAGT TCAGCCTTTT AGGTAGTTGA AGGGAAGTAC  
1551 ACCCCGTATT CAGCACATGT TGAGTTTCTT ACACCAGGAA TTTTCAATAT

```

1601 GTATATTGAT GAAAACAAGC TCAATTCAAA CTGGACAGTT TTAAGATAAT
1651 GTTAAAATCA GCACTTTTAG AGACAACGAA GGCCAAGAAT CAGTACAGTA
1701 GTATTCCAAA ATGATTTTCT CTAGAAATTT GAAAGTAGAT CGAACAGAAT
1751 GTTGTCAACC GCCTACCAGT ACAATCTTTT GTGGAAGATA CTTTGAAATC
5 1801 ACTTTCTACT TTGTTAGTAA AGTTCTGTCT TTCCAGAGCT GCAAGTTTAA
1851 AAGTGTTACT TATACAGACC AACCAAGAAT AGTGCTGAAT TAAGTGGCAT
1901 TTAGTATCTA GAAGCCATTT TGATCCAAGA AGCTACTTAA GTGTCAAAGT
1951 CAGCATGCAG CACATGTAGC TTTTCTGTAA ACAAGGGTGT GATATGAAAG
2001 CTGCTTTTTT AAGAAGAGTA AAAGCACATT CCATATACGT AAGTGAATTT
10 2051 TAAAAATAAA TTGAGGCAAA CAGTTAAGTT TTATTTTATG AGCAACAAGT
2101 TAACTGTAAA TATTTTAATG TTAGTTTGCT CATCTATGAT CTGAGATCAT
2151 GCCGAAGTGA GAAAAATCTC CCCAAAATAC AATTTAATGC ATTGGGAAAA
2201 AAAAACTTTA ACAGTAATTC CAGCCACAAT CTTTAGATCA CCCTTGTAAT
2251 GTGTTACGGG TCCATTTTTC CTGGAATCGT TTAATCTAAA GCAGTTTCCC
15 2301 CTGTTTTGGA GATTTTGTAG TTAATTTTAA TTTTGGCTAT TGTGTTGAAA
2351 AGATGAGCTG TCTGTGTAGA TATGAAGTAT AGTTTTTTCC ATAAAACAGA
2401 TGTTTATTTT GTATTAAAAA ATACCACTGT ACTTGTTTTA CACCATTTGT
2451 ATACATGTGG TGATATTAAT GCTAAACTGT AAAATTTCAGG AATTAAAAATG
2501 TGACCCTGTA ATTCCAAAAA AAAAAAAA
20

```

## BLAST Results

-----

```

25 Entry AF016448_8 from database TREMBL:
   gene: "F41E6.3"; Caenorhabditis elegans cosmid F41E6.
   Score = 390, P = 5.0e-32, identities = 73/184, positives =
   118/184,
   frame +3
30 Entry HS211256 from database EMBL:
   human STS SHGC-15844.
   Score = 977, P = 5.5e-38, identities = 199/202
35

```

## Medline entries

-----

```

40 No Medline entry

```

## Peptide information for frame 3

-----

```

45 ORF from 132 bp to 980 bp; peptide length: 283
   Category: putative protein
   Classification: no clue
50 1 MNKDLLRRVL VLMNSKHTFL ALCALRFMR R IIGLKDEFYN RYITKGNLFE
   51 PVINALLDNG TRYNNLSAV IELFEFIRVE DIKSLTAHIV ENFYKALES I
   101 EYVQTFKGLK TKYEQEKDRQ NQKLNSVPSI LRSNRFRRDA KALEEDEEMW
   151 FNEDEEEEGK AVVAPVEKPK PEDDFPDNYE KFMETKKAKE SEDKENLPKR
55 201 TSPGGFKFTF SHSASAANGT NSKSVAQIP PATSNGSSSK TTNLPTSVTA
   251 TKGSLVGLVD YPDDEEEDDE EESSPRKRPR LGS

```

No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_12i1, frame 3

10

Pedant information for DKFZphamy2\_12i1, frame 3

## 15

```

[LENGTH] 326
[MW] 37261.10
[pI] 5.60
[HMOL] TREMBL:AF016448_8 gene: "F41Eb.3"; Caenorhabditis
elegans cosmid F41Eb. 1e-3b
[FUNCAT] 01.05.04 regulation of carbohydrate utilization [S.
cerevisiae, YNL201c] 2e-08
[BLOCKS] BL00357 Histone H2B proteins
[BLOCKS] BP02232B
[BLOCKS] PR01073C
[BLOCKS] BP03050C
[BLOCKS] BP03580F
[BLOCKS] PR00893F
[KW] All_Alpha
[KW] LOW_COMPLEXITY 10.43 %

```

35	SEQ	IVGSNKNNTICPDNYQTAQLLALILELLTFCVEHHTYHIKNYIMNKDLLRRVLVLMNSKH
	SEG	.....xxxxxxxxx.....
	PRD	ccccccccccccccccchhhhhhhhhhhhhhhhhhhcccccchhhhhhhhhhhhhhhhhhhhhccch
40	SEQ	TFLALCALRFMRRIIGLKDEFYNRYITKGNLFEPVINALLDNGTRYNLLNSAVIELFEFI
	SEG	.....
	PRD	hhhhhhhhhhhhhhhhhhhhccchhhhhhhccccccchhhhhhhhhhhccccccccccchhhhhhhhhhh
	SEQ	RVEDIKSLTAHIVENFYKALESIEYVQTFKGLKTKYEQEKDRQNAQLNSVPSILRSNRFR
	SEG	.....
	PRD	hheeehhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhhhccccccccccccccccccchhh
45	SEQ	RDAKALEEDEEMWFNEDEEEEGKAVVAPVEKPKPEDDFPDNYEKFMETKKAKESDKENL
	SEG	.....xxxxxxxxxxxxxxxxx.....
	PRD	hhhhhhhhhhhhhhhhhhhhccccccccceeeeeeeccccccccccccccccchhhhhhhhhhhhhhhhhhhcccccc
50	SEQ	PKRTSPGGFKFTFSHSASAANGTNSKSVVAQIPPATSNNGSSSKTTNLPSTVTATKGS LVG
	SEG	.....
	PRD	ccccccccccccceeeccce
55	SEQ	LVDYPDDEEEDEEEESSPRKRPRLG
	SEG	.....xxxxxxxxxxx.....
	PRD	eeccccccccchhhhhhhcccccccccccccc

-90-

(No Pfam data available for DKFZphamy2\_1211.3)



DKFZphamy2\_13g19

-----

5 group: amygdala derived

DKFZphamy2\_13g19 encodes a novel 281 amino acid protein without similarity to known proteins.

10 The novel protein contains a PROSITE ASP\_PROTEASE motif and seem to be expressed Ubiquitously.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

15 The new protein can find application in studying the expression profile of amygdala-specific genes.

20 unknown protein

perhaps complete cds.

Pedant: SIGNAL\_PEPTIDE

25 Sequenced by EMBL

Locus: /chromosome="12p13.3"

Insert length: 2754 bp

30 Poly A stretch at pos. 2743, polyadenylation signal at pos. 2724

```

      1 GCAATCTCGG GAAATTGGAG ACTGACGCGG CTGCTCCTGC ATGTTATTTA
      51 TTTTTCCTCT TTCCCTCCCG TGGAGACCCT CCTGTTGGAA AGAGAGCTGC
35 101 AGCACGGGAC AGAGACAGGC AGGAAGAAGC AGAGAGGACT CGGTGACGCC
    151 CCCACCGAGC AGCCCTTGGC CCACTCCTCC AGCAGGGGCC ATGAGCACCA
    201 AGCAGGAGGC CAGGAGAGAT GAGGGAGAAG CCAGGACGAG GGGGCAGGAG
    251 GCACAGCTTC GAGACCGAGC CCACCTGAGC CAGCAGCGCC GGCTCAAACA
    301 GGCCACCCAG TTCCTGCACA AGGACTCGGC CGACCTGCTC CCGCTGGACA
40 351 GCCTCAAGAG GCTCGGCACC TCCAAGGACT TGCAGCCGCG CAGTGTGATC
    401 CAAAGACGCC TGGTGGAGGG AAACCCGAAT TGGCTTCAGG GGGAGCCTCC
    451 CCGGATGCAG GACCTGATTC ATGGCCAGGA GAGCAGGAGG AAGACCAGCA
    501 GGACAGAGAT TCCAGCTCTT CTGGTCAACT GCAAGTGCCA GGACCAGCTG
    551 CTTAGAGTGG CCGTTGACAC AGGCACCCAA TACAATCGGA TCTCTGCTGG
45 601 ATGTCTCAGC CGCTGGGGT TAGAGAAAAG GGTCTTAAAA GCCTCAGCTG
    651 GGGACCTGGC CCCTGGGCCC CCAACCCAGG TGGAGCAGTT GGAGCTACAG
    701 CTGGGGCAGG AGACTGTGGT GTGCTCGGCA CAGGTGGTGG ATGCTGAGAG
    751 TCCTGAATTC TGCTGGGCC TGCAGACTCT GCTTTCTCTC AAGTGCTGCA
    801 TCGACCTGGA GCACGGAGTG CTGCGGCTGA AAGCCCCGTT CTCAGAGCTA
50 851 CCCTTCCTGC CTTTGTACCA AGAGCCTGGC CAGTGACTGC TGTCTCAGTC
    901 AGTCCCCAGA GGGAAAGACC TTGCCTTAGA AGAAGAGGCG TGTGGGGAAC
    951 GGGGGCTCTT GAAGCCAGGT AGCTGGGGAC TATGGTGTCT GCCCTTCCAA
   1001 TCACCTCCCT GACCCCTGCT GTCCCATTTT CCCCAGCTGG CCGCATTCCT
   1051 CTCTGCTTCT CAGCAGCTGT CTTACTCCCC AGGACGAGTT TTCCTAGAG
55 1101 GGCCACGAT GCCAGGATTC TGATTATCT TCCTCCCAAG AAAAGCAAAG
   1151 CCAAATCAAG ACCACAGATA GGAACCTAAG CACAATGGGG TGCCTGCTTG
   1201 GGCTGGGTCT AAGGCTCTGC TGACTGCTGT CTTGTCCAT CACCCAATAC
   1251 CACCCCAAAC ACAACTCAAC TTCCACACC ACCATGTCTC TCACCACACC

```

```

1301 TTCTGGGCCT CATTATCTCC CACAACCTAGA CCGCCATGCC TCACCAACCT
1351 ATGTCCCTGG ACCTCCTGGT GTCTGCCTCT CGGAGTCTGT GCACATCTGC
1401 TCACAGTTGA GTGGGGGAAG AAACAGCCAG AATTCAATAC AACAAAGAGC
1451 GGGAGTTAGT ATAGGAATGT CCATCTCATA AGGCTGAGAG CTATTTTTTC
5 1501 CTGTGGCTGC AAATGTCTGA AGCCAGTTAG TTTGATTACC CTGTGCAAAA
1551 CCTTGGACAT ACTTCTGCTA TTAACGCTAT AGGTATTTAT CCGTTTCCAC
1601 TGGCTTTTTG TACCCACCGA GCCCCTGAGC CTTGCGTGTG TGTGTGTGGA
1651 AGAGCCTTGT AGAGAACTGC TCCTGTGAGG CAGACAGGAC AGTGAGGTTG
1701 TCACCACTCA GACTTCACCT ATTCAGCATT CTTTCTGATT TCTAGAACTA
10 1751 TCCACCTCAT TAGGCCTTCT TCCTATCCCC ATCTCTGGCC TCTTGAGCTT
1801 AAGCTTGTAT TGTCTGGAA TCAGTGGCTT TCTAACCCCC TGCCAGGCTT
1851 TGCCAAAGCA AAAAGACAGA GGCTTTTTTT TTTTTTTTAA AGTTGGGGT
1901 CTGTCAGGAG ACAGAGGCTT TTTTGAATTC ACTGTGAAGA GAAGAACCCG
1951 AACCTTAAGA CGCCAGATCC CTGAGAGTCT TTCTGGCTGG TTTGAGTCTC
15 2001 TCAAATCATG GATTAGGAGT AAAGAAAGAG GCAGGCGCAA TGGCTCATGC
2051 CTGTAATCCC AGCACTTTGG GAGGCTGAGG TGGGTGGATC ACTTGAGGTC
2101 AGGAGTTTGA GACCAGCCTG GGTAATATGG CAAAACCCCA TCTCTACTAA
2151 AAAATACAAA AATTAGCCAG GTATGGTGGT GAACACCTGT AATCCCAGCT
2201 ACTTGGAAGG CTGAGGCATA GGAGTTGCTT GAACCTGGGA GATGGGGGTT
20 2251 GTAGTGAGCC AAGTTCGTGC CATCGGACTC CAGCCTGGGT GAAGGAGTGA
2301 GACCCTGTCT CCAAAAACAA ACAAAAAGG AGCAGAGAAA GACAGTGGTA
2351 CAGCTAACCT GAACAAGGGA ACTGGGACCG TTGGGCTGAA ACAGTCTTGA
2401 GCCTGGGGTT GACTGGGTTA GAGAAGAACC GGGATGCAAG GAGCTGCCTG
2451 TGACACCTGG CCTGCCCTTT CTCAGCTGCC TCCCCTGCCC TTTCTCAGCT
25 2501 GCCTCCCCTG CCCTCAGAAG GAAAGGAGAG GGCTCACTTA TCACTTGTGC
2551 CATAGCACCT GGTCTCAAAA TCCTAAAAGC TTTCTCGCC CTCCTGCCT
2601 TGCTCCACAA GGTCCACTTT CCTGGGTCTT GTGCTGTGCC TTTCTTGTG
2651 TGCTCCTGCT TGCTTCTGTA ACTGCAGACC CCAGGCCCAA TTGCAAGCCC
2701 TCGGCTCAGC TGCTTCTCCA TTGGAATAAA CTCTTGTTTC TCTAAAAAAA
30 2751 AAAA

```

## BLAST Results

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35

No BLAST result

## Medline entries

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40

No Medline entry

45

## Peptide information for frame 2

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50

ORF from 41 bp to 883 bp; peptide length: 281  
 Category: putative protein  
 Classification: no clue  
 Prosite motifs: ASP\_PROTEASE (173-184)

55

```

1 MLFIFPLSLP WRPSCWKESC STGQRQAGRS REDSVTPPPS SPWPTPPAGA
51 MSTKQEARRD EGEARTRGQE AQLRDRAHLS QQRRLKQATQ FLHKDSADLL
101 PLDSLKRLGT SKDLQPRSVI QRRLVEGNPN WLQGEPPRMQ DLIHQESRR
151 KTSRTEIPAL LVNCKCQDQL LRVAVDTGTQ YNRISAGCLS RLGLEKRVLK

```

201 ASAGDLAPGP PTQVEQLELQ LGQETVVCSA QVVDAESPEF CLGLQTLLSL  
 251 KCCIDLEHGV LRLKAPFSEL PFLPLYQEPG Q

5

## BLASTP hits

No BLASTP hits available

10

Alert BLASTP hits for DKFZphamy2\_13g19, frame 2

PIR:S50646 hypothetical protein YER143w - yeast (*Saccharomyces cerevisiae*), N = 1, Score = 90, P = 0.26

15

TREMBL:RND060\_1 product: "DNA (cytosine-5-)-methyltransferase";  
*Rattus norvegicus* mRNA for DNA (cytosine-5-) -methyltransferase, partial  
 cds.,  
 N = 1, Score = 81, P = 0.89

20

>PIR:S50646 hypothetical protein YER143w - yeast (*Saccharomyces cerevisiae*)

Length = 428

25

## HSPs:

Score = 90 (13.5 bits), Expect = 3.0e-01, P = 2.6e-01  
 Identities = 28/112 (25%), Positives = 48/112 (42%)

30

Query: 155 TEIPALLVNCKCQDQLLRVAVDTGTQYNRISAGCLSRLGLEKRVLKASAGD-  
 --LAPGPP 211

T++P L +N + + ++ VDTG Q +S + GL + + K G+

+ G

35

Sbjct: 199  
 TQVPMYINIEINNYPVKAFVDTGAQTTIMSTRLAKKTGLSRMIDKRFIGEARGVGTGKI 258

Query: 212 XXXXXXXXXXXXXXXX-  
 CSAQVVDAESPEFCLGLQTLLSLKCCIDLEHGVRL 263

40

CS V+D + + +GL L C+DL+

VLR+

Sbjct: 259 IGRIHQAAQVKIETQYIPCSFTVLDTDI-  
 DVLIGLDMKRLHLACVDLKENVLRI 310

45

Pedant information for DKFZphamy2\_13g19, frame 2

-----

## Report for DKFZphamy2\_13g19.2

50

[[LENGTH]] 281  
 [[MW]] 31330.97  
 [[pI]] 8.75  
 55 [[BLOCKS]] PRO0049D  
 [[BLOCKS]] BP01921G  
 [[PROSITE]] ASP\_PROTEASE 1  
 [[KW]] All\_Alpha

[[KW]] SIGNAL\_PEPTIDE 17  
 [[KW]] LOW\_COMPLEXITY 9.96 %

```

5  SEQ  MLFIFPLSLPWRPSCWKES CSTGQRQAGRSREDSVTPPPSSPWPTPPAGAMSTKQEARRD
   SEG  .....-XXXXXXXXXXXXX.....
   PRD  cccccccccccccceeeccccccccccccceeeccccccccccccccccchhhhhhhhhh

10  SEQ  EGEARTRGQEAQLRDRAHLSQQRRRLKQATQFLHKDSADLLPLDSLKRLGTSKDLQPRSVI
   SEG  .....
   PRD  cccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccccccccccccchhhh

15  SEQ  QRRLVEGNPNWLQGEPPRMQDLIHGQESRRKTSRTEIPALLVNCKCQDQLLRVAVD TGTD
   SEG  .....
   PRD  hhhhccccccccccccccccccccccccccccccccccccchhhhhhhchhhhhhhhhccce

20  SEQ  YNRISAGCL SRLGLEKRVLKASAGDLAPGPPTQVEQLQLGQETVVCSAQVVDAESPEF
   SEG  .....-XXXXXXXXXXXXXXXXX.....
   PRD  eeccccchhhhhhhhhhhhhhhhhhhhhccccccccccccchhhhhhhhhccceeeccceeeccccc

25  SEQ  CLGLQTL LSLKCCIDLEHGVLRLKAPFSELPFLPLYQEPGQ
   SEG  .....
   PRD  cccchhhhhhhhhhhcchhhhhhhcccccccccccccccccccc

```

Prosites for DKFZphamy2\_13g19.2

```

30  PS00141      173->185  ASP_PROTEASE      PD0C00128

```

(No Pfam data available for DKFZphamy2\_13g19.2)

DKFZphamy2\_14b5

-----

5 group: intracellular transport and trafficking

DKFZphamy2\_14b5 encodes a novel 771 amino acid protein which shows 61% identity to the human TYL protein and 48% identity to the human Tic protein.

10

Both proteins show similarity to Sec7 of *Saccharomyces cerevisiae*, which takes function in vesicular trafficking. The new protein shows also significant similarity to human ARN03, which is involved in the control of Golgi structure and function.

15

DKFZphamy2\_14b5 is predominantly expressed in the cns and germ cells.

20

The new protein can find application in diagnosis/therapy of diseases related to vesicular trafficking e.g. in synapses of the central nervous system and in studying expression profiles.

similarity to TYL protein (Homo sapiens)

25

Sequenced by EMBL

Locus: /map="445.7 cR from top of Chr5 linkage group"

30

Insert length: 4528 bp

Poly A stretch at pos. 4511, polyadenylation signal at pos. 4489

```

35      1 CTGCTCAGC CTCTCCACAT CGCGGCTCCG GCACCTGAAG GGACGCGGGC
      51 GGGCGCGGGC AGCTCCGACC GGC GGCGGGC GGGCGGGACA GGCAGCCCCG
     101 CGGCCTCCGA TGGCCCCGCC GTGAGAGGCC GGACCCGCGG CGGGGACCAG
     151 CAGCGGTCTA GAGGAGTCCC AGGAGCAGCC AGGACAGGCG GAAGCAGTGG
     201 CTGCCATGGA GGAGGACAAG CTCTTATCTG CAGTGCCTGA GGAAGGCGAT
     251 GCCACCCGTG ACCCCGGTCC AGAGCCTGAA GAGGAGCCAG GGGTCCGGAA
     40  301 TGGGATGGCC AGTGAGGGCC TGAACAGCAG CCTCTGCAGC CCAGGGCAGC
     351 AGCGAAGGGG CACCCAGCG GACACTGAGG AACCACGAA GGACCCAGAT
     401 GTGGCCTTCC ATGGCCTCAG CCTTGGCCTC TCTCTACCA ATGGCCTAGC
     451 CCTGGGGCCA GACTTGAACA TTCTGGAAGA TTCAGCGGAG TCCAGGCCCT
     501 GGAGGGCTGG CGTGCTGGCA GAGGGGGACA ATGCTTCCAG GAGCCTCTAC
     45  551 CCAGATGCTG AGGACCCTCA GCTGGGGTTG GATGGTCCCG GGGAGCCAGA
     601 TGTGCGGGAT GGCTTCAGCG CCACGTTTGA GAAGATTCTG GAGTCAGAGC
     651 TGCTGCGGGG CACCCAGTAC AGCAGCCTCG ACTCCCTAGA CGGGCTGAGC
     701 CTCACGGATG AGAGCGACAG CTGCGTCAGC TTCGAGGCCC CCCTCACACC
     751 CCTCATCCAG CAGCGGGCCC GTGACAGCCC TGAGCCAGGG GCTGGGTGTTG
     50  801 GCATTGGGGA CATGGCGTTT GAGGGGGACA TGGGGGCAGC TGGTGGTGAT
     851 GGGGAGCTGG GCAGCCCCCT GCGGCGCTCC ATCTCCAGCA GCCGCTCTGA
     901 GAATGTCCTG AGCCGCCTGT CTCTCATGGC CATGCCCAAT GGATTCCATG
     951 AAGATGGCCC TCAGGGCCCA GGGGGGGATG AGGATGATGA TGAGGAGGAC
    1001 ACGGACAAGT TGCTGAACTC AGCCAGTGAC CCCAGCCTGA AGGATGGCCT
    55 1051 GTCAGACTCA GACTCTGAGC TCAGCAGCTC GGAGGGGTTG GAGCCTGGTA
    1101 GTGCAGACCC TCTGGCCAAC GGGTGCCAGG GGGTCAGTGA AGCTGCTCAT
    1151 CGGCTGGCAC GCCGTCTCTA CCACCTCGAG GGCTTCCAGC GCTGTGATGT
    1201 GGCCCGGCAG CTGGGCAAGA ACAACGAGTT TAGCAGGCTG GTGGCCGGGG

```

	1251	AGTACCTCAG	TTTCTTCGAC	TTCTCGGGCT	TGACTCTGGA	CGGAGCACTC
	1301	AGAACATTCT	TGAAGGCCTT	CCCCGTGATG	GGGGAGACAC	AAGAGCGTGA
	1351	GCGGGTCCTC	ACACACTTCT	CCCCCGGTA	CTGCCAGTGC	AACCCTGATG
	1401	ACAGCACTTC	GGAAGATGGG	ATCCACACGC	TCACCTGTGC	CCTGATGCTG
5	1451	CTCAACACGG	ACCTGCACGG	CCACAACATT	GGCAAAAAGA	TGTCCTGTCA
	1501	GCAATTTCATT	GCCAACCTTG	ACCAGCTGAA	TGATGGCCAA	GACTTTTGCCA
	1551	AAGACCTGCT	GAAGACCCCT	TACAACCTCCA	TCAAGAATGA	AAAGCTGGAA
	1601	TGGGCCATTG	ATGAGGATGA	GCTGAGGAAA	TCCCTGTCTG	AGCTGGTGGA
	1651	TGACAAGTTC	GGGACAGGCA	CGAAGAAGGT	GACGCGAATC	CTGGATGGTG
10	1701	GCAACCCCTT	CCTGGATGTC	CCACAGGCGC	TCAGTGCCAC	CACCTACAAG
	1751	CACGGCGTCC	TGACCCGGAA	GA CTCACGCT	GACATGGATG	GCAAGAGGAC
	1801	GCCCCGTGGG	AGGCGTGGCT	GGAAGAAATT	CTACGCAGTG	CTCAAAGGGA
	1851	CCATCCTGTA	CCTGCAGAAG	GATGAGTACA	GGCCTGACAA	AGCTCTATCG
	1901	GAGGGTGACC	TGAAGAACGC	CATTTCGCGTG	CATCACGCTC	TGGCCACCAG
15	1951	GGCCTCTGAC	TACAGCAAGA	AGTCCAACGT	GCTGAAGCTT	AAGACAGCCG
	2001	ACTGGAGGGT	ATTCTCTTTC	CAGGCACCGA	GCAAGGAAGA	AATGCTGTCC
	2051	TGGATCCTCA	GGATCAACCT	GGTGGCAGCC	ATCTTCTCTG	CCCCGGCCTT
	2101	CCCAGCCGCT	GTCAGCTCCA	TGAAGAAGTT	CTGTCGGCCC	CTGCTGCCCT
	2151	CCTGCACCAC	CCGCCTCTGC	CAGGAGGAGC	AACTGCGGTC	TCATGAGAAT
20	2201	AAGTTGAGGC	AGCTGACTGC	GGAGCTGGCC	GAACACAGGT	GTCACCCAGT
	2251	CGAGAGGGGC	ATCAAGTCCA	AGGAGGCCGA	GGAGTACCGG	TTGAAGGAGC
	2301	ACTATCTCAC	CTTCGAGAAA	AGCCGTTATG	AGACCTATAT	CCACCTCCTG
	2351	GCTATGAAAA	TCAAAGTGGG	CTCAGATGAT	CTGGAGCGGA	TTGAGGCCCG
	2401	GCTGGCCACT	CTGGAAGGGG	ATGACCCCTC	TCTCCGGAAG	ACACATTCAA
25	2451	GCCCTGCCCT	CAGCCAGGGC	CATGTGACTG	GCAGCAAAAC	CACAAAGGAT
	2501	GCCACTGGGC	CTGATACTTA	GCTGACATGG	ATTTGCAGAC	CCCAGGGTGG
	2551	GCAGATGTCT	CCAGTGGGGT	CAGTGAGCAC	AATTCCAGCC	AGGGGCCACT
	2601	TGGACCAAGC	TCCAGTCAGT	TGATGGGCAG	CTAGAGGGGT	GCAGAAAGCC
	2651	TGTGGGCCCA	GGAGATGGAG	ATGCCGTTTG	TGGCGTTGAT	CTCCTTGCGT
30	2701	CCTTGGGCAT	CTCCGGGCAT	CAGACCCCTC	CCCTGGCCCT	TGTTTTCTCT
	2751	TCCACCATGG	AGCCTCATTT	TGTAGGCCAG	TTGTGTGCAT	GCTCTAGACA
	2801	CCACCTCGCT	GGAGAAGCTG	GAAGGGCTGT	TGTCTTCCCA	GGTCTTTCTC
	2851	TTCTCATCAA	GCTCCTCTCC	TCATCTTTTT	TGTGTGTGAG	GGCAGGTCTT
	2901	GACTCTAGGT	CTCAGCTGGA	ACCCACCCCT	TTCTCCTCCT	CCTTCTCTCT
35	2951	AGTTGACCAG	CAGCAGGTCT	GCCGACCACC	AGCACCATCC	TCTCCTCCCA
	3001	GCAGCCTCCA	GAACCATGCC	CAGGTCTCCT	GCCTCACATC	ACAATAACTCT
	3051	GGGACCCAGG	CTTGTGCCCT	TTCAGTGTA	AGCTGACTCC	ATCATATGTG
	3101	CATCCACTTC	TTTTTCATCCA	TTGAGATCAC	ACTGCCTCCT	TTTTATACAG
	3151	ACACAAATAT	ACATCTATAA	GAATAATATA	TACATAAGGA	ACCCCTGAAA
40	3201	GATGGTTTTG	GAAC TGGAAT	CAGTTAGAGG	ATGAAATCAG	ATAAAGGAAA
	3251	AGCCTATTTT	GGAGCTTCCC	CTGTTAGGAA	GGATGGCTGC	ACCTGGCCCC
	3301	CTGGCATTCC	TGACGCTCTA	GGAGGGAAGG	GGGAGGCAGT	GCTGGCCTCC
	3351	CTTGCCCTGT	TTTTCCCTCT	TCCAGCTGAC	CTGTGACTTA	TACTGCTCTT
	3401	ACCGATGATA	CTTTTGGA	AAATAGAGCG	TGTATGCACC	GCCCCGTTTG
45	3451	TCCCATGGAT	ATCCTGGGGT	GTGAGTCGGA	TGGGACCACG	GCCCTGTTTA
	3501	TATTTGGGTC	TTTATGTTGG	TGCTGCCAGG	TCTCTGAGCT	CCAGAGGTGG
	3551	CCTCTTGAC	AGATCTACTG	CTATAGGAAT	AAAAGACACT	CTGTCTCGCA
	3601	AATGGCTGCT	TGTCAACAAG	CCCAAAGATG	CTTGTGCGAG	GACGGTTATG
	3651	GAAGCCCTTA	ATTCTTGTTT	GTGGGAAAAG	GTGGAATGAC	AAGTTATTGA
50	3701	TTGTTTTTCT	GTCGCTATTT	CTTTCATTTG	TCTAGTGAAT	CAGAAAGGCT
	3751	TAGCCAAGGC	CACATCTGGG	AAGAGTGGAG	AAATTTGCCA	CTTGACGATC
	3801	ACGGATTAGC	TAGCACCTTT	AAGCCCTGCA	TTTCTCCAAC	TGACAAGTGG
	3851	GTGGGGGTGA	TGGCACATTC	AGTGTGGCTA	TGAAGAGCGA	ATCCTCTCTA
	3901	TTGTTTAAAT	AGATTACTGT	AGTTTGGCCA	GGAATTTGGC	GTCAGTGGTA
55	3951	ACACACTTAG	TTAATAAAAT	AAGCCAGGCT	TGCAACTAAG	TATCTAACTT
	4001	TACAGGCCCA	CTCACATTTG	AGGCAAGGGG	CTATTGAGTA	TGTGGAGAGA
	4051	TGTAGTGATT	TAAATTCAGA	TTATTTAAGT	TGGATCAGCT	GAAGTGTGTT
	4101	TTAGACCCAA	ACCATCTGGC	CCCTTCGTTT	TGCTCAGAGG	AAGTAAATGT

4151 TCACTTAAAT GAAATTGAAA ACGCCATGTG GCACCACAAA AGAGCTCTCT  
 4201 GTACTTTCCC CATGCTGCCT CAAAAGTTCT GTGAGTTTCG GGGTCAGTGT  
 4251 CCCACCCCTC ACTTCCCGAG GCGGGGTGAG TGGAGAGCAG AGCCAGGAGC  
 4301 TCTGGCAGCT GTGGACAGAT GTGCTTCCTG AGCATGGGTT GTGCCTCCCA  
 5 4351 TCAGTAAAAA AATGTTTAGT TCACTTCCTT AATTGTATAA TTATTTATTT  
 4401 GTAAATTATA TACATGTACT ACTGTACTAA AATATTATGT ACATTATAAA  
 4451 ACATACACAA AAATAGAAAT TAAAAAAGA TGAGATGAAA ATAAATCTAA  
 4501 GTCAAAGTTC CAAAAAAGTTC AAAAAAAGTTC

10

## BLAST Results

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No BLAST result

15

## Medline entries

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20 98086482:

Perletti L, Talarico D, Trecca D, Ronchetti D, Fracchiolla NS, Maiolo AT, Neri A.; Identification of a novel gene, PSD, adjacent to

25 NFKB2/lyt-10, which contains Sec7 and pleckstrin-homology domains.

Genomics 46:251-259(1997)

30

## Peptide information for frame 2

-----

ORF from 206 bp to 2518 bp; peptide length: 771

35 Category: similarity to known protein

Classification: Cell signaling/communication

1 MEEDKLLSAV PEEGDATRDP GPEPEEEPGV RNGMASEGLN SSLCSPGHER  
 51 RGTPADTEEP TKDPPDVAFHG LSLGLSLTNG LALGPDNLIL EDSAESRPWR  
 40 101 AGVLAEGDNA SRSLYPDAED PQLGLDGPGE PDVRDGFSA FEKILESELL  
 151 RGTQYSSLD LDGLSLTDES DSCVSFEAPL TPLIQQRARD SPEPGAGLGI  
 201 GDMAFEGDMG AAGDGELGS PLRRSISSSR SENVLSRLSL MAMPNGFHED  
 251 GPQGPGGDED DDEEDTDKLL NSASDPSLKD GLSDSDSELS SSEGLEPGSA  
 301 DPLANGCQGV SEAAHRLARR LYHLEGFQRC DVARQLGKNN EFSRLVAGEY  
 45 351 LSFFDFSGLT LDGALRTFLK AFPLMGETQE RERVLT HFSR RYCQCNPD DS  
 401 TSEDGIHTLT CALMLLNTDL HGHNIGKKMS CQQFIANLDQ LNDGQDFAKD  
 451 LLKTLYNSIK NEKLEWAIDE DELRKSLSEL VDDKFGTGTK KVTRILDGGN  
 501 PFLDVPQALS ATTYKHGVL T RKTHADMDGK RTPRGRRGWK KFYAVLKG TI  
 551 LYLQKDEYRP DKALSEGDLK NAIRVHHALA TRADYSKKS NVLKLKTADW  
 50 601 RVFLFQAPSK EEMLSWILRI NLVAAIFSAP AFPAAVSSMK KFCRPLLPSC  
 651 TTRLCQEEQL RSHENKLRQL TAELAEHRCH PVERGIKSKE AEEYRLKEHY  
 701 LTFEKSRYET YIHLLAMKIK VGSDDLRIE ARLATLEGDD PSLRKTHSSP  
 751 ALSQGHVTGS KTTKDATGPD T

55

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_14b5, frame 2

5 PIR:G01205 TYL protein - human, N = 2, Score = 1421, P = 8.6e-150

TREMBL:AB023159\_1 gene: "KIAA0942"; product: "KIAA0942 protein"; Homo sapiens mRNA for KIAA0942 protein, partial cds., N = 1, Score = 1251, P = 2.3e-127

10 TREMBL:U63127\_1 gene: "TIC"; product: "Tic"; Human SEC7 homolog Tic (TIC) mRNA, complete cds., N = 1, Score = 1050, P = 4.6e-106

15 >PIR:G01205 TYL protein - human  
Length = 645

20 HSPs:

Score = 1421 (213.2 bits), Expect = 8.6e-150, Sum P(2) = 8.6e-150

25 Identities = 280/452 (61%), Positives = 336/452 (74%)

Query: 301  
DPLANGCQGVSEAAHRLARRLYHLEGFQRCDDVARQLGKNNEFSRLVAGEYLSFFDFSGLT 360  
D L+NG + EAA RLA+RLY L+GF++ DVAR LGKNN+FS+LVAGEYL

30 FF F+G+T  
Sbjct: 166  
DTLSNGQKADLEAAQRLAKRLYRLDGFRKADVARHLGKNNDFSKLVAGEYLKFFVFTGMT 225

Query: 361  
35 LDGALRTFLKAFPLMGETQERERVLTHFSRRYCQCNPDDSTSEDGIHTLTALMLLNTDL 420  
LD ALR FLK LMGETQERERVL HFS+RY QCNP+ +SEDG  
HTLTALMLLNTDL  
Sbjct: 226  
LDQALRVFLKELALMGETQERERVLAHFSQRYFQCNPALSSSEDGAHTLTALMLLNTDL 285

40 Query: 421  
HGHNIGKKMSCQQFIANLDQLNDGQDFAKDLLKTLYNSIKNEKLEWAIDEDELKSLSEL 480  
HGHNIGK+M+C FI NL+ LNDG DF ++LLK  
LY+SIKNEKL+WAIDE+ELR+SLSEL

45 Sbjct: 286  
HGHNIGKRMTGDFIGNLEGLNDGGDFPRELLKALYSSIKNEKLQWAIDEEELRRSLSEL 345

Query: 481 VDDKFGTGTKKVTRIL----  
DGGNPFLDVPQALSATTYKHGVLTRKTHADMDGKRTPRGR 536  
D K + RI G +PFLD+ A YKHG L RK HAD D  
++TPRG+

50 Sbjct: 346 ADPN----  
PKVIKRISGGSGSGSSPFLDLTPEPGAAYKHGALVRKVHADPDCRKTPRGK 401

55 Query: 537  
RGWKKFYAVLKGITILYLQKDEYRPDKALSEGDLKNAIRVHHALATRASDYSSKSNVLKLLK 596  
RGWK F+ +LKG ILYLQK+EY+P KALSE +LKNAI  
+HHALATRASDYSSK+ +V L+



Sbjct: 402  
RGWKSFGILKGMILYLQKEEYKPGKALSETELKNAISIHHALATRASDYSKRPHVFYLR 461

Query: 597  
5 TADWRVFLFQAPSKEEMLSWILRINLXXXXXXXXXXXXXXXXSMKKFCRPLLPSCTTRLQ 656  
TADWRVFLFQAPS E+M SWI RIN+ S KKF

RPLLPS TRL Q

Sbjct: 462  
10 TADWRVFLFQAPSLQMQSWITRINVVAAMFSAPPFPAAVSSQKKFSRPLLPSAATRLSQ 521

Query: 657  
EEQLRSHENKLRQLTAELAEHRCHPVERGIKSKEAEEYRLKEHYLTFEKSR YETIYIHLA 716  
EEQ+R+HE KL+ + +EL EHR + + + KEAEE R KE YL FEKSR Y  
TY LL

15 Sbjct: 522  
EEQVRTHEAKLKAMASELREHRAAQLGKKGRGKEAEEQRQKEAYLEFEKSRYSTYAALLR 581

Query: 717 MKIKVGSDDLERIEARLATLEGDDPSLRKTHSSPAL 752  
+K+K GS++L+ +EA LA + L +HSSP+L

20 Sbjct: 582 VKLKAGSEELDAVEAALAQAGSTEDGLPPSHSSPSL 617

Score = 63 (9.5 bits), Expect = 8.6e-150, Sum P(2) = 8.6e-150  
Identities = 19/64 (29%), Positives = 23/64 (35%)

25 Query: 132 DVRDGFSAFTEKILESELLRGTQYXXXXXXXXXXXXXXXXXX-  
CVSFEAPLTPLIQQRARD 190  
D D FS FE ILES +GT Y +FE P P

+  
Sbjct: 18  
30 DGPDSFSCVF EAILSHRAKGTSYTSLASLEALASPGPTQSPFFTFELPPQPPAPRPDPP 77

Query: 191 SPEP 194  
+P P

35 Sbjct: 78 APAP 81

Pedant information for DKFZphamy2\_14b5, frame 2

40 Report for DKFZphamy2\_14b5.2

45 [LENGTH] 771  
[MW] 84660.55  
[pI] 5.04  
[HOMOL] PIR:G01205 TYL protein - human 1e-158  
[FUNCAT] 30.09 organization of intracellular transport vesicles  
[S. cerevisiae, YDR170c] 5e-22  
50 [FUNCAT] 30.08 organization of golgi [S. cerevisiae, YDR170c]  
5e-22  
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae,  
YDR170c] 5e-22  
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S.  
cerevisiae, YDR170c] 5e-22  
55 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YPR095c]  
4e-04  
[BLOCKS] BL01277B  
[BLOCKS] BP02373F

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[BLOCKS] PRO0655C
[BLOCKS] PRO1088F
[BLOCKS] PRO0229B
[BLOCKS] BP02646D
5 [BLOCKS] PRO0391A
[BLOCKS] DM01354M
[BLOCKS] PF01369B
[BLOCKS] PF01369A
[SCOP] dlbtn__ 2.41.1.1.2 beta-spectrin [mouse (Mus
10 musculus) brain 1e-39
[PIRKB] transmembrane protein 1e-20
[SUPFAM] Caenorhabditis elegans K06H7.4 protein 7e-24
[SUPFAM] pleckstrin repeat homology 7e-24
[PFAM] PH (pleckstrin homology) domain
15 [KW] Irregular
[KW] 3D
[KW] LOW_COMPLEXITY 18.42 %

20 SEQ MEEDKLLSAVPEEGDATRDPGPEPEEEPGVRNGMASEGLNSSL CSPGHERRGTPADTEEP
SEG .....xxxxxxxxxxxxx.....
lbtn-
.....

25 SEQ TKDPDVAFHGLSLGLSLTNGLALGPDLNILED SAESRPWRAGVLAEGDNASRSLYPDAED
SEG .....xxxxxxxxxxxxxxxxx.....
lbtn-
.....

30 SEQ PQLGLDGPGE PDVRDGF SATFEKILESELLRGTQYSSLD SL DGLSLTDES DSCVSFEAPL
SEG .....xxxxxxxxxxxxxxxxxxxxx.....
lbtn-
.....

35 SEQ TPLIQQRARDSPEPGAGLGIGDMAFEGDMGAAGGDGELGSPLRRSISSSRSENVLSRLSL
SEG .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
lbtn-
.....

40 SEQ MAMPNGFHEDGPQGP GGDEDDDEEDTDKLLNSASDPSLKDGLSDSDSELSSSEGLEPGSA
SEG .....xxxxxxxxxxxxxxxxxxxxx.....xxxxxxxxxxxxxxxxxxxxxxxxxxxxx
lbtn-
.....

45 SEQ DPLANGCQGVSEAAHRLARRLYHLEGFQRC DVARQLGKNNEFSRLVAGEYLSFFDFSGLT
SEG .....
lbtn-
.....

50 SEQ LDGALRTFLKAFPLMGETQERERVLTHFSRRYCQCNPD DSTSEDGIHTLT CALMLLNTDL
SEG .....
lbtn-
.....

55 SEQ HGHNIGKKMSCQQFIANLDQLNDGQDFAKDLLKTL YNSIKNEKLEWAIDEDELKSLSEL
SEG .....
lbtn-
.....

```

```

SEQ  VDDKFGTGTKKVTRILDGGNPFLDVPQALSATTYKHGVLTRKTHADMDGKRTPRGRRGWK
SEG  .....
lbtn- .....EEEEEEEEETTTEET--
5   TTTCEE

SEQ  KFYAVLKGITILYLQKDEYRPDKALSEGDLKNAIRVHHALATRASDYSKKSNNVLKLKTADW
SEG  .....
lbtn- EEEEEETTTEEEECCHHHHHHCCBTTT-
10  TCCEETTTTEEEETTTTTCTTTEEEETTTT

SEQ  RVFLFQAPSKEEMLSWILRINLVAAIFSAFPAAVSSMKKFCRPLLPSCTTRLCQEEQL
SEG  .....xxxxxxxxxxxxxxxxxxxx.....
lbtn- .....
15  CEEEEECCHHHHHHHHHHH.....

SEQ  RSHENKLRQLTAELAEHRCHPVERGIKSKEAEEYRLKEHYLTFEKSRYETYIHLAMKIK
SEG  .....
lbtn- .....
20  .....

SEQ  VGSDDLERIEARLATLEGDDPSLRKTHSSPALSQGHVTGSKTTKDATGPD
SEG  .....
lbtn- .....
25  .....

```

(No Prosite data available for DKFZphamy2\_14b5.2)

30 Pfam for DKFZphamy2\_14b5.2

HMM\_NAME PH (pleckstrin homology) domain

```

35  HMM
    *dvIREGWMyKWgswrkstg.....nWqrRWFvLrndpnrLiYYkddk
                                + ++G + +++ + ++          W++ ++VL++ + L++
KD+
Query           512  TTYKHGVLTRKTHADMDGKRTPRGRRGWKKFYAVLKG--
40  TILYLQKDE-    557

HMM
dekPr.....YMlIdld.cWrMidVEidWmmdndHCFiIWtrq.rtYYF
                                +P+          + ++D ++ +++ +++T +
45  R+++F
Query           558  -YRPDKALSEGDLKNAIRVHHALATRASDYSKK-
SNVLKLKTADWRVFLF    605

HMM
QAeNeEEMmeWMsaIrRaIw*
50  QA+++EEM +W+ I+ + +
Query           606  QAPSKEEMLSWILRINLVAA      625

```

DKFZphamy2\_14m1b

-----

5 group: transcription factors

DKFZphamy2\_14m1b.p1 encodes a novel 252 amino acid protein with similarity to the homeotic protein emx2 of man, mouse and zebra fish as well as to the gene "empty spiracles" of *Drosophila melanogaster*.

Homoeobox genes are known to play important roles in developmental processes. In zebrafish emx2 mRNAs are found in the dorsal telencephalon, parts of the diencephalon and the otocyst. The human homologue Emx2 appears to be already expressed in 8.5 day embryos. It is also expressed in the presumptive cerebral cortex, olfactory bulbs, in some neuroectodermal areas in embryonic head including olfactory placodes in earlier stages and olfactory epithelia later in development. Mutants of the *D. melanogaster* gene "empty spiracles" display spiracles devoid of filzkörper, no antenna and an open head.

The new protein can find application in modulating the expression of genes controlled by this transcription factor and modulation of neuronal development.

strong similarity to homeotic protein emx2 (*Homo sapiens*)

perhaps differential splicing

Sequenced by EMBL

Locus: /chromosome="10"

Insert length: 241b bp

Poly A stretch at pos. 2378, polyadenylation signal at pos. 2373

```

1  GAAAAAAAAA GAAAAAAAAA GAAAAAAAAAT TACCCCAATC CACGCCTGCA
40  51 AATTCTTCTG GAAGGATTTT CCCCCCTCTC TTCAGGTTGG GCGCGTTTGG
    101 TGCAAGATTG TCGGGATCCT CGGCTTTGCC TCTCCCTCTC CCTCCCCCT
    151 CTTTTCTTTT TTCCTTTCCT TTCCTTTCTT TCTTCTTTTC CTTCCCCCA
    201 CCCCCACCCC CACCCCAAAC AAACGAGTCC CCAATTCTCG TCCGTCTCTG
    251 CCGCGGGCAG CGGGCGGGCG AGGCAGCGTG CGGCGGTCGC CAGGAGCTGG
45  301 GAGCCAGGGG CGCCCGCTCC TCGGCGCAGC ATGTTCCAGC CGGCGCCCAA
    351 GCGCTGCTTC ACCATCGAGT CGCTGGTGGC CAAGGACAGT CCCCTGCCCCG
    401 CCTCGCGCTC CGAGGACCCC ATCCGTCCCG CGGCACTCAG CTACGCTAAC
    451 TCCAGCCCCA TAAATCCGTT CCTCAACGGC TTCCACTCGG CCGCCGCCGC
    501 CGCCGCCGGT AGGGGCGTCT ACTCCAACCC GGAAGTGGTG TTCGCCGAGG
50  551 CGGTCTCGCA CCGCCCCAAC CCGCCGTGCG CAGTGCACCC GGTGCCGCCG
    601 CCGCACGCCC TGGCCGCCCA CCCCCTACCC TCCTCGCACT CGCCACACCC
    651 CCTATTGCGC TCGCAGCAGC GGGATCCGTC CACCTTCTAC CCCTGGCTCA
    701 TCCACCGCTA CCGATATCTG GGTATCGCT TCCAAGGGAA CGACACTAGC
    751 CCGGAGAGTT TCCTTTTGCA CAACGCGCTG GCCCGAAAGC CCAAGCGGAT
55  801 CCGAACCGCC TTCTCCCCGT CCCAGCTTCT AAGGCTGGAA CACGCCTTTG
    851 AGAAGAATCA CTACGTGGTG GCGCGCGAAA GGAAGCAGCT GGCACACAGC
    901 CTCAGCCTCA CGGAAACTCA GGTAAAAGTA TGGTTTCAGA ACCGAAGAAC
    951 AAAGTTCAAA AGGCAGAAGC TGGAGGAAGA AGGCTCAGAT TCGCAACAAA

```

```

1001 AGAAAAAAGG GACGCACCAT ATTAACCGGT GGAGAATCGC CACCAAGCAG
1051 GCGAGTCCGG AGGAAATAGA CGTGACCTCA GATGATTAAA AACATAAACC
1101 TAACCCACACA GAAACGGACA ACATGGAGCA AAAGAGACAG GGAGAGGTGG
1151 AGAAGGAAAA AACCTACAA AAAAAAACA AACCGCATAC ACGTTCACCG
5 1201 AGAAAGGGAG AGGGAATCGG AGGGAGCAGC GGAATGCGGC GAAGACTCTG
1251 GACAGCGAGG GCACAGGGTC CCAAACCGAG GCCGCGCCAA GATGGCAGAG
1301 GATGGAGGCT CTTTCATCAA CAAGCGACCC TCGTCTAAAG AGGCAGCTGA
1351 GTGAGAGACA CAGAGAGAAG GAGAAAGAGG GAGGGAGAGA GAGAAAGAGA
1401 GAGAAAGAGA GAGAGAGAGA GAGAGAAAGC TGAACGTGCA CTCTGACAAG
10 1451 GGGAGCTGTC AATCAAACAC CAAACCGGGG AGACAAGATG ATTGGCAGGT
1501 ATTCCGTTTA TCACAGTCCA CTAAAAAAT GATGATGATG AAAAAACCA
1551 CGACCCAACC AGGCACAGGA CTTTTTTGTT TTTTGCATT CGCTGTGTTT
1601 CCCCCCATC TTAAAAAATA ATTAGTAATA AAAAACAAAA ATTCCATATC
1651 TAGCCCCATC CCACACCTGT TTCAAATCCT TGAAATGCAT GTAGCAGTTG
15 1701 TTGGGCGAAT GGTGTTTAAA GACCGAAAAT GAATTGTAAT TTTCTTTTCC
1751 TTTTAAAGAC AGGTTCTGTG TGCTTTTAT TTTGATTTT TTTCCCAAGA
1801 AATGTGCAGT CTGTAAACAC TTTTGTATC CTTCTGATGT CAAAGTGATT
1851 GTGCAAGCTA AATGAAGTAG GCTCAGCGAT AGTGGTCCTC TTACAGAGAA
1901 ACGGGGAGCA GGACGACGGG GGGGCTGGGG GTGGCGGGGG AGGGTGCCCA
20 1951 CAAAAAGAAT CAGGACTTGT ACTGGGAAAA AAACCCCTAA ATTAATTATA
2001 TTTCTTGGAC ATTCCCTTTC CTAACATCCT GAGGCTTAAA ACCCTGATGC
2051 AAACCTCTCC TTTCAGTGGT TGGAGAAATT GGCCGAGTTC AACCATTAC
2101 TGCAATGCCT ATTCCAACT TTAAATCTAT CTATTGCAA ACCTGAAGGA
2151 CTGTAGTTAG CGGGGATGAT GTTAAGTGTG GCCAAGCGCA CGGCGGCAAG
25 2201 TTTTCAAGCA CTGAGTTTCT ATTCCAAGAT CATAGACTTA CTAAAGAGAG
2251 TGACAAATGC TTCCTTAATG TCTTCTATAC CAGAATGTAA ATATTTTGT
2301 GTTTTGTGTT AATTTGTTAG AATTCTAACA CACTATATAC TTCCAAGAAG
2351 TATGTCAATG TCAATATTTT GTCAATAAAG ATTTATCAAT ATGCCCTCAC
30 2401 AAAAAAAAAA AAAAAA

```

## BLAST alert EMBL/EMBLNEW

-----

```

35 EMBLNEW:AL133353 Human DNA sequence *** SEQUENCING IN PROGRESS
*** from
clone RP11-483F11; N = 2, Score = 3108, P = 5.3e-134

EMBL:HSEMX2 H.sapiens EMX2 mRNA; N = 1, Score = 2385, P = 5.1e-
40 101

```

## Medline entries

-----

```

45 92331606:
Simeone A, Gulisano M, Acampora D, Stornaiuolo A, Rambaldi M,
Boncinelli E.;
Two vertebrate homeobox genes related to the Drosophila empty
spiracles gene are expressed in the embryonic cerebral cortex.
50 EMB0 J
1992 Jul;11(7):2541-50

```

55

## Peptide information for frame 1

-----

ORF from 331 bp to 1086 bp; peptide length: 252  
 Category: questionable ORF  
 Classification: unset  
 Prosite motifs: HOME0B0X\_1 (187-210)

5

1 MFQPAKRCF TIESLVAKDS PLPASRSEDP IRPAALSYAN SSPINPFLNG  
 51 FHSAAAAAAG RGVYSNPDLV FAEAVSHPPN PAVPVHPVPP PHALAAHPLP  
 101 SSHSPHPLFA SQQRDPSTFY PWLIHRYRYL GHRFQGNQTS PESFLLHNAL  
 151 ARKPKRIRTA FSPSQLLRLE HAFEKNHYVV GAERKQLAHS LSLTETQVKV  
 201 WFQNRRTKFK RQKLEEEGSD SQQKKKGTH INRWRIATKQ ASPEEIDVTS  
 251 DD

15

Alert BLASTP hits for DKFZphamy2\_14m1b, frame 1

PIR:I51737 homeotic protein emx2 - zebra fish; N = 2, Score =  
 753, P =  
 1e-105

20

PIR:S22722 homeotic protein emx2 - human (fragment); N = 1, Score =  
 763, P = 1.3e-75

25

TREMBL:0LA132403\_1 gene: "emx2"; product: "Emx2 protein";  
 Oryzias  
 latipes mRNA for Emx2 protein, partial; N = 2, Score = 513, P =  
 4.5e-72

30

>PIR:S22722 homeotic protein emx2 - human (fragment)  
 Length = 158

HSPs:

35

Score = 763 (114.5 bits), Expect = 1.3e-75, P = 1.3e-75  
 Identities = 144/144 (100%), Positives = 144/144 (100%)

Query: 109

40

FASQQRDPSTFYPWLIHRYRYLGHRFQGNQTS PESFLLHNALARKPKRIRTA FSPSQLLR 168

FASQQRDPSTFYPWLIHRYRYLGHRFQGNQTS PESFLLHNALARKPKRIRTA FSPSQLLR

Sbjct: 15

FASQQRDPSTFYPWLIHRYRYLGHRFQGNQTS PESFLLHNALARKPKRIRTA FSPSQLLR 74

45

Query: 169

LEHAFEKNHYVVGAERKQLAHSLSLTETQVKVWFQNRRTKFKRQKLEEEGSDSQQKKKG 228

LEHAFEKNHYVVGAERKQLAHSLSLTETQVKVWFQNRRTKFKRQKLEEEGSDSQQKKKG

50

Sbjct: 75

LEHAFEKNHYVVGAERKQLAHSLSLTETQVKVWFQNRRTKFKRQKLEEEGSDSQQKKKG 134

Query: 229 HHINRWRIATKQASPEEIDVTSDD 252

HHINRWRIATKQASPEEIDVTSDD

55

Sbjct: 135 HHINRWRIATKQASPEEIDVTSDD 158

Pedant information for DKFZphamy2\_14m1b, frame 1

## Report for DKFZphamy2\_14mlb.1

```

5  [LENGTH]          362
   [MW]              40749.28
   [pI]              10.51
   [HOMOL]           PIR:I51737 homeotic protein emx2 - zebra fish le-
                        113
10  [FUNCAT]          30.10 nuclear organization      [S. cerevisiae,
   YML027w] 5e-05
   [FUNCAT]          04.99 other transcription activities [S.
   cerevisiae, YML027w] 5e-05
   [FUNCAT]          03.07 pheromone response, mating-type
15  determination, sex-specific proteins [S.
   cerevisiae, YCR097w] 5e-04
   [FUNCAT]          04.05.01.04 transcriptional control [S.
   cerevisiae, YDL106c] 7e-04
   [FUNCAT]          01.04.04 regulation of phosphate utilization
20  [S. cerevisiae, YDL106c] 7e-04
   [FUNCAT]          01.03.13 regulation of nucleotide metabolism
   [S. cerevisiae, YDL106c] 7e-04
   [BLOCKS]          PR00049D
   [BLOCKS]          PR00909H
25  [BLOCKS]          PR00487F
   [BLOCKS]          PR00796G
   [BLOCKS]          BL00035C
   [BLOCKS]          BL00027 'Homeobox' domain proteins
   [BLOCKS]          PR00026A
30  [BLOCKS]          BL00032C
   [BLOCKS]          BL00032B 'Homeobox' antennapedia-type protein
   [SCOP]             d1au7b1 1.4.1.1.6 Pit-1 POU homeodomain Pit-1
   Pit-1 [Rat (Rattus 5e-16
   [SCOP]             d1yrna_1.4.1.1.2 mating type protein A1
35  Homeodomain mat alpha 2e-15
   [SCOP]             d1enh_1.4.1.1.1 engrailed Homeodomain
   [(Drosophila melanogaster 2e-13
   [PIRKW]            nucleus 1e-67
   [PIRKW]            heart 3e-10
40  [PIRKW]            DNA binding 1e-67
   [PIRKW]            leukemia 3e-15
   [PIRKW]            alternative splicing 1e-10
   [PIRKW]            proto-oncogene 3e-15
   [PIRKW]            transcription factor 1e-11
45  [PIRKW]            embryo 9e-12
   [PIRKW]            transcription regulation 1e-67
   [PIRKW]            homeobox 1e-67
   [SUPFAM]           homeobox homology 1e-67
   [SUPFAM]           homeotic protein Hox A5 7e-10
50  [SUPFAM]           homeotic protein Hox B3 3e-10
   [SUPFAM]           homeotic protein Hox B2 3e-11
   [SUPFAM]           homeotic protein Hox B1 7e-11
   [SUPFAM]           unassigned homeobox proteins 1e-67
   [SUPFAM]           homeotic protein goosecoid 4e-10
55  [SUPFAM]           homeotic protein Hox D4 9e-12
   [PROSITE]          HOMEBOX_1 1
   [PFAM]             Homeobox domain
   [KW]               Irregular

```

[[KW]] 3D  
 [[KW]] LOW\_COMPLEXITY 25.69 %

```

5  SEQ
   EKRRKKKKKNYPNPRLLQILLEGFSPLSSGWARLVQDSRDPRCLSLSLPPPFLFPFLSFL
   SEG
   .xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
   lfj1a
10  .....

   SEQ
   SSFSPSPHPHPKQTSPQFSSVLAAGSGRRRQRAAVARSWEPRAPAPRRSMFQAPAPKRCF
   SEG
15  xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
   lfj1a
   .....

   SEQ
20  TIESLVAKDSPLPASRSEDPIRPAALSYANSSPINPFLNGFHSAAAAAAGRGVYSNPDLV
   SEG
   .....xxxxxx.....
   lfj1a
   .....

25  SEQ
   FAEAVSHPPNPAVPVHPVPPPHALAAHPLSSHSPHPLFASQQRDPSTFYPLIHRYRYL
   SEG
   .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
30  lfj1a
   .....

   SEQ
   GHRFQGNDTSPESFLLHNALARKPKRIRTAFFSPSQLLRLEHAFEKNHYVVGAEKQLAHS
35  SEG
   .....
   lfj1a
   .....CCCCCCCCCHHHHHHHHHHHHHHTTTTCHHHHHHHHHHH

40  SEQ
   LSLTETQVKVWFQNRRTKFKRQKLEEEGSDSQQKKKGTHHINRWRIATKQASPEEIDVTS
   SEG
   .....
   lfj1a
45  HCCCHHHHHHHHHHHHHHHHHHHHH.....

   SEQ      DD
   SEG      ..
   lfj1a    ..
50

```

Prosites for DKFZphamy2\_14m16.1

55 PS00027 297->321 HOME0BOX\_1 PD0C00027

Pfam for DKFZphamy2\_14m16.1



HMM\_NAME Homeobox domain

HMM

5 \*RRRpRTtFTreQLdELEREFHfNrYPTRqRREELAQmLNlTERQVKIWF  
+R RT+F+ +QL++LE +F+ N+Y+ ++R

+LA++L+LTE+QVK+WF

Query 264

PKRIRTAfSPSQLLRLEHAFEKNHYVVGAERKQLAHSLSLTETQVKVWF 312

10

HMM QNRRMKWKRMH\*

QNRR+K KR+

Query 313 QNRRTKFKRQK 323

15

5 group: amygdala derived

DKFZphamy2\_16e14.p3 encodes a novel 328 amino acid protein,  
similar to carbonic anhydrase-related proteins.

10 A similar cDNA encoding a protein of the same length was  
identified in sheep. This protein shows a strong signal sequence,  
which indicates that it is a secreted protein. The new protein  
belongs to a protein family, which was designated carbonic  
15 anhydrase-related protein XI (CA-RP XI), encoded by CA11 (human)  
and Car11 (mouse, rat). Despite potentially inactivating changes  
in the active-site residues, CA-RP XI is evolving very slowly in  
mammals, a property indicative of an important function, which  
has also been observed in the two other "acatalytic" CA isoforms,  
CA-RP VIII and CA-RP X.  
20 No informative BLAST results; No predictive prosite, pfam or SCOP  
motife.

The new protein can find application in studying the expression  
profile of amygdala-specific genes.

25

similarity to carbonic anhydrase-related protein (Homo sapiens)

ESTs ending at appr. 1800 have polyA-signal

30

Sequenced by EMBL

Locus: /map="17q24; 5.13cR from GATA41C05"

35 Insert length: 2267 bp

Poly A stretch at pos. 2252, polyadenylation signal at pos. 2231

40 1 GGATGGAAAT AGTCTGGGAG GTGCTTTTTC TTCTTCAAGC CAATTTTCATC  
51 GTCTGCATAT CAGCTCAACA GAATTCACCA AAAATCCATG AAGGCTGGTG  
101 GGCATACAAG GAGGTGGTCC AGGGAAGCTT TGTTCAGTT CCTTCTTTCT  
151 GGGGATTGGT GAACTCAGCT TGGGAATCTTT GCTCTGTGGG GAAACGGCAG  
201 TCGCCAGTCA ACATAGAGAC CAGTCACATG ATCTTCGACC CCTTTCTGAC  
251 ACCTCTTCGC ATCAACACGG GGGGCAGGAA GGTCAGTGGG ACCATGTACA  
45 301 ACACTGGAAG ACACGTATCC CTTCGCCTGG ACAAGGAGCA CTTGGTCAAC  
351 ATATCTGGAG GGCCCATGAC ATACAGCCAC CGGCTGGAGG AGATCCGACT  
401 ACACTTTGGG AGTGAGGACA GCCAAGGGTC GGAGCACCTC CTCAATGGAC  
451 AGGCCTTTCTC TGGGGAGGGT CAGCTCATCC ACTATAACCA TGAGCTATAT  
501 ACGAATGTCA CAGAAGCTGC AAAGAGTCCA AATGGATTGG TGGTAGTTTC  
50 551 TATATTTATA AAAGTTTCTG ATTCATCAAA CCCATTTCTT AATCGAATGC  
601 TCAACAGAGA TACTATCACA AGAATAACAT ATAAAAATGA TGCATATTTA  
651 CTACAGGGGC TTAATATAGA GGAAGTATAT CCAGAGACCT CTAGTTTTCAT  
701 CACTTATGAT GGGTCGATGA CTATCCCACC CTGCTATGAG ACAGCAAGTT  
751 GGATCATAAT GAACAAACCT GTCTATATAA CCAGGATGCA GATGCATTCC  
55 801 TTGCGCCTGC TCAGCCAGAA CCAGCCATCT CAGATCTTTC TGAGCATGAG  
851 TGACAACTTC AGGCCTGTCC AGCCACTCAA CAACCGCTGC ATCCGCACCA  
901 ATATCAACTT CAGTTTACAG GGGGAAGGACT GTCCAAACAA CCGAGCCCAG  
951 AAGCTTCAGT ATAGAGTAAA TGAATGGCTC CTCAAGTAGG GAACAAAGCC

```

1001 AAGAAGAATC CCACCTCAGT GAAATGCTAC AACTGTGAAT TGACGTAACC
1051 TAGAATGTCC CCTTCTTGC TTCTCTCTCC TTCTTTCCCC CAAGCCTCAT
1101 TCATTCTTGG GATTGGCCCT TTCTTCATGA AAAGTGTCTG CAAAACCATG
1151 GCAGAGGAAT ACATCTCTCA CACATACTCA CAAACACACA CACAAGCACT
5 1201 TGCACATACA TACAAACACA TGCAAAACATA CCTACACACA CACACACTCT
1251 TACAACCTCC ATCATGGGAA GTCAAGTTTC AGAAACAAAA GTCTCATTCA
1301 TAAGAGGTCT TAGAAGAAAA TAACCAGTTA ACCTGATTTT AATTTTGATA
1351 CCGTTTTCTT GAACATAATA ATCTACCCAA TGAGACTTTT CAGCCTTTGT
1401 ACATACAAAA TTCTTCCAAA AGAGAGAGGA GAAAATACAG CTCTGATGGC
10 1451 ATCAAAACGGA CTTTGCATCA AGTAATTTCA GATAGTGTCC TAGGATCCTT
1501 TGAGGGTGCT GGTAGCAGGT GAGCAGGACA AAGTTGACCA AGGACACTTA
1551 TTTCTAGATT ATGATTCTTC TGTTTACTCA ACAATTTACA AAGAAAAAAA
1601 GGACAGACAT TGAAGAGCTA CACATTGTAT ATATATCACC ACAGACTATA
1651 AGGAAATGGA ATTATTTCCC TCTTTGTCAC ATATCTGTAG TAGGATTTGC
15 1701 CAAGATCAGA AATGATCCAT TTGCTGTTTC TTGTTTTCCA AAGGTCATAC
1751 ATTGTGTTTG GTTATTGTTA CCAGCTCAAT AAATGTGTTT AACGAGTTAA
1801 TTTCATTTTT CTGGCTTTGG TCTGTTCTCC TTCCTTACAG GCTAAGCCCT
1851 GGCTCCATGC AACTGCATTC TTTGATTTCA CTTGTTCTTT CATCTACATG
1901 TTTTGTTTCAT TTGCAGCCAG TTTTACTGA GTTTGTGGCA ATCAGGAATG
20 1951 CATTTGCTAA GCAAGTATGA CTTTAATTCC ACTCCATGGC TCAATCATTC
2001 ACATGAGGTG AGCTTCAGCC TGAGATAGCA GGCACAGAC TTCTTGCGTT
2051 TCAAAACTGC CATGCCCCCC TGTGATGCTC CCGTGAAGGA ATGCACTTTG
2101 CCTTGTAAGT TCCTGGGAAA GGGGTATGTT TTCTCTCCAG GTGCAGCCAG
2151 ATCTCACAAA GTACAAAACG AATGCCTTTC TTTTCTTGTT TATAATGGTC
25 2201 ACTCACTGTG TTTGGTTACT GTCAAGAAAT CAATAAATGT GTTTAACAAG
2251 TCAAAAAAAA AAAAAAA

```

## BLAST alert EMBL/EMBLNEW

30

```

EMBL:AF064854 Homo sapiens map 17q24; 5.13cR from GATA41C05
repeat
region, complete sequence.; N = 2, Score = 8784, P = 0

```

35

```

EMBLNEW:AC005883 Homo sapiens chromosome 17 clone RP11-958E11 map
17,
WORKING DRAFT SEQUENCE, 2 ordered pieces.; N = 3, Score = 6260, P
= 0

```

40

## Medline entries

```

9097349:
45 Lovejoy DA, Hewett-Emmett D, Porter CA, Cepoi D, Sheffield A,
Vale WW,
Tashian RE.; Evolutionarily conserved, "acatalytic" carbonic
anhydrase-related protein XI
contains a sequence motif present in the neuropeptide sauvagine:
50 the
human
CA-RP XI gene (CA11) is embedded between the secretor gene
cluster and
the
55 DBP gene at 19q13.3. Genomics 1998 Dec 15;54(3):484-9

```

## Peptide information for frame 3

-----

5 ORF from 0 bp to 986 bp; peptide length: 329  
 Category: similarity to known protein  
 Classification: unclassified

10 1 MEIVWEVLFL LQANFIVCIS AQQNSPKIHE GWWAYKEVVQ GSFVPVPSFW  
 51 GLVNSAWNLC SVGKRQSPVN IETSHMIFDP FLTPLRINTG GRKVSGMTYN  
 101 TGRHVSLRLD KEHLVNISGG PMTYSHRLEE IRLHFGSEDS QGSEHLLNGQ  
 151 AFSGEVQLIH YNHELYTNVT EAAKSPNGLV VVSIFIKVSD SSNPFLNRML  
 201 NRDTITRITY KNDAYLLQGL NIEELYPETS SFITYDGSMT IPPCYETASW  
 251 IIMNKPVIIT RMQMHSRLRL SQNQPSQIFL SMSDNFRPVQ PLNNRCIRTN  
 15 301 INFSLQGKDC PNNRAQKLQY RVNEWLLK

## Alert BLASTP hits for DKFZphamy2\_16el4, frame 3

20 PIR:JED375 carbonic anhydrase-related protein - human; N = 1,  
 Score =  
 937, P = 4.6e-94

25 SWISSNEW:CAHB\_SHEEP CARBONIC ANHYDRASE-RELATED PROTEIN 2  
 PRECURSOR  
 (CARP 2) (CA-RP II) (CA-XI).; N = 1, Score = 935, P = 7.5e-94

30 >PIR:JED375 carbonic anhydrase-related protein - human  
 Length = 328

## HSPs:

Score = 937 (140.6 bits), Expect = 4.6e-94, P = 4.6e-94  
 35 Identities = 169/287 (58%), Positives = 223/287 (77%)

Query: 30  
 EGWWAYKEVVQGSFVPVPSFWGLVNSAWNLC SVGKRQSPVNIETSHMIFDPFLTPLRINT 89  
 E WW+YK+ +QG+FVP P FWGLVN+AW+LC+VGKRQSPV++E  
 40 +++DPFL PLR++T  
 Sbjct: 32  
 EDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVEVKRVLYDPFLPPLRLST 91

Query: 90  
 45 GGRKVSGMTMYNTGRHVSLRLDKEHLVNISGGPMYSHRLEEIRLHFGSEDSQGSEHLLNG 149  
 GG K+ GT+YNTGRHVS +VN+SGGP+ YSHRL E+RL FG+ D  
 GSEH +N  
 Sbjct: 92  
 GGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINH 151

50 Query: 150  
 QAFSGEVQLIHYNHELYTNVTEAAKSPNGLVVVSIFIKVSDSSNPFLNRMLNRDTITRIT 209  
 Q FS EVQLIH+N ELY N + A++ PNGL ++S+F+ V+  
 +SNPFL+R+LNRDTITRI+  
 55 Sbjct: 152  
 QGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSLFVNVASTSNPFLSRLLNRDTITRIS 211

Query: 210

YKNDAYLLQGLNIEELYPETSSFITVDGSM TIPPCYETASWIIMNKPVYITRMQMHSRL 269  
YKNDAY LQ L++E L+PE+ FITY GS++ PPC ET +WI++++ + IT

+QMHSRL

5 Sbjct: 212

YKNDAYFLQDLSELELLFPESFGFITYQGSLSSTPPCSETVTWILIDRALNITSLQMHSRL 271

Query: 270 LSQNPSPQIFLSMSDNFRPVQPLNNRCIRTNINFSLQGKDC--PNNR 314

LSQN PSQIF S+S N RP+QPL +R +R N + + C PN R

10 Sbjct: 272 LSQNPSPQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGPNYR 318

Pedant information for DKFZphamy2\_16e14, frame 3

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15 Report for DKFZphamy2\_16e14.3

[LENGTH] 328  
 [MW] 37563.19  
 20 [pI] 8.22  
 [HOMOL] PIR:JED375 carbonic anhydrase-related protein -  
 human 1e-101  
 [BLOCKS] DM011098  
 [BLOCKS] BL00162F  
 25 [BLOCKS] BL00162E  
 [BLOCKS] BL00162D  
 [BLOCKS] BL00162C Eukaryotic-type carbonic anhydrases  
 proteins  
 [BLOCKS] BL00162A Eukaryotic-type carbonic anhydrases  
 30 proteins  
 [SCOP] d1znca\_ 2.56.1.1.3 Carbonic anhydrase [human  
 (Homo sapiens 1e-103  
 [SCOP] d2cba\_ 2.56.1.1.2 Carbonic anhydrase [human  
 (Homo sapiens 9e-97  
 35 [EC] 4.2.1.1 Carbonate dehydratase 1e-36  
 [EC] 3.1.3.48 Protein-tyrosine-phosphatase 2e-20  
 [PIRKW] blocked amino end 8e-29  
 [PIRKW] carbon-oxygen lyase 1e-36  
 [PIRKW] zinc 1e-36  
 40 [PIRKW] polymorphism 2e-20  
 [PIRKW] hydro-lyase 1e-36  
 [PIRKW] transmembrane protein 3e-23  
 [PIRKW] tyrosine-specific phosphatase 2e-20  
 [PIRKW] brain 6e-16  
 45 [PIRKW] acetylated amino end 1e-36  
 [PIRKW] phosphatidylinositol linkage 2e-19  
 [PIRKW] receptor 2e-20  
 [PIRKW] liver 3e-29  
 [PIRKW] phosphoprotein 2e-20  
 50 [PIRKW] saliva 2e-21  
 [PIRKW] glycoprotein 2e-22  
 [PIRKW] mitochondrion 1e-32  
 [PIRKW] monomer 3e-32  
 [PIRKW] alternative splicing 6e-16  
 55 [PIRKW] lipoprotein 2e-19  
 [PIRKW] pyroglutamic acid 2e-21  
 [PIRKW] metalloprotein 6e-35  
 [PIRKW] muscle 4e-31

[[PIRKW]] membrane protein 2e-19  
 [[PIRKW]] phosphoric monoester hydrolase 2e-20  
 [[PIRKW]] homodimer 3e-23  
 5 [[SUPFAM]] fibronectin type III repeat homology 2e-20  
 [[SUPFAM]] carbonic anhydrase homology 1e-36  
 [[SUPFAM]] protein-tyrosine-phosphatase, receptor type zeta  
 6e-16  
 [[SUPFAM]] carbonate dehydratase 1e-36  
 10 [[SUPFAM]] protein-tyrosine-phosphatase, receptor type gamma  
 2e-20  
 [[SUPFAM]] protein-tyrosine-phosphatase homology 2e-20  
 [[SUPFAM]] leukocyte common antigen cytosolic domain  
 homology 2e-20  
 [[PFAM]] Eukaryotic-type carbonic anhydrases  
 15 [[KW]] All\_Beta  
 [[KW]] 3D  
 [[KW]] SIGNAL\_PEPTIDE 22

20 SEQ  
 MEIVWEVLFLLDANFIVCISAQQNSPKIHEGWWAYKEVVQGSFVPVPSFWGLVNSAWNLC  
 Luc-  
 .....

25 SEQ  
 SVGKRQSPVNIETSHMIFDPFLTPLRINTGGRKVS GMTMYNTGRHVSLRLDKEHLVNISGG  
 Luc- ..TTTTCCCEETTTTTEETTTTCEEEEEET-  
 TTCEEEEEETTTTEEEECTTTTTEEEEE

30 SEQ  
 PMTYSHRLEEIRLHFGSEDSQGSHELLNGQAFSGEVQLIHYNHELYTNVTEAAKSPNGLV  
 Luc- TTCCCEEEEEEEEEETTTTCTTTEETTBCCEEEEEEEEEEGG-  
 GTTHHHHCTTTTEE

35 SEQ  
 VVSIFIKVSDSSNPFLNRMLNRDTITRITYKNDAYLLQGLNIEELYPETSSFITVDGSM  
 Luc- EEEEEEEEC-CCCGGGHHH--  
 HHGGGCTTTEEEETTTTCGGGGCCCCCEEEEECCC

40 SEQ  
 IPPCYETASWIIMNKPVIYITRMQMHSLRLLSQNQPSQIFLSMSDNFRPVQPLNNRCIRTN  
 Luc-  
 TTTTCCCEEEEEECCEEECHHHHHHHHCCBCCTTTTCCCBTTTTCCCCCTTTTCCEEC

45 SEQ INFSLQGKDCPNNRAQKLQYRVNEWLLK  
 Luc- .....

50 (No Prosite data available for DKFZphamy2\_1be14.3)  
 Pfam for DKFZphamy2\_1be14.3

55 HMM\_NAME Eukaryotic-type carbonic anhydrases  
 HMM  
 \*WCYgeHWGPEHH.....WHkhYPIAW....GDRQSPINIQWkearYDPS

W Y E + W+++ + + G RQSP+NI ++  
 +DP  
 Query 33  
 WAYKEVVQGSFVPVPSFWGLVNSAOWNLCSVGKRQSPVNIETSHMIFDPF 81  
 5 HMM  
 LKPWrv.SYYpaWCrEWeIWNNGHSFQVeFDDSDMSVLSGGPLPgHPYR  
 L P+R+ ++ +++++ ++ N+G+ + +D +SGGP++  
 ++R  
 10 Query 82 LTPLRINTGGRKVS--TMYNTGRHVSLRLDK-  
 EHLVNISGGPMTY-SHR 127  
 HMM  
 15 LkQFHFHUGGASSNDWGSEHTVDGmkYPMELHLVHWNStKYnNYdEAQdq  
 L + ++H G S++ +GSEH ++G +++ E+ L+H+N +Y N+  
 EA++  
 Query 128 LEEIRLHFG--  
 SEDSQGSEHLLNGQAFSGEVQLIHYNHELYTNVTEAAKS 175  
 20 HMM  
 PDGLAVIGVFMKVGNyqENPyLQKVv..DALdnIKYKGKratMTNFDPsC  
 P+GL V+ +F+KV NP L++ + D + I YK +  
 +++++  
 Query 176 PNGLVVVSIFIKVS-  
 25 DSSNPFLNRMLNRDTITRITYKNDAYLLQGLNIEE 224  
 HMM  
 LLPpPnCRDYWTYPGSLTTPPCHECVTWIVCKEPIsISsEQMWKFRsLLF  
 L P+ + TY GS+T+PPC+E WI+ P+ I + QM +R  
 30 L  
 Query 225 LYPE--  
 TSSFITYDGSMTIPPCYETASWIIMNKPVIYITRMQMHSLRLLSQ 272  
 HMM  
 35 NhEGEeeVpMVDNWRPPQPLKhRvVRASF\*  
 N +M DN+RP QPL++R +R +  
 Query 273 NQPSQIFLSMSDNFRPVQPLNNRCIRTNI 301

DKFZphamy2\_1c12

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5 group: nucleic acid management

DKFZphamy2\_1c12 encodes a novel 422 amino acid protein with partial identity to I-kappa-B-related protein and to BRCA1.

10 I-kappa-B-related protein interacts with transcription factors and BRCA1 has a function in DNA damage response. I-kappa-B-alpha mutations contribute to constitutive NF-kappaB activity in cultured and primary HRS (Hodgkin/Reed-Sternberg) cells and are therefore involved in the pathogenesis of Hodgkin's disease (HD)

15 patients.

The new protein can find application in modulating DNA repair and mutagenesis and also in expression profiling in HD related syndroms.

20

similarity to I-kappa-B-related protein

Sequenced by MediGenomix

25

Locus: unknown

Insert length: 1645 bp

Poly A stretch at pos. 1626, polyadenylation signal at pos. 1605

30

```

      1 GGATTTTCCT TGGTCTTAAG ATGGGTTAGAA ATGTGATGCG ACACATGTCT
    51 GATGACTTAG GAAGTTATGT TTCTCTTTTCG TGTGATGACT TTTCTTCACA
   101 GGAATTAGAG ATTTTCATTT GTCCTTTTTC CTCTCCTGG CTTCAAATGT
   35 151 TTGTTGCAGA GGCAGTCTTT AAAAAGTTGT GTCTACAGAG CTCTGGCAGT
      201 GTTTCTTCTG AGCCACTCTC TCTTCAGAAA ATGGTATATT CCTATTTACC
      251 AGCCTTG GGGG AAAACTGGTG TGCTTGGGTC TGGAAAGATT CAGGTGTCAA
      301 AGAAATAGG ACAGCGGCCT TGTTTTGACT CTCAGAGAAC CTTACTAATG
      351 CTGAATGGTA CTAAACAAAA ACAAGTCGAA GGGCTGCCAG AGTTACTAGA
   40 401 CCTGAACCTT GCTAAATGTT CCTCATCATT AAAAAAATTG AAAAAGAAGT
      451 CAGAAGGAGA ATTGTCATGT TCCAAGGAGA ATTGCCCTC TGTAGTTAAA
      501 AAGATGAATT TTCACAAGAC TAATCTAAAA GGAGAAACAG CCCTGCATAG
      551 AGCTTGCATA AATAACCAAG TGGAGAAATT GATTCTTCTT CTCTCTTTGC
   45 601 CAGGAATAGA CATCAATGTT AAAGACAATG CTGGCTGGAC GCCTTTGCAT
      651 GAAGCCTGTA ACTATGGCAA CACAGTGTGT GTCCAGGAAA TTTTGCAACG
      701 TTGTCCAGAG GTAGATCTGC TCACTCAAGT GGACGGGGTG ACTCCTTTGC
      751 ATGATGCACT GTCAAACGGA CATGTAGAAA TTGGCAAGCT GCTACTACAG
      801 CATGGGGGCC CAGTGCTTTT ACAACAGAGG AATGCTAAGG GAGAATTGCC
      851 CTTGGATTAT GTGGTTTCAC CTCAAATCAA AGAAGAACTG TTTGCTATTA
   50 901 CAAAAATAGA AGATACAGTG GAGAACTTTC ATGCACAAGC AGAGAAACAT
      951 TTTCAATTACC AGCAACTTGA ATTTGGCTCC TTTTACTTA GTAGGATGTT
  1001 GCTAAATTTT TGTTCAATTT TTGATTTATC TTCAGAGTTC ATTTTAGCTT
  1051 CCAAAGGGTT AACTCATCTA AATGAACTGC TTATGGCTTG TAAAAGTCAT
  1101 AAAGAAACCA CCAGTGTTCA TACTGACTGG TTAAGGATC TTTATGCTGG
   55 1151 AAATATAAAG ACATTGCAGA AACTCCCACA CATTCTTAAG GAACTGCCTG
      1201 AGAATTTGAA AGTGTGTCTT GGGGTACACA CTGAGGCCTT GATGATAACA
      1251 TTGGAAATGA TGTGTCGGTC AGTCATGGAG TTTTCATGAT GATGCTAGAA
      1301 AGTATGGATT GACTTTCTAA ATCTGTTTCAG TTTGCATTGG TACTTACTGT

```



1351 GGA CTT CATA GCT TACT GAC AGA TAGT AAT TTG ATTT ATT TATT GAC AGA  
 1401 CTTT GCAG CC TTG CTA AAT TTAAA AGCAT TTTTAAAAA ACTTCTACAA  
 1451 AACTCTAGTA TGGGCTTCTG ACTTTTCCA GGGTGTAGAA TTTGACTCAA  
 1501 AAGTAAAAAT AATTTTGTTC TAGTATATTC TACTTTCATT AATGTTTTTT  
 5 1551 TGTTC TGAAG GTGATATTAT ATTGTACATG TAAAAATTAAT TTAAATATTT  
 1601 TTTCAAATAA AAATGTAATG TCCTGTAAAA AAAAAAAAAA AAAAA

## BLAST Results

10

No BLAST result

## Medline entries

15

No Medline entry

## Peptide information for frame 3

20

25 ORF from 21 bp to 1286 bp; peptide length: 422  
 Category: similarity to known protein  
 Classification: Cell signaling/communication

30 1 MGRNVMRHMS DDLGSYVSLG CDDFSSQELE IFICSFSSSW LQMFVAEAVF  
 51 KKLCLQSSGS VSSEPLSLQK MVYSYLPALG KTGVLGSGKI QVSKKIGQRP  
 101 CFDSQRTLLM LNKTKQKQVE GLPELLDLNL AKCSSSLKKL KKKSEGE LSC  
 151 SKENCPSVVK KMNFKHTNLK GETALHRACI NNQVEKLILL LSLPGIDINV  
 201 KDNAGWTPLH EACNYGNTVC VQELQRCPE VDLLTQVDGV TPLHDALSNG  
 251 HVEIGKLLLQ HGGPVLLQQR NAKGELPLDY VVSPQIKEEL FAITKIEDTV  
 35 301 ENFHAQAEKH FHYQQLFEGS FLLSRMLLN FCSIFDLSEF ILASKGLTHL  
 351 NELLMAKSH KETTSVHTDW LLDLYAGNIK TLQKLPHILK ELPENLKVCP  
 401 GVHTEALMIT LEMMCRSVME FS

40

## BLASTP hits

No BLASTP hits available

45

## Alert BLASTP hits for DKFZphamy2\_1c12, frame 3

PIR:A56429 I-kappa-B-related protein - human, N = 1, Score = 242,  
 P =  
 4.6e-18

50

TREMBLNEW:AF038042\_1 gene: "BARD1"; product: "BRCA1-associated  
 RING  
 domain protein"; Homo sapiens BRCA1-associated RING domain  
 protein

55

(BARD1) gene, exons 10, 11 and complete cds., N = 1, Score = 236,  
 P =  
 6.9e-17

>PIR:A56429 I-kappa-B-related protein - human  
Length = 481

5 HSPs:

Score = 242 (36.3 bits), Expect = 4.6e-18, P = 4.6e-18  
Identities = 52/118 (44%), Positives = 71/118 (60%)

10 Query: 156  
PSVVKKMNFHKTNLKGETALHRACINNQVEKLILLLSLPGIDINVKDNAGWTPLEACNY 215  
P K +++ N GET LHRACI Q+ ++ L+ G +N +D  
GWTPLEACNY  
Sbjct: 354 PGAAGKSKWNRRNDMGETLLHRACIEGQLRRVQDLVR-  
15 QGHPLNPRDYCGWTPLEACNY 412  
  
Query: 216 GNTVCVQELQRCPEVDLL--  
TQVDGVTPLHDALSNGHVEIGKLLQLHGGPVLLQQRNA 272  
G+ V+ +L VD +G+TPLHDAL+ GH E+ +LLL+ G V  
20 L+ R A  
Sbjct: 413  
GHLEIVRFLLDHGAAVDDPGGQGCEGITPLHDALNCGHFEVAELLRLRGASVTLRTRKA 471

25 Pedant information for DKFZphamy2\_1c12, frame 3  
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Report for DKFZphamy2\_1c12.3

30 [LENGTH] 422  
[MW] 47071.18  
[pI] 6.57  
[HOMOL] PIR:A56429 I-kappa-B-related protein - human 3e-19  
35 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YIL112w]  
3e-11  
[FUNCAT] 06.13.01 cytoplasmic degradation [S. cerevisiae,  
YGR232w] 4e-06  
40 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YIR033w]  
2e-04  
[FUNCAT] 04.05.01.07 chromatin modification [S. cerevisiae,  
YIR033w] 2e-04  
[SCOP] dlawcb\_ 1.91.3.1.2 GA binding protein (GABP) alpha  
45 GA bindini 6e-24  
[EC] 3.1.3.53 Myosin-light-chain-phosphatase 9e-06  
[PIRKW] phosphotransferase 3e-07  
[PIRKW] tandem repeat 9e-06  
[PIRKW] transmembrane protein 7e-10  
50 [PIRKW] serine/threonine-specific protein kinase 3e-07  
[PIRKW] phosphoprotein 3e-10  
[PIRKW] integrin binding 3e-07  
[PIRKW] alternative splicing 3e-11  
[PIRKW] peripheral membrane protein 2e-09  
55 [PIRKW] transcription regulation 3e-06  
[PIRKW] phosphoric monoester hydrolase 9e-06  
[PIRKW] cytoskeleton 4e-10  
[PIRKW] smooth muscle 9e-06

[SUPFAM] ankyrin 3e-11  
 [SUPFAM] ankyrin repeat homology 3e-11  
 [SUPFAM] unassigned ankyrin repeat proteins 7e-10  
 [PFAM] Ank repeat  
 5 [KW] Irregular  
 [KW] 3D  
 [KW] LOW\_COMPLEXITY 8.53 %

10 SEQ MGRNVMRHMSDDLGSYVSLSCDDFSSQELEIFICSFSSSWLQMFVAEAVFKKLC LQSSGS  
 SEG .....xxxxxx  
 lawcB .....  
 15 SEQ VSSEPLSLQKMVYSYLPALGKTGVLGSGKIQVSKKIGQRPCFDSQR TLLMLNGTKQKQVE  
 SEG xxxxxxxx.....  
 lawcB .....  
 20 SEQ GLPELLDLNLAKCSSSLKKLKKKSEGELSCSKENCPSVVKMNFHKT NLKGETALHRACI  
 SEG .....xxxxxxxxxxxxxxxxxxxxxxxx.....  
 lawcB .....  
 25 SEQ NNQVEKLILLLSLPGIDINVKDNAGW TPLHEACNYGNTVCVQ EILQRCPEVDLLTQVDGV  
 SEG .....  
 lawcB .....TTTT CCHHHHHHHHCCHHHHHHHHCCCTTTTCTTTTC-  
 30 SEQ TPLHDALSNGHVEIGKLLLQHG GPVLLQQRNAKGELPLDYV VSPQIKEELFAITKIEDTV  
 SEG .....  
 lawcB CHHHHHHHHTTHHHHHHHHCCCTT.....  
 35 SEQ ENFHAQAEKHFHYQQL EFGSFLLSRMLLNFC SIFDL SSEFILASKGLTHLNELL MACKSH  
 SEG .....  
 lawcB .....  
 40 SEQ KETTSVHTDWLLDLYAGNIKTLQ KLP HILKELPENLKVCPGVHTEALMITLEMMCRSVME  
 SEG .....  
 lawcB .....  
 45 SEQ FS  
 SEG ..  
 lawcB ..

50 (No Prosite data available for DKFZphamy2\_1c12.3)

Pfam for DKFZphamy2\_1c12.3

55

HMM\_NAME Ank repeat

HMM \*GyTPLHIAARYNNvEMVr1LLQH.GADIN\*

Query 171 G+T+LH A+++N+VE LLL+ G DIN  
 171 GETALHRACINNQVEKLILLLSLPGIDIN 179

34.48 (bits) f: 205 t: 232 Target: dkfzphamy2\_1c12.3  
 similarity to I-kappa-B-related protein

Alignment to HMM consensus:

Query \*GyTPLHIAARyNNvEMVr1LLQHGADIN\*  
 G+TPLH A+ Y+N+ +V+ LQ+ + ++  
 dkfzphamy2 205 GWTPLHEACNYGNTVCVQEILQRCPEVD 232

Query f: 239 t: 266 Target: dkfzphamy2\_1c12.3  
 similarity to I-kappa-B-related protein

Alignment to HMM consensus:

HMM \*GyTPLHIAARyNNvEMVr1LLQHGADIN\*  
 G TPLH A +++VE+ +LLLQHG +  
 Query 239 GVTPLHDALSNHGVEIGKLLLQHG GPVL 266

DKFZphamy2\_1i1

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group: nucleic acid management

DKFZphamy2\_1i1 encodes a novel 629 amino acid protein with  
 similarity to the murine hemin-sensitive initiation factor 2.

The hemin-sensitive initiation factor 2 is expressed  
 predominantly in liver, spleen, colon and uterus and contains 2  
 protein kinase motifs. The mouse homologue inhibits protein  
 synthesis in stress conditions by phosphorylation of eif-2-alpha.  
 Four different eIF2alpha kinases have been identified in  
 mammalian cells, the heme-regulated inhibitor (HRI), the  
 interferon-inducible RNA-dependent kinase (PKR), the endoplasmic  
 reticulum-resident kinase (PERK) and MGCN2. The new protein  
 represents a new member of this family

The new protein can find application in modulating/blocking of  
 translation.

similarity to hemin-sensitive initiation factor 2 (Mus musculus),  
 complete cds.alpha kinase

complete cds.

probably complete in genomic clone DJ0042M02

Sequenced by MediGenomix

Locus: /map="37.2 cR from top of Chr7 linkage group"

Insert length: 2863 bp

Poly A stretch at pos. 2844, polyadenylation signal at pos. 2824

1 GCAGTGCTGG GCTGGCCGGC GGGCTGGGCT GCGGCCCGCG CGCGGCCGGC  
 51 GATGCAGGGG GGCAACTCCG GGGTCCGCAA GCGCGAAGAG GAGGGCGACG  
 101 GGGCTGGGGC TGTGGCTGCG CCGCCGGCCA TCGACTTTCC CGCCGAGGGC  
 151 CCGGACCCCG AATATGACGA ATCTGATGTT CCAGCAGAAA TCCAGGTGTT

	201	AAAAGAACCC	CTACAACAGC	CAACCTTCCC	TTTTGCAGTT	GCAAACCAAC
	251	TCTTGCTGGT	TTCTTTGCTG	GAGCACTTGA	GCCACGTGCA	TGAACCAAAC
	301	CCACTTCGTT	CAAGACAGGT	GTTTAAAGCTA	CTTTGCCAGA	CGTTTATCAA
5	351	AATGGGGCTG	CTGTCTTCTT	TCACTTGTAG	TGACGAGTTT	AGCTCATTGA
	401	GACTACATCA	CAACAGAGCT	ATTACTCACT	TAATGAGGTC	TGCTAAAGAG
	451	AGAGTTCGTC	AGGATCCTTG	TGAGGATATT	TCTCGTATCC	AGAAAATCAG
	501	ATCAAGGGAA	GTAGCCTTGG	AAGCACAAAC	TTACAGTTAC	TTAAATGAAT
	551	TTGAAGAACT	TGCCATCTTA	GGAAAAGGTG	GATACGGAAG	AGTATACAAG
	601	GTCAAGGAATA	AATTAGATGG	TCAGTATTAT	GCAATAAAAA	AAATCCTGAT
10	651	TAAGGGTGCA	ACTAAAACAG	TTTGATGAA	GGTCCTACGG	GAAGTGAAGG
	701	TGCTGGCAGG	TCTTCAGCAC	CCCAATATTG	TTGGCTATCA	CACCGCGTGG
	751	ATAGAACATG	TTCATGTGAT	TCAGCCACGA	GACAGAGCTG	CCATTGAGTT
	801	GCCATCTCTG	GAAGTGCTCT	CCGACCAGGA	AGAGGACAGA	GAGCAATGTG
	851	GTGTTAAAAA	TGATGAAAGT	AGCAGCTCAT	CCATTATCTT	TGCTGAGCCC
15	901	ACCCCAAGAA	AAGAAAAACG	CTTTGGAGAA	TCTGACACTG	AAAATCAGAA
	951	TAACAAGTCG	GTGAAGTACA	CCACCAATTT	AGTCATAAGA	GAATCTGGTG
	1001	AACTTGAGTC	GACCCTGGAG	CTCCAGGAAA	ATGGCTTGGC	TGGTTTGTCT
	1051	GCCAGTTCAA	TTGTGGAACA	GCAGCTGCCA	CTCAGGCGTA	ATTCCACCT
	1101	AGAGGAGAGT	TTACATCCA	CCGAAGAATC	TTCCGAAGAA	AATGTCAACT
20	1151	TTTTGGGTCA	GACAGAGGCA	CAGTACCACC	TGATGCTGCA	CATCCAGATG
	1201	CAGCTGTGTG	AGCTCTCGCT	GTGGGATTGG	ATAGTCGAGA	GAAACAAGCG
	1251	GGGCCGGGAG	TATGTGGACG	AGTCTGCCTG	TCCTTATGTT	ATGGCCAATG
	1301	TTGCAACAAA	AATTTTTCAA	GAATTGGTAG	AAGGTGTGTT	TTACATACAT
	1351	AACATGGGAA	TTGTGCACCG	AGATCTGAAG	CCAAGAAATA	TTTTTCTTCA
25	1401	TGGCCCTGAT	CAGCAAGTAA	AAATAGGAGA	CTTTGGTCTG	GCCTGCACAG
	1451	ACATCCTACA	GAAGAACACA	GACTGGACCA	ACAGAAACGG	GAAGAGAACA
	1501	CCAACACATA	CGTCCAGAGT	GGGTACTTGT	CTGTACGCTT	CACCCGAACA
	1551	GTTGGAAGGA	TCTGAGTATG	ATGCCAAGTC	AGATATGTAC	AGCTTGGGTG
30	1601	TGGTCCTGCT	AGAGCTCTTT	CAGCCGTTTG	GAACAGAAAT	GGAGCGAGCA
	1651	GAAGTTCTAA	CAGGTTTAAAG	AACTGGTCAG	TTGCCGGAAT	CCCTCCGTAA
	1701	AAGGTGTCCA	GTGCAAGCCA	AGTATATCCA	GCACTTAACG	AGAAGGAACT
	1751	CATCGCAGAG	ACCATCTGCC	ATTCACTGCT	TGCAGAGTGA	ACTTTTCCAA
	1801	AATTCTGGAA	ATGTTAACTT	CACCCTACAG	ATGAAGATAA	TAGAGCAAGA
	1851	AAAAGAAATT	GCAGAACTAA	AGAAGCAGCT	AAACCTCCTT	TCTCAAGACA
35	1901	AAGGGGTGAG	GGATGACGGA	AAGGATGGGG	GCGTGGGATG	AAAGTGGACT
	1951	TAACTTTTAA	GGTAGTTAAC	TGGAATGTAA	ATTTTAAATC	TTTATTAGGG
	2001	TATAGTTGGT	ACAATGCTTC	GTTGTATTTA	GTAAGCCTTT	ACAAGACTTG
	2051	TTAAAGATGT	CAGAGTGCCC	CAAGCTGCCG	TTCTTCCCTT	TCCTGCCCCA
40	2101	CAAGCTCCTT	TTCTTGAATT	TCCTACCTAA	ATATTAACCA	TATGCCTAGT
	2151	CTCTGAAACT	AAAAACTTGG	ACCTCATCCT	CAATTATTTT	CTCCTTTCAA
	2201	CTCTGTTGAC	CCTCTGTCTG	GTCTTCTCTT	AGAAGGTTCT	ACCGCAGAAA
	2251	TTGATGTGTG	CTCCCTGCCC	TCGTCACTGC	CCAAGCCCCG	GCCTGCACAT
	2301	ACTCACTGGA	CTGTTCCAGT	TTTGACAGCT	GCCAGTCTTC	CTGCCCCCTT
	2351	CACACTGCAG	CTGAAGTTCA	TTACCTGAAG	GACGCCCTCAT	CATTTTCATTC
45	2401	CTTGGCTCCA	AACCTTCTGC	TGCCTCTAAG	ATAAAAGCTC	AACTTCTTAA
	2451	CAGTGTACAG	TGTGCAACTT	CCAACCTTTT	TATCTGTTCT	CTCCACCTTC
	2501	AGTTTAGCGT	CATTCCAAAA	CCACACCCTT	GCAAAGCTTT	GTAATCCGCA
	2551	CCCCAGATGA	TCTCCAGGCA	GCTCAGATCT	CTTTCCTGCC	TTTGCCCTGC
	2601	ACTGTTCCCC	GGTACTTCCT	CCTTTATTGT	AGCACTCAGC	TCCCCAGCCA
50	2651	ATCTGTACAT	CCCTCAGAGG	CAGCGATCTG	ATGAATTGGT	TTTTGAATCC
	2701	CAGAAAGGGT	CTGCCATGGA	GTTGGCAGTC	ATCACGGTAG	ATGGCGTATG
	2751	ATTTTGCTGA	ATTTTAAATA	AAATGAAAAC	CATAAATTAC	ATGATGCTTT
	2801	TATTGACACT	TGACAACCTGG	CCTAAATAAA	AAGACTCTGA	CTCCAAAAAA
55	2851	AAAAAAAAAA	AAA			

BLAST Results

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Entry AF028808 from database EMBL:  
Mus musculus hemin-sensitive initiation factor 2 alpha kinase  
mRNA,

5 complete cds.

Score = 6688, P = 2.7e-296, identities = 1922/2534

Entry AC005995 from database EMBL:

Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 13

10 unordered

pieces.

Score = 5116, P = 0.0e+00, identities = 1090/1148

15

#### Medline entries

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99042009:

20 Berlanga J.-J., Herrero S., de Haro C.; Characterization of the  
hemim-sensitive eukaryotic initiation factor 2alpha kinase from  
mouse

nonerythroid cells; J. Biol. Chem. 273(48):32340-32346(1998).

25

#### Peptide information for frame 1

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30

ORF from 52 bp to 1938 bp; peptide length: 629

Category: similarity to known protein

Classification: Protein management

Prosite motifs: PROTEIN\_KINASE\_ATP (173-196)

35 PROTEIN\_KINASE\_ATP (173-197)

PROTEIN\_KINASE\_ST (437-449)

40

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1 MGGGNSGVK REEEGDGAGA VAAPPAIDFP AEGPDPEYDE SDVPAEIQVL
51 KEPLQPTFP FAVANQLLV SLLEHLSHVH EPNPLRSRQV FKLLCQTFIK
101 MGLLSSTCS DEFSSRLHH NRAITHLMRS AKERVQDPC EDISRIQKIR
151 SREVALEAQT SRYLNEFEEL AILGKGGYGR VYKVRNKLDG QYYAIKKILI
201 KGATKTVCMK VLREVKVLAG LQHPNIVGYH TAWIEHVHVI QPRDRAAIEL
251 PSLEVLSDQE EDREQCGVKN DESSSSSIIF AEPTPEKEKR FGESDTENQN
45 301 NKSVKYTTNL VIRESGELES TLELQENGLA GLSASSIVEQ QLPLRRNSHL
351 EESFTSTES SEENVNVLGQ TEAQYHMLH IQMQLCELSL WDWIVERNKR
401 GREYVDESAC PYVMANVATK IFQELVEGVF YIHNMGIVHR DLKPRNIFLH
451 GPDQVVKIGD FGLACTDILQ KNTDWTNRNG KRTPTHTSRV GTCLYASPEQ
501 LEGSEYDAKS DMYSLGVVLL ELFQPFGTET ERAEVLTLGLR TGQLPESLRK
50 551 RCPVQAKYIQ HLTRRNSSQR PSAIQLLQSE LFQNSGNVNL TLQMKIIEQE
601 KEIAELKKQL NLLSQDKGVR DDGKDDGGVG

```

55

#### BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_111, frame 1

No Alert BLASTP hits found

5 Pedant information for DKFZphamy2\_111, frame 1

## Report for DKFZphamy2\_111.1

10

[LENGTH] 646

[MW] 72738.78

[pI] 5.80

[HOMOL] SWISSNEW:HRI\_MOUSE HEME-REGULATED EUKARYOTIC

15 INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HEME-REGULATED INHIBITOR) (HRI) (HEME-CONTROLLED REPRESSOR) (HCR) (HEMIN-SENSITIVE INITIATION FACTOR-2 ALPHA KINASE). 0.0

[FUNCAT] 05.07 translational control [S. cerevisiae, YDR283c] 2e-43

20 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YDR283c] 2e-43

[FUNCAT] 10.02.11 key kinases [S. cerevisiae, YOR231w] 8e-14

[FUNCAT] 03.04 budding, cell polarity and filament formation

[S. cerevisiae, YOR231w] 8e-14

25 [FUNCAT] 03.01 cell growth [S. cerevisiae, YOR231w] 8e-14

[FUNCAT] 11.01 stress response [S. cerevisiae, YOR231w] 8e-14

[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YOR231w] 8e-14

30 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKL101w] 8e-12

[FUNCAT] 99 unclassified proteins [S. cerevisiae, YPL150w] 8e-12

[FUNCAT] 03.13 meiosis [S. cerevisiae, YDR523c] 2e-11

35 [FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YDR523c] 2e-11

[FUNCAT] 09.01 biogenesis of cell wall [S. cerevisiae, YPL140c] 4e-11

[FUNCAT] 10.03.11 key kinases [S. cerevisiae, YCR073c] 9e-11

40 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YHR082c] 1e-10

[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YLR362w] 2e-10

[FUNCAT] 10.05.11 key kinases [S. cerevisiae, YLR362w] 2e-10

[FUNCAT] 10.04.11 key kinases [S. cerevisiae, YLR362w] 2e-10

45 [FUNCAT] 10.99 other signal-transduction activities [S. cerevisiae, YDL101c] 3e-10

[FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision repair) [S. cerevisiae, YDL101c] 3e-10

[FUNCAT] 03.25 cytokinesis [S. cerevisiae, YDR507c] 3e-10

50 [FUNCAT] 04.05.01.01 general transcription activities [S. cerevisiae, YDL108w] 1e-09

[FUNCAT] 03.16 dna synthesis and replication [S. cerevisiae, YBR160w] 1e-09

55 [FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YLR113w] 4e-09

[FUNCAT] 02.19 metabolism of energy reserves (glycogen, trehalose) [S. cerevisiae, YPL031c] 1e-08

- 1 [FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YPL031c] 1e-08  
 [FUNCAT] 01.04.04 regulation of phosphate utilization [S. cerevisiae, YPL031c] 1e-08  
 5 [FUNCAT] c energy conversion [M. genitalium, MG109] 2e-08  
 [FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YOR351c] 1e-07  
 [FUNCAT] 03.22.01 cell cycle check point proteins [S. cerevisiae, YPL153c] 1e-07  
 10 [FUNCAT] 10.05.09 regulation of g-protein activity [S. cerevisiae, YBL016w] 7e-07  
 [FUNCAT] 04.03.99 other trna-transcription activities [S. cerevisiae, YIL035c] 1e-06  
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 15 [FUNCAT] 06.13.04 lysosomal and vacuolar degradation [S. cerevisiae, YGL180w] 1e-06  
 [FUNCAT] 04.99 other transcription activities [S. cerevisiae, YER129w] 2e-06  
 20 [FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YDR122w] 2e-06  
 [FUNCAT] 30.07 organization of endoplasmatic reticulum [S. cerevisiae, YHR079c] 3e-06  
 [FUNCAT] 01.06.10 regulation of lipid, fatty-acid and sterol biosynthesis [S. cerevisiae, YHR079c] 3e-06  
 25 [FUNCAT] 08.99 other intracellular-transport activities [S. cerevisiae, YKL198c] 1e-05  
 [FUNCAT] 10.04.99 other nutritional-response activities [S. cerevisiae, YKL198c] 1e-05  
 30 [FUNCAT] 09.04 biogenesis of cytoskeleton [S. cerevisiae, YNL020c] 9e-05  
 [FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation, palmitylation, farnesylation and processing) [S. cerevisiae, YFL033c] 4e-04  
 35 [FUNCAT] 01.02.04 regulation of nitrogen and sulphur utilization [S. cerevisiae, YNL183c] 7e-04  
 [BLOCKS] BL00107A Protein kinases ATP-binding region proteins  
 [SCOP] d1ir3a\_ 5.1.1.2.6 insulin receptor Complex (transferase/substrate) 1e-22  
 40 [SCOP] d1fgkb\_ 5.1.1.2.5 Fibroblast growth factor receptor 1 [Human (Homo)] 9e-27  
 [SCOP] d1phk\_ 5.1.1.1.6 gamma-subunit of glycogen phosphorylase kinase 2e-23  
 [SCOP] d1abo\_ 5.1.1.1.14 Protein kinase (CK2, alpha) subunit [Maize (Zea)] 1e-23  
 45 [SCOP] d3lck\_ 5.1.1.2.2 Lymphocyte kinase (lck) [Human (Homo sapiens)] 3e-22  
 [SCOP] d2erk\_ 5.1.1.1.11 MAP kinase Erk2 [Rat (Rattus norvegicus)] 7e-20  
 50 [SCOP] d1cdkb\_ 5.1.1.1.2 cAMP-dependent PK, catalytic subunit Comple 6e-19  
 [SCOP] d1hcl\_ 5.1.1.1.1 Cyclin-dependent PK [Human (Homo sapiens)] 5e-21  
 [EC] 2.7.1.112 Protein-tyrosine kinase 1e-08  
 55 [EC] 2.7.1.126 beta-Adrenergic-receptor kinase 2e-08  
 [EC] 2.7.1.117 Myosin-light-chain kinase 1e-09  
 [EC] 2.7.1.37 Protein kinase 5e-12



	[[EC]]	2.7.1.123 Ca <sup>2+</sup> /calmodulin-dependent protein kinase 4e-09
	[[PIRKW]]	phosphotransferase 0.0
	[[PIRKW]]	nucleus 9e-09
5	[[PIRKW]]	RNA binding 2e-21
	[[PIRKW]]	duplication 8e-10
	[[PIRKW]]	tandem repeat 4e-09
	[[PIRKW]]	zinc 5e-12
	[[PIRKW]]	cell cycle control 2e-09
10	[[PIRKW]]	serine/threonine-specific protein kinase 0.0
	[[PIRKW]]	transmembrane protein 2e-09
	[[PIRKW]]	zinc finger 8e-10
	[[PIRKW]]	oncogene 6e-12
	[[PIRKW]]	autophosphorylation 0.0
15	[[PIRKW]]	coat protein 1e-11
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	[[PIRKW]]	receptor 9e-09
20	[[PIRKW]]	phosphoprotein 0.0
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	[[PIRKW]]	glycoprotein 9e-09
	[[PIRKW]]	growth factor receptor 9e-11
	[[PIRKW]]	signal transduction 2e-12
25	[[PIRKW]]	serine/threonine/tyrosine-specific protein kinase 8e-10
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	[[PIRKW]]	transforming protein 2e-12
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30	[[PIRKW]]	purine nucleotide binding 2e-10
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	[[PIRKW]]	meiosis 1e-08
	[[PIRKW]]	alternative splicing 1e-11
	[[PIRKW]]	P-loop 2e-10
35	[[PIRKW]]	proto-oncogene 2e-12
	[[PIRKW]]	segmentation 4e-10
	[[PIRKW]]	stress-induced protein 1e-09
	[[PIRKW]]	EF hand 4e-09
	[[PIRKW]]	cell division 1e-09
40	[[PIRKW]]	calmodulin binding 4e-09
	[[SUPFAM]]	LIM protein kinase 8e-10
	[[SUPFAM]]	calcium-dependent protein kinase 4e-09
	[[SUPFAM]]	rat protein kinase raf 5e-12
	[[SUPFAM]]	AMP-activated protein kinase 2e-08
45	[[SUPFAM]]	protein kinase byr2 5e-09
	[[SUPFAM]]	SH2 homology 1e-08
	[[SUPFAM]]	unassigned Ser/Thr or Tyr-specific protein kinases 0.0
	[[SUPFAM]]	leucine-rich alpha-2-glycoprotein repeat homology 9e-09
50	[[SUPFAM]]	double-stranded RNA-binding repeat homology 2e-21
	[[SUPFAM]]	histidine--tRNA ligase homology 6e-42
	[[SUPFAM]]	SAM homology 5e-09
	[[SUPFAM]]	avian retrovirus IC10 gag-Rmil-env polyprotein 1e-11
	[[SUPFAM]]	LIM metal-binding repeat homology 8e-10
55	[[SUPFAM]]	GCN2 protein 6e-42
	[[SUPFAM]]	protein kinase homology 0.0
	[[SUPFAM]]	protein kinase C zinc-binding repeat homology 2e-12
	[[SUPFAM]]	Ca <sup>2+</sup> /calmodulin-dependent protein kinase II 4e-08

[SUPFAM] beta-adrenergic-receptor kinase 2e-08  
 [SUPFAM] kinase-related transforming protein 6e-12  
 [SUPFAM] protein kinase A-raf 2e-12  
 [SUPFAM] SH3 homology 1e-08  
 5 [SUPFAM] Ca<sup>2+</sup>/calmodulin-dependent protein kinase 4e-09  
 [SUPFAM] protein kinase Xa21 9e-09  
 [SUPFAM] calmodulin repeat homology 4e-09  
 [SUPFAM] protein kinase DUN1 9e-09  
 [SUPFAM] pleckstrin repeat homology 9e-09  
 10 [SUPFAM] protein kinase TIK 2e-21  
 [SUPFAM] protein-tyrosine kinase tec 1e-08  
 [SUPFAM] kinase interaction domain homology 9e-09  
 [PROSITE] PROTEIN\_KINASE\_ATP 2  
 [PROSITE] PROTEIN\_KINASE\_ST 1  
 15 [PFAM] Eukaryotic protein kinase domain  
 [KW] Irregular  
 [KW] 3D  
 [KW] LOW\_COMPLEXITY 10.99 %  
 [KW] COILED\_COIL 5.26 %  
 20  
 SEQ AVLGWPA GWAAARARPAMQGGNSGVRKREEEGDGAGAVAAPPAIDFPAEGPDPEYDES DV  
 SEG .....XXX.....  
 COILS  
 25 .....  
 1jstA  
 .....  
 SEQ PAEIQVLKEPLQQTFFFAVANQLLLVSLLEHL SHVHEPNPLRSRQVFKLLCQTFIKMGL  
 30 SEG .....XXX.....  
 COILS  
 .....  
 1jstA  
 .....  
 35 SEQ LSSFTCSDEFSSLRLHHNRAITHLMRS AKERV RQDP CEDISRIQKIRSREVALEAQT SRY  
 SEG .....  
 COILS  
 .....  
 40 1jstA  
 .....  
 SEQ LNEFEELAILGKGGYGRVYKVRNKLDGQYYAIKKILIKGATKTVC MKVLREV KVLAGLQH  
 45 SEG .....  
 COILS  
 .....  
 1jstA  
 TTTEEEEEEECCBTTBCEEEEEETTTTCEEEEEEECCTTTTTTTTHHHHHHHHHHHHTTTB  
 50 SEQ PNIVGYHTAWIEHVHVIQPRDRAAIELPSLEVLSDQ EEDREQCGVKND ESSSSSIIFAEP  
 SEG .....  
 COILS  
 .....  
 1jstA  
 55 TTBC.....  
 SEQ TPEKEKRFGESDTENQNNKSVKYTTNLVIRESGELESTLELQENGLAGLSASSIVEQQLP  
 SEG .....

COILS

ljsta

5

SEQ LRRNSHLEESFTSTEESEENVNVLGQTEAQYHMLHIQMQLCELSLWDWIVERNKRGRE  
 SEG .....XXXXXXXXXXXXX.....  
 COILS

10

ljsta

SEQ YVDESACPYVMANVATKIFQELVEGVFYIHNMGIVHRDLKPRNIFLHGPDAQVKIGDFGL  
 SEG .....

15

COILS

ljsta

20

SEQ ACTDILQKNTDWTNRNGKRTPTHTSRVGTCLYASPEQLEGSEYDAKSDMYSLGVVLELF  
 SEG .....

ljsta

25

SEQ QPFGTEMERAQVLTGLRTGQLPESLRKRCVPQAKYIQHLTRRNSSQRPQSAIQLLQSELFQ  
 SEG .....

30

ljsta

SEQ NSGNVNLTLQMKIIEQEKEIAELKKQLNLLSQDKGVRDDGKDGQGVG  
 SEG .....XXXXXXXXXXXXX.....  
 COILS ..CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.....  
 ljsta .....

40

## Prosite for DKFZphamy2\_lil.1

PS00107	190->214	PROTEIN_KINASE_ATP	PD0C00100
PS00107	190->215	PROTEIN_KINASE_ATP	PD0C00100
45 PS00108	454->467	PROTEIN_KINASE_ST	PD0C00100

## Pfam for DKFZphamy2\_lil.1

50

HMM\_NAME Eukaryotic protein kinase domain

HMM

55 \*YeigRiIGeGsFGtVYkCiWr.TGeIVAIIK.krsms.....FIREI  
 +E + I+G+G++G+VYK++++ +G+ +AIK+I K ++  
 +LRE+

Query 184  
 FEELAILGKGGYGRVYKVRNKLDGQYYAIAKKILIKGATKTVCMKVLREV 232

5 HMM qIMRrLnHPNIIRFYDwFedddDHI\*  
 ++++ L+HPNI+ + +++ ++ H+  
 Query 233 KVLAGLQHPNIVGYHTAWI-EHVHV 256

10 HMM  
 \*IYMIMEYMeGGDLFDYIrrng.....pMsEweInfIMyQIL  
 +++ M+++E +L+D+I++++ ++ + + +I+  
 +++  
 Query 396 LHIQMQLCCL-  
 SLWDWIVERNKRGREYVDESACPYVMANVATKIFQELV 443

15 HMM  
 rGMeYLHSMgIIHRDLKPENILIDeN.gqIKIcDFGLARqMn.....  
 +G+ Y+H+MGI+HRDLKP+NI++ + Q+KI+DFGLA+  
 Query 444  
 EGVFYIHNMGI VHRDLKPRNIFLHGPDQQVKIGDFGLACTDILQKNTDWT 493

20 HMM  
 .....nYerMttfCGTPWYMMAPEVImgnyYttkVDMWSFGCILWEMMT  
 + T+++GT Y +PE ++G++Y+ K+DM+S+G++L  
 E++  
 25 Query 494 NRNGKRTPTHTSRVGTCLYA-SPEQ-  
 LEGSEYDAKSDMYSLGVLLELF- 540

30 HMM  
 GepPFyd..dnMemImrIiqr.frrpfWpnCSeElyDFMrwCWnyDPekR  
 +PF ++ E + ++ + ++ ++ +C+ +++ + + +++  
 ++R  
 Query 541 --QPFGTEMERA EVLTGLRTGQLPESLRKRCVPVQAKYIQ-  
 HLTRRNSSQR 587

35 HMM  
 PTFrQILnHPWF\*  
 P++ Q+L++ F  
 Query 588 PSAIQLLQSELF 599

DKFZphamy2\_1114

-----

5 group: transmembrane proteins

DKFZphamy2\_1114 encodes a novel 617 amino acid protein with similarity to the human 1(3)mbt protein homolog.

10 Mutations of the Drosophila 1(3)mbt gene lead to malignant brain tumors. The novel protein contains 1 transmembrane domain. No informative BLAST results; No predictive prosite, pfam or SCOP motife

15 The new protein can find application in studying the expression profile of oncogenes and amygdala-specific genes and as a new marker for amygdala cells.

20 similarity to Human 1(3)mbt protein homolog mRNA

> 14 exons (HS756623 (EMBLNEW))

Pedant: TRANSMEMBRANE 1

25 Sequenced by MediGenomix

Locus: /map="22q13.31-13.33"

Insert length: 3071 bp

30 Poly A stretch at pos. 3052, no polyadenylation signal found

```

      1 GGCAGGCCAA TATGGCTTCC TGCACCTGGT GACGCTTGGC GAAACTGAGG
      51 TCTCATGGAG AAGCCCCGGA GTATTGAGGA GACCCCATCT TCAGAACCAA
35    101 TGGAGGAAGA GGAAGATGAC GACTTGGAGC TGTTTGGTGG CTATGATAGT
      151 TTCCGGAGTT ATAACAGCAG TGTGGGCAGT GAGAGCAGCT CCTATCTGGA
      201 GGAGTCAAGT GAAGCAGAAA ATGAGGATCG GGAAGCAGGG GAACTGCCGA
      251 CCTCCCCGCT GCATTTGCTC AGCCCTGGGA CTCCTCGCTC CTTGGATGGC
      301 AGTGGTTCTG AGCCAGCTGT CTGTGAGATG TGTGGTATCG TGGGTACAAG
40    351 GGAAGCCTTC TTCTCCAAGA CCAAGAGGTT CTGCAGCGTC TCCTGTCTCA
      401 GGAGCTACTC CTCCAACCTC AAGAAAGCCA GTATCTTGGC TAGATTACAG
      451 GGAAAACACAC CGACCAAAAA AGCCAAAGTC CTGCACAAGG CTGCCTGGTC
      501 TGCCAAAATT GGAGCCTTCC TCCACTCTCA AGGGACAGGA CAGCTGGCAG
      551 ATGGGACACC AACAGGACAA GACGCTCTGG TCTTGGGCTT CGACTGGGGG
45    601 AAGTTCCTGA AGGATCACAG TTACAAGGCT GCTCCCGTCA GCTGTTTCAA
      651 GCACGTCCCA CTCTATGACC AGTGGGAGGA TGTGATGAAA GGGATGAAGG
      701 TGGAGGTGCT CAACAGTGAT GCTGTGCTCC CCAGCCGGGT GACTGGATC
      751 GCCTCTGTCA TCCAGACAGC AGGGTATCGG GTGCTGCTTC GGTATGAAGG
      801 CTTTGAAAAT GACGCCAGCC ATGACTTCTG GTGCAACCTG GGAACAGTGG
50    851 ATGTCCACCC CATTGGCTGG TGTGCCATCA ACAGCAAGAT CCTAGTGCCC
      901 CCACGGACCA TCCATGCCAA GTTCACCGAC TGGAAAGGGCT ACCTCATGAA
      951 ACGGCTGGTG GGCTCCAGGA CGCTTCCCGT GGATTTCAC ATCAAGATGG
100  1001 TGGAGAGCAT GAAGTACCCC TTTAGGCAGG GCATGCGGCT GGAAGTGGTG
105  1051 GACAAGTCCC AGGTGTCACG CACTCGCATG GCTGTGGTGG ACACAGTAAT
55  1101 CGGGGGTCCG CTACGGCTCC TCTACGAGGA TGGTGACAGT GACGACGACT
      1151 TCTGGTGCCA CATGTGGAGC CCCCTGATCC ACCCAGTGGG TTGGTCACGA
      1201 CGTGTGGGCC ACGGCATCAA GATGTCAGAG AGGCGAAGTG ACATGGCCCA
      1251 TCACCCACCC TTCCGGAAGA TCTACTGTGA TGCCGTTTCT TACCTCTTCA

```

```

1301 AGAAGGTACG AGCAGTCTAC ACAGAAGGCG GTTGGTTTGA GGAAGGGATG
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1401 TGTCTGTAAG GTTCTCCTGG ATGGATACCT GATGATCTGT GTGGACGGGG
1451 GGCCCTCCAC AGATGGCTTG GACTGGTTCT GCTACCATGC CTCTTCCCAC
5 1501 GCCATCTTCC CGGCCACCTT CTGTCAGAAG AATGACATTG AGCTCACACC
1551 GCCAAAAGGT TATGAGGCAC AGACTTTCAA CTGGGAGAAC TACTTGAGAG
1601 AGACCAAGTC GAAAGCCGCT CCATCGAGAC TCTTTAACAT GGATTGCCCA
1651 AACCATGGCT TCAAGGTGGG CATGAAGCTG GAGGCCGTGG ACCTGATGGA
1701 GCCCCGGCTC ATCTGTGTGG CCACGGTGAA ACGAGTGGTG CATCGGCTCC
10 1751 TCAGCATCCA CTTTGACGGC TGGGACAGCG AGTACGACCA GTGGGTGGAC
1801 TGCGAGTCCC CAGACATCTA CCCCCTCGGC TGGTGTGAGC TCACCGGCTA
1851 CCAGCTCCAG CCTCCTGTGG CCGCAGGTGT GGGCTCTCGT GGCCCTAAGA
1901 GGCTCTGACT TTCTTTCTCT TTCTTTTTC CTTCTTCCCC CGCCCTGTG
1951 CCCATCTCCG TTCTTTGGCA TGAGGTGGAG ATGTCTCATG GACCACTTTA
15 2001 AGTAGAGAGT GAGCCCCGTC ACCCAGCCCC TGCTCCTGAC TTCTCTGTCT
2051 CCCTTTCCCT CTGGCCTGCA GAGCTCCTTC CTTCATCTTG CCCACTCTGT
2101 CATATGTTCT TGCCCTTGTG CACCCAGGTA AACTACCCAG GTCCCTCTGA
2151 GCAGCCCTGG TAACAAGGGT GGGGAAGAAG GACAGCTGTT CTCCGGCCCC
2201 TCCTCCAGCC CCGCCCTCTC CTCATTGCCC AGGTTTGGCT TCCTGTCTTG
20 2251 GGGTGTCTCG TGTGGGAGGG TGGATGGGGT CTCGGGATGC GCCTGTGCCC
2301 TGTGTCCTCC CAGGGACCCT CTTCTCATCT CTTTCACCCT TGTCTTTCAA
2351 CAACAGAACC GGCCACACCG CTGAAGGCCA AAGAGGCCAC AAAGAAGAAA
2401 AAGAAACAGT TTGGGAAGAA AAGGAAAAGA ATCCCGCCCA CTAAGACGCG
2451 ACCCCTCAGA CAGGGGTCCA AGAAGCCCTT GCTGGAGGAC GACCCTCAGG
25 2501 GTGCCAGGAA GATCTCGTCG GAGCCTGTTT CTGGCGAGAT CATTGCTGTG
2551 CGTGTGAAGG AAGAGCATCT AGACGTGGCC TCGCCCGACA AGGCTTCAAG
2601 TCCAGAGCTG CCTGTCTCCG TCGAGAACAT CAAGCAGGAA ACAGACGACT
2651 GAGCCTTCCT GCCTCCAGCC TGGCTTCTAG CTGGAAGCCA GCCCAGCGTT
2701 TCTCTACCAC CACCACCATG CCTCCACCTG ACTTTGGCTT GGAGACTGAT
30 2751 CCTCTCTGTG TAAATTCTGC CCGGTGCTGT GAAGGCTGGA CGGTGGAGGA
2801 CCTGCTGGGG TCTCCTGGGA CCGCCTGTT GCTTCTGCCC TCCCCTGTGG
2851 AAAGGTCTAT ATGACGGGCC GCCTGAGGCC CCAGAACTCG TCTGTGAACC
2901 ACCTTTTCCA GCCAGAGTTC CCAAAGCTGG AACGCTAGCT GCCTGCTCTT
2951 CCTTAAGATG GCCTCCCCC GACCCGCCAC GGCCCTCAGT TGCCAGGGAT
35 3001 GGGGCCACCA CTGTCACACT GTGGAATACA AGACAGTGAA CTCTGTCTGC
3051 CTAACAAAAA AAAAAAAAAA A

```

## BLAST Results

40

Entry HS756623 from database EMBLNEW:  
 Human DNA sequence from clone 756623 on chromosome 22q13.31-13.33  
 Score = 3939, P = 0.0e+00, identities = 875/954

45

Entry U89358\_1 from database TREMBL:  
 product: "1(3)mbt protein homolog"; Human 1(3)mbt protein  
 homolog  
 mRNA, complete cds.  
 50 Score = 505, P = 7.2e-45, identities = 123/320, positives =  
 170/320,  
 frame +1

55

Entry AB014581\_1 from database TREMBL:  
 gene: "KIAA0681"; product: "KIAA0681 protein"; Homo sapiens  
 mRNA for  
 KIAA0681 protein, partial cds.

Score = 503, P = 1.4e-46, identities = 122/307, positives = 163/307,  
frame +1

5

## Medline entries

-----

10 No Medline entry

## Peptide information for frame 1

15

ORF from 55 bp to 1905 bp; peptide length: 617  
Category: similarity to known protein  
Classification: unclassified

20

1 MEKPRSIEET PSSEPMEEEE DDDLELFGGY DSFRSYNSSV GSESSSYLEE  
51 SSEAENEDRE AGELPTSPLH LLSPGTPRSL DSGSGSEPAVC EMCGIVGTRE  
101 AFFSKTKRFC SVSCSRSYSS NSKKASILAR LQGKPPTKKA KVLHKAAWSA  
151 KIGAFLLHSQG TGQLADGTPT GQDALVLGFD WKGFLKDHSY KAAPVSCFKH  
25 201 VPLYDQWEDV MKGMKVEVLN SDAVLPSRVY WIASVIQTAG YRVLLRYEGF  
251 ENDASHDFWC NLGTVDVHPI GWCAINSKIL VPPRTIHAKF TDWKGYYLMKR  
301 LVGSRTLPLVD FHIKMVESMK YPFRQGMRL VVDKSQVSRT RMAVVDTVIG  
351 GRLRLLYEDG DSDDDFWCHM WSPLIHPVGW SRRVGHGKIM SERRSDMAHH  
401 PTFRKIYCDV VPYLFKKVRA VYTEGGWFEE GMKLEAIDPL NLGNICVATV  
30 451 CKVLLDGYLM ICVDGGPSTD GLDWFCYHAS SHAIFFPATFC QKNDIELTPP  
501 KGYEAQTFNW ENYLEKTKSK AAPSRLFNMD CPNHGFKVGM KLEAVDLMEP  
551 RLICVATVKR VVHRLLSIHF DGWDSEYDQW VDCESPDIYP VGWCELTGYQ  
601 LQPPVAAGVG SRGPKRL

35

## BLASTP hits

No BLASTP hits available

40

Alert BLASTP hits for DKFZphamy2\_1114, frame 1

TREMBL:AB014581\_1 gene: "KIAA0681"; product: "KIAA0681 protein";  
Homo  
45 sapiens mRNA for KIAA0681 protein, partial cds., N = 1, Score =  
503, P  
= 3.9e-48

50

TREMBL:U89358\_1 product: "1(3)mbt protein homolog"; Human  
1(3)mbt  
protein homolog mRNA, complete cds., N = 1, Score = 505, P =  
6.2e-48

55

>TREMBL:U89358\_1 product: "1(3)mbt protein homolog"; Human  
1(3)mbt protein  
homolog mRNA, complete cds.  
Length = 772

## HSPs:

Score = 505 (75.8 bits), Expect = 6.2e-48, P = 6.2e-48  
 5 Identities = 123/313 (39%), Positives = 170/313 (54%)

Query: 293 WKG YLMKRLVGSRTL PVDFH--  
 IKMVE SMKYPFRQGMRLVVDK SQVSRTRMAVVDTVIG 350  
 W+ YL ++ + T PV + V K F+ GM+LE +D S +

10 V V G  
 Sbjct: 208 WESYLEEQK--  
 AITAPVSLFQDSQAVTHNKNGFKLG MKLEGIDPQHPSMYFILTVAEVC G 265

Query: 351 GRLRLLYEDGDS D-DFWCHMW SPLIHPVGWSRRVGHG IKMSE--  
 15 RRS DMAHHP TFRKIY 407  
 RLRL + DG S+ DFW + SP IHP GW + GH +++ + + + +  
 Sbjct: 266 YRLRLHF-  
 DGYSECHDFWVNANSPDIHPAGWF EKTGHKLQLPKGYKEEEFSWSQYMCSTR 324

20 Query: 408 CDAVP-  
 YLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATVCKVLLDGYLMICVDGG 466  
 A P ++F G F+ GMKLEA+D +N +CVA+V V+ D  
 ++ D  
 Sbjct: 325 AQAAPKHM FVSQSHSPPLG-FQVGMKLEAVDRMNPSLVCVASVTDVV-  
 25 DSRFLVHFDNW 382

Query: 467 PSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGY-  
 EAQTFN WENYLEKTKSKAAPSR 525  
 T D++C SS I P +CQK LTPP+ Y + F WE YLE+T  
 30 + A P+  
 Sbjct: 383 DDT--YDYWC-  
 DPSSPYIHPVGWCQKQ GKPLTPPQDYPDPDNFCWEKYLEETGASAVPTW 439

Query: 526  
 35 LFNMDCPNHGFKVGMKLEAVDLMEPR LICVATVKRVVHRLLSIHFDGWDSEYDQWVDCES 585  
 F + P H F V MKLEAVD P LI VA+V+ V + IHFDGW  
 YD W+D +  
 Sbjct: 440 AFKVR-  
 PPHSFLVNMKLEAVDRRNPALIRVASVEDVEDHRIKIHF DGW SHGYDFWIDADH 498

40 Query: 586 PDIYPVGWCELTGYQLQPPV 605  
 PDI+P GWC TG+ LQPP+  
 Sbjct: 499 PDIHPAGWCSKTGHPLQPP L 518

45 Score = 333 (50.0 bits), Expect = 4.1e-27, P = 4.1e-27  
 Identities = 103/324 (31%), Positives = 151/324 (46%)

Query: 179 FDW GKFLKDHSYKAAPVSCFKHVPLYDQWEDVMK-  
 GMKVEVLNSDAVLPSRVYWIASVIQ 237  
 50 + W +L++ APVS F+ ++ K GMK+E + D PS  
 +Y+I +V +  
 Sbjct: 206 WSWESYLEEQKAITAPVSLFQDSQAVTHNKNGFKLG MKLEGI--DPQHPS-  
 MYFILTVAE 262

55 Query: 238  
 TAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYL 297  
 GYR+ L ++G+ HDFW N + D+HP GW L P+ +  
 W Y+



Sbjct: 263 VCGYRLRLHFDGYSE--  
CHDFWVNANSPDIHPAGWFEKTGHKLQLPKGYKEEEFSWSQYM 320

Query: 298 MKRLVGSRTLVPVDFHIKMVESMKYP---  
5 FRQGMRLLEVVDKSQVSRTRMAVVDTVIGGRLR 354  
+R H+ + +S P F+ GM+LE VD+ S +A V

V+ R  
Sbjct: 321 CS----  
10 TRAQAAPKHMFSQSHSPPLGFQVGMKLEAVDRMNPSLVCVASVTDVVDSRFL 376

Query: 355 LLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGKMSERRSD---  
MAHHPTFRKIYCDAY 411  
+ +++ D D+WC SP IHPVGW ++ G + + D

+ AV

15 Sbjct: 377  
VHFDNWDDTYDYWCDPSSPYIHPVGWCQKQKPLTPPQDYDPDNFCWEKYLEETGASAV 436

Query: 412  
PYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDG 471  
20 P KVR ++ F MKLEA+D N I VA+V V D + I

DG + G

Sbjct: 437 PTWAFKVRPPHS----FLVNMKLEAVDRRNPALIRVASVEDVE-  
DHRIKIHFDGW--SHG 489

25 Query: 472 LDWFCYHASSHAIFPATFCQKNDIELTPPKG 502  
D F A I PA +C K L PP G

Sbjct: 490 YD-FWIDADHPDIHPAGWCSKTGHPLQPPLG 519

30 Score = 236 (35.4 bits), Expect = 2.5e-16, P = 2.5e-16  
Identities = 47/110 (42%), Positives = 66/110 (60%)

Query: 499 PPKGYEAQTFNWENYLEKTKSKAAPSRLE-NMDCPNH---  
GFKVGMKLEAVDLMEPRLIC 554

P G + + ++WE+YLE+ K+ AP LF + H GFK+GMKLE +D

35 P +  
Sbjct: 197  
PATGEKKECWSWESYLEEQKAITAPVSLFQDSQAVTHNKNGFKLGMKLEGIDPQHPSMYF 256

40 Query: 555 VATVKRVVHRLLSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPP  
604

+ TV V L +HFDG+ +D WV+ SPDI+P GW E TG++LQ P  
Sbjct: 257 ILTVAEVCGYRLRLHFDGYSECHDFWVNANSPDIHPAGWFEKTGHKLQLP  
306

45 Pedant information for DKFZphamy2\_1114, frame 1  
-----

Report for DKFZphamy2\_1114.1

50 [LENGTH] 617

[MW] 69264.11

[pI] 6.05

55 [HOMOL] TREMBL:U89358\_1 product: "1(3)mbt protein  
homolog"; Human 1(3)mbt protein homolog mRNA, complete cds. 1e-47

[BLOCKS] BL01206A Amiloride-sensitive sodium channels proteins

[[KW]] TRANSMEMBRANE 1  
[[KW]] LOW\_COMPLEXITY 9.40 %

```
5  SEQ  MEKPRSIEETPSSEPMEEEEDDDLELFGGYDSFRSYNSSVGSESSSYLEESSEAENEDRE
   SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
   PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
   MEM  .....

10  SEQ  AGELPTSPLHLLSPGTPRSLDGSSEPAVCEMCGIVGTREAFFSKTKRFCSVSCSRYSYS
   SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
   PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
   MEM  .....

15  SEQ  NSKKASILARLQGKPPTKKAKVLHKAAWSAKIGAF LHSQGTGQLADGTPTGQDALVLGFD
   SEG  xxxxxx.....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
   PRD  ccchhhhhhhhhhhccccccccchhhhhhhhhhhhhhhhhhhcccccccccccccccccccccc
   MEM  .....

20  SEQ  W GKFLKDHSYKAAPVSCFKHVPLYDQWEDVMKGMKVEVLNSDAVLPSRVYWIASVIQTAG
   SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
   PRD  chhhhhhhccccccccccccccccccccccccchhhhhhheeeeecccccccccccccccccccc
   MEM  .....

25  SEQ  YRVLLRYEGFENDASHDFWCNLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKR
   SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
   PRD  cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccchhhhhh
   MEM  .....

30  SEQ  LVGSRTL PVD FHIKMVESMKYPFRQGMRLVV DKSQVSRTMAVVDTVIGGRLRLLYEDG
   SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
   PRD  hcccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
   MEM  .....

35  SEQ  DSDDDFWCHMWSPLIHPVGWSRRVGHGIKMSERRSDMAHHPTFRKIYCDAVPYLFKKVRA
   SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
   PRD  cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccchhhhhh
   MEM  .....

40  SEQ  VYTEGGWFEEGMKLEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCYHAS
   SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
   PRD  cccccchhhhhhheeeeecccccccccccccccccccccccccccccccccccccccccccccccc
   MEM  .....MMMMMMMMMMMMMMMMMMMM.....

45  SEQ  SHAI FPATFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKAAPSR LFNMDCPNHGFKVGM
   SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
   PRD  cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccchhhhhh
   MEM  .....

50  SEQ  KLEAVDLMEPRLICVATVKRVVHRLLSIHFDGW DSEYDQWVDCESPDIYPVGWCELTGYQ
   SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
   PRD  eecccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
   MEM  .....

55  SEQ  LQPPVAAGVGSRGPKRL
   SEG  .....
   PRD  ccccccccccccccccccc
   MEM  .....
```

(No Prosite data available for DKFZphamy2\_1114.1)

5 (No Pfam data available for DKFZphamy2\_1114.1)

DKFZphamy2\_1i24

-----

5 group: differentiation/development

DKFZphamy2\_1i24 encodes a novel 835 amino acid protein without partial similarity to *rattus norvegicus* Notch2 protein.

10 Notch family molecules are thought to be negative regulators of neuronal differentiation in early brain development. Notch2 is expressed not only by neuronal cells in the embryonic brain, but also by glial cells in the postnatal brain. The new protein represents a new member of this family and may be involved in  
15 specific differentiation or developmental pathways of the nervous system.

The new protein can find application in modulating development and differentiation of amygdala cells.

20

putative protein

probably complete cds.

25

Sequenced by MediGenomix

Locus: unknown

30

Insert length: 2768 bp

Poly A stretch at pos. 2714, polyadenylation signal at pos. 2697

```

1 AGAAATCTTC AGCCAAACAG CTGCAGGAAG TAGAGAAGGT TAAACCCAG
35 51 AGTGAGAAAG TTCATCAGAC TCTGATTCTG GACCCAGCAC AGAGGAAGAG
101 ACTCCAGCAG CAGATGCAGC AGCAGGTTCA GCTCTTGACC CAAATCCACC
151 TTCTTGCCAC CTGCAACCCC AACCTCAATC CGGAGGCCAC TACCACCAGG
201 ATATTTCTTA AAGAGCTGGG AACCTTTGCT CAAAGCTCCA TCGCCCTTCA
251 CCATCAGTAC AACCCCAAGT TTCAGACCCT GTTCCAACCC TGTAACCTGA
40 301 TGGGAGCTAT GCAGCTGATT GAAGACTTCA GCACACATGT CAGCATTGAC
351 TGCAGCCCTC ATAAAACTGT CAAGAAGACT GCGAATGAAT TTCCCTGTTT
401 GCCAAAGCAA GTGGCTTGGG TTCTGGCCAC AAGCAAGGTT TTCATGTATC
451 CAGAGTTACT TCCAGTGTGT TCCCTGAAGG CAAAGAATCC CCAGGATAAG
501 ATCGTCTTCA CCAAGGCTGA GGACAATTTG TTAGCTTTAG GACTGAAGCA
45 551 TTTTGAAGGA ACTGAGTTTC CTAATCCTCT AATCAGCAAG TACCTTCTAA
601 CCTGCAAAAC TGCCCACCAA CTGACAGTGA GAATCAAGAA CCTCAACATG
651 AACAGAGCTC CTGACAACAT CATTAAATTT TATAAGAAGA CCAAACAGCT
701 GCCAGTCCTA GGAAAATGCT GTGAAGAGAT CCAGCCACAT CAGTGGGAAGC
751 CACCTATAGA GAGAGAAGAA CACCGGCTCC CATTCTGGTT AAAGGCCAGT
50 801 CTGCCATCCA TCCAGGAAGA ACTGCGGCAC ATGGCTGATG GTGCTAGAGA
851 GGTAGGAAAT ATGACTGGAA CCACTGAGAT CAACTCAGAT CGAAGCCTAG
901 AAAAAGACAA TTTGGAGTTG GGGAGTGAAT CTCGGTACCC ACTGCTATTG
951 CCTAAGGGTG TAGTCCTGAA ACTGAAGCCA GTTGCCACCC GTTCCCCAG
1001 GAAGGCTTGG AGACAGAAGC GTTCATCAGT CCTGAAGCCC CTCCTTATCC
55 1051 AACCCAGCCC CTCTCTCCAG CCCAGCTTCA ACCCTGGGAA AACACCAGCC
1101 CGATCAACTC ATTCAGAAGC CCCTCCGAGC AAAATGGTGC TCCGGATTCC
1151 TCACCCAATA CAGCCAGCCA CTGTTTACCA GACAGTTCCA GGTGTCCCTC
1201 CACTGGGGGT CAGTGGAGGT GAGAGTTTTG AGTCTCCTGC AGCACTGCCT

```

```

1251 GCTGTGCCCC CTGAGGCCAG GACAAGCTTC CCTCTGTCTG AGTCCCAGAC
1301 TTTGCTCTCT TCTGCCCCCTG TGCCCCAAGGT AATGCTGCCC TCCCTTGCCC
1351 CTTCTAAGTT TCGAAAGCCA TATGTGAGAC GGAGACCCTC AAAGAGAAGA
1401 GGAGTCAAGG CCTCTCCCTG TATGAAACCT GCCCCTGTTA TCCACCACCC
5 1451 TGCATCTGTT ATCTTCACTG TTCCTGCTAC CACTGTGAAG ATTGTGAGCC
1501 TTGGCGGTGG CTGTAACATG ATCCAGCCTG TCAATGCGGC TGTGGCCCAG
1551 AGTCCCCAGA CTATTTCCAT CACTACCCTC TTGGTTAACC CTACTTCCTT
1601 CCCCTGTCCA TTGAACCAGT CCCTTGTGGC CTCCTCTGTC TCACCCTTAA
1651 TTGTTTCTGG CAATTCTGTG AATCTTCCTA TACCATCCAC CCCTGAAGAT
10 1701 AAGGCCCACG TGAATGTGGA CATTGCTTGT GCTGTGGCTG ATGGGGAAAA
1751 TGCCTTTTCA GGCCTAGAAC CCAAATTAGA GCCCCAGGAA CTATCTCCTC
1801 TCTCTGCTAC TGTTTTCCCG AAAGTGGAAC ATAGCCCAGG GCCTCCACTA
1851 GCAGATGCAG AGTGCCAAGA AGGATTGTCA GAGAATAGTG CCTGTGCTG
1901 GACCGTTGTG AAAACAGAGG AGGGGAGGCA AGCTCTGGAG CCGCTCCCTC
15 1951 AGGGCATCCA GGAGTCTCTA AACAACCCTA CCCCTGGGGA TTTAGAGGAA
2001 ATTGTCAAGA TGGAACCTGA AGAAGCTAGA GAGGAAATCA GTGGATCCCC
2051 TGAGCGTGAT ATTTGTGATG ACATCAAAGT GGAACATGCT GTGGAATTGG
2101 ACACTGGTGC CCCAAGCGAG GAGTTGAGCA GTGCTGGAGA AGTAACGAAA
2151 CAGACAGTCT TACAGAAGGA AGAGGAGAGG AGTCAGCCAA CTAACACCCC
20 2201 TTCATCTTCT CAAGAGCCCC CTGATGAAGG AACCTCAGGG ACAGATGTGA
2251 ACAAAGGATC ATCAAAGAAT GCTTTGTCTT CAATGGATCC TGAAGTGAGG
2301 CTTAGTAGCC CCCAGGGGAA GCCAGAAGAT TCATCCAGTG TTGATGGTCA
2351 GTCAGTGGGG ACTCCAGTTG GGCCAGAAAC TGGAGGAGAG AAGAATGGGC
2401 CAGAAGAAGA GGAAGAAGAG GACTTTGATG ACCTCACCCA AGATGAGGAA
25 2451 GATGAAATGT CATCAGCTTC TGAGGAATCT GTGCTTTCTG TCCCAGAACT
2501 CCAGGTGAGA GCTGGAGAAT ATTCTCAAGT ATTTCTGTTG CTCAGTAATA
2551 TGTATCACTT ATTGATATGC CACCTGCTTG CTTGCTGCAC TATGGATAGT
2601 CCTAAAATCA TTTGTATTTG ATTTGTGAAT GCATTATGGG ACATGATTGT
2651 GGAGTTGAGG TGAAATGAGA TGGAAGGAT GAAATTTTAC TTATTATATT
30 2701 AAACTCGTTT ACACATTAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2751 AAAAAAAAAA AAAAAAAAAA

```

## BLAST Results

35

Entry RNN0TCHX from database EMBL:

Rat notch 2 mRNA.

Score = 818, P = 1.6e-26, identities = 216/277

40

## Medline entries

45

No Medline entry

50

## Peptide information for frame 3

ORF from 114 bp to 2618 bp; peptide length: 835

Category: putative protein

55

Classification: Differentiation/Development

```

1 MQQHVQLLTQ IHLLATCNPN LNPEATTTTRI FLKELGTFAQ SSIALHHQYN
51 PKFQTLFQPC NLMGAMQLIE DFSTHVSIDC SPHKTVKKTA NEFPCLPKQV

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5

10

15

## 20

25

Pedant information for DKFZphamy2\_li24, frame 3

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30.

Report for DKFZphamy2\_li24.3

35

40

50

55

[illegible]

55 (No Prosite data available for DKFZphamy2\_li24.3)  
(No Pfam data available for DKFZphamy2\_li24.3)

DKFZphamy2\_1j19

5 -----

group: differentiation/development

10 DKFZphamy2\_1j19 encodes a novel 150 amino acid protein with high similarity to the allograft inflammatory factor-1 of *Cyprinus carpio*.

15 Allograft inflammatory factor-1 (AIF-1) is a protein involved in allograft rejection. In experimental autoimmune encephalomyelitis (EAE), neuritis(EAN) and uveitis (EAU) it is produced by macrophages and microglia cells.

20 The new protein can find clinical application in the development of tools to enhance the compatibility of transplanted tissues as well as in expression profiling of autoimmune diseases and infections.

25 strong similarity to allograft inflammatory factor-1 (*Cyprinus carpio*)

identical to DKFZphamy2\_1n1

30 Sequenced by MediGenomix

Locus: /map="504.9 cR from top of Chr9 linkage group"

Insert length: 3381 bp

35 Poly A stretch at pos. 3362, polyadenylation signal at pos. 3344

```

      1 GCCGGAGCCC GGACCAGGCG CCTGTGCCTC CTCCTCGTCC CTCGCCGCGT
      51 CCGCGAAGCC TGGAGCCGGC GGGAGCCCCG CGCTCGCCAT GTCGGGCGAG
40    101 CTCAGCAACA GGTTCCAAGG AGGGAAGGCG TTCGGCTTGC TCAAAGCCCCG
      151 GCAGGAGAGG AGGCTGGCCG AGATCAACCG GGAGTTTCTG TGTGACCAGA
      201 AGTACAGTGA TGAAGAGAAC CTTCAGAAA AGCTCACAGC CTTCAAAGAG
      251 AAGTACATGG AGTTTGACCT GAACAATGAA GCGGAGATTG ACCTGATGTC
      301 TTAAAGAGG ATGATGGAGA AGCTTGGTGT CCCCAGACC CACCTGGAGA
45    351 TGAAGAAGAT GATCTCAGAG GTGACAGGAG GGGTCAGTGA CACTATATCC
      401 TACCGAGACT TTGTGAACAT GATGCTGGGG AAACGGTCGG CTGTCCTCAA
      451 GTTAGTCATG ATGTTTGAAG GAAAAGCCAA CGAGAGCAGC CCCAAGCCAG
      501 TTGGCCCCCC TCCAGAGAGA GACATTGCTA GCCTGCCCTG AGGACCCCGC
      551 CTGGACTCCC CAGCCTTCCC ACCCCATACC TCCCTCCCGA TCTTGCTGCC
50    601 CTTCTTGACA CACTGTGATC TCTCTCTCTC TCATTTGTTT GGTCATTGAG
      651 GGTTTGTTTG TGTTTTCATC AATGTCTTTG TAAAGCACAA ATTATCTGCC
      701 TTAAAGGGGG TCTGGGTGCG GGAATCCTGA GCCTTGGGTC CCCTCCCTCT
      751 CTTCTTCCCT CTTCCCCCGC TCCCTGTGCA GAAGGGCTGA TATCAAACCA
      801 AAAACTAGAG GGGGCAGGGC CAGGGCAGGG AGGCTTCCAG CCTGTGTTCC
55    851 CCTCACTTGG AGGAACCAGC ACTCTCCATC CTTTCAGAAA GTCTCCAAGC
      901 CAAGTTCAGG CTCACTGACC TGGCTCTGAC GAGGACCCCA GGCCACTCTG
      951 AGAAGACCTT GGAGTAGGGA CAAGGCTGCA GGGCCTCTTT CGGGTTTCCT
1001 TGGACAGTGC CATGGTTCCA GTGCTCTGGT GTCACCCAGG ACACAGCCAC

```



```

1051 TCGGGGCCCC GCTGCCCCAG CTGATCCCCA CTCATTCCAC ACCTCTTCTC
1101 ATCCTCAGTG ATGTGAAGGT GGGGAAGGAAA GGAGCTTGGC ATTGGGAGCC
1151 CTTCAAGAAG GTACCAGAAG GAACCTCCA GTCTGCTCT CTGGCCACAC
1201 CTGTGCAGGC AGCTGAGAGG CAGCGTGCAG CCTACTGTC CCTTACTGGG
5 1251 GCAGCAGAGG GCTTCGGAGG CAGAAGTGAG GCCTGGGGTT TGGGGGGAAA
1301 GGTCAAGCTCA GTGCTGTTCC ACCTTTTAGG GAGGATACTG AGGGGACCAG
1351 GATGGGAGAA TGAGGAGTAA AATGCTCACG GCAAAGTCAG CAGCACTGGT
1401 AAGCCAAGAC TGAGAAATAC AAGGTTGCTT GTCTGACCCC AATCTGCTTG
1451 AAACCTGACT CTGCTTCTCT CATTGTCTT CCTACCCTAC TCACATAATT
10 1501 CACTCATTGA CTCACTCATT CACCAGATAT TTATTGACCT GCTATTATAA
1551 GCTTTACATC CTCCCAGTGT GTCCGTGGCAT GTGCAGTATA CACGGCTAA
1601 CTCATCTCTC CCCAGATCTC TCAGAACCCTT GAGCTTGGGA ATTGAACTGG
1651 GGTACCTGT GTCTTTCTT ATGGACTCGC AGGATTTTAG AACCTAATG
1701 CACCCTGGAG GGTAAGCTGGG CCAGACTTCT CATTTACAG GTGAGGAGAC
15 1751 TGGTGCCCCA CAGGGATTAA GTGCCTTGCC CAAGGTCAGG CTTATCTCCA
1801 GAGGGAGGTG CCCTGGACTG GGGCCAGAT GTTCAGGGAC CCTGCCTACA
1851 CCTCATTTCC AGTGTGGGCT GCCTTAGTTA GTTATGAGAA CAGGGAAGGG
1901 CTGGGAAGAG ACAGCCTCCA AGGTCAACAC TTGGAGAGGG TTTACTTGC
1951 TCTGAAGACC CTGGTCCAGG ATTCGCCCTC TCCCATGCCT TCAAGTCAGC
20 2001 ATCAGGCTTA GGGCAAAGAC CAGGCCTCTG AAGCTGCCTC TTGTAATTCA
2051 TGCAGGAAGA TGTCAAAGTC AGCCCCATCT TGGCTGATCA GGGTGTTCAG
2101 CCTTAACCCC ACCTGTGTTT TGAAGTCTCT TACCCTACCT GCTCAGGACT
2151 GAGACAGTTA TTCACTGAAC ATATTTATTA AGCACTTGCT GTAGGCCAAC
2201 AGTTAAGAAT CCAATAATGA AATGGACAGA TTCATGGAAC TTAGAGTCCA
25 2251 ATAGGAAAGT GAGACCCAGA CAATGACAAT GAGATAAATG TTAGGAAGGG
2301 GGAGGTATGG GGTGACTTCC CTGCAGTCCT GGGGGCCTAC ATGGGCCCCA
2351 GACTGGGTGA GAGTCTTGGC AGAGCCTTTG CAACACCTTA AGTGGACAGG
2401 ACTGGGAGGT CTTGGTGGTT GGAGCCAACG TGGGTTCCTT GCGGCTCCTT
2451 AGTCACCTCT GATAGCAGAT TGAGGGAGGA AAACAGGTAA GGCATGAGGA
30 2501 AATGGCCAGG TTGGGTAAAC CCACTGGTTT CAACCAGTTC AGGAATGAGG
2551 TTATTTGGCC ATGACTGGCT GATCTTGAGC TCAAGGATCT GCTTCAAATG
2601 CACACAGGCC TAGTTGAAGT TTAAACCCCA GCAAAACATT CCTCCCTGTA
2651 AATGGAAAAT CCTACTTCTA CCCCCACCCT GCCCTGTTTT TTGTTTTTTT
2701 TTTCCCCAAG ATCATTAGAT GTCCTCACCC CTCCTCACTG CCTCTCCTCT
35 2751 CTGGGACAGG CTGGGACCTT TGAGGAAGAT AAAGCCTTCC TTGACTACCC
2801 ATCATATTCA GTGTCCCTGT TCCTCACTCA GAGAGGAAGG CAGAACCAGT
2851 CAGGCTTATT TCAGTAAGTT CCACAGTTCT ACAAGACTGC AGGAATTCTC
2901 CTTAAGGGAG GAGAGCAAGC AGGTGTGGCC CCAGCTTCTG GAAATGGCAG
2951 AAGAGAGGGT TTTCTCATTG AATGGGGGTG GGGGCTCGTG TGTCTTGGGA
40 3001 AACCCCATCA GTCCCTTCAT TTCTTGAGAC TCAACTCCTG GGAGGAGAGG
3051 GTCTCAAGAG TTGTCCCTGG AAGGAGGGCG GGGGCAGTCT GCATCTATTT
3101 CAGGTTGTGG CTCTTGGTTC TAGGACTCTT ACTTCTCTGG CTAAGGGCTC
3151 AGCTTCTTGG GACTTCAACC ATCTTCTTTC TGAAAGACCA AATCTAATGT
3201 AACCAGTAAC GTGAGGACTG CCAAGTATGG CTTTGTCCCT ATGACTCAGA
45 3251 GGAGGGTTTG TCGGGCAAAT TCAGGTGGAT GAAGTATGTG TGTGCGTGTG
3301 CATGGGAGTG TCGGTGGACT GGGATATCAT CTCTACAGCC TGCAATAAAA
3351 CCAGACAAAC TTAAAAAAA AAAAAAAAAA A

```

50

## BLAST Results

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Entry AB012309\_1 from database TREMBL:

product: "allograft inflammatory factor-1"; Cyprinus carpio mRNA

55 for

allograft inflammatory factor-1, complete cds.

Score = 575, P = 3.7e-54, identities = 113/146, positives = 128/146,

frame +2

5

## Medline entries

-----

No Medline entry

10

## Peptide information for frame 2

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15 ORF from 89 bp to 538 bp; peptide length: 150

Category: strong similarity to known protein

Classification: unclassified

1 MSGELSNRFQ GGKAFGLLKA RQERRLAIEIN REFLCDQKYS DEENLPEKLT  
 20 51 AFKEKYMED LNNEGEIDLK SLKRMMEKLG VPKTHLEMKK MISEVTGGVS  
 101 DTISYRDFVN MMLGKRSAVL KLVMMFEGKA NESSPKPVGP PPERDIASLP

25

## BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_1j19, frame 2

30

No Alert BLASTP hits found

Pedant information for DKFZphamy2\_1j19, frame 2

-----

35

## Report for DKFZphamy2\_1j19.2

40 [LENGTH] 150  
 [MW] 17067.86  
 [pI] 6.63  
 [HOMOL] TREMBL:AB012309\_1 product: "allograft inflammatory  
 factor-1"; Cyprinus carpio mRNA for allograft inflammatory  
 factor-1, complete cds. 2e-59  
 45 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae,  
 YBR109c] 5e-04  
 [FUNCAT] 03.07 pheromone response, mating-type determination,  
 sex-specific proteins [S. cerevisiae, YBR109c] 5e-04  
 [FUNCAT] 08.19 cellular import [S. cerevisiae, YBR109c] 5e-04  
 50 [FUNCAT] 10.02.99 other morphogenetic activities [S.  
 cerevisiae, YBR109c] 5e-04  
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae,  
 YBR109c] 5e-04  
 [FUNCAT] 03.04 budding, cell polarity and filament formation  
 55 [S. cerevisiae, YBR109c] 5e-04  
 [FUNCAT] 03.01 cell growth [S. cerevisiae, YBR109c] 5e-04  
 [FUNCAT] 30.05 organization of centrosome [S. cerevisiae,  
 YBR109c] 5e-04

[[SCOP]] d2mysb\_ 1.37.1.5.15 Myosin Essential Chain Myosin  
 Regulatory Chai 5e-20  
 [[SCOP]] dlwdcb\_ 1.37.1.5.14 Myosin Essential Chain Myosin  
 Regulatory Chai 3e-05  
 5 [[SCOP]] dlosa\_ 1.37.1.5.13 Calmodulin [(Paramecium  
 tetraurelia) 3e-16  
 [[SCOP]] dlauib\_ 1.37.1.5.19 Calcineurin regulatory subunit  
 (B-chain 2e-16  
 [[PIRKW]] duplication 7e-06  
 10 [[PIRKW]] mitosis 7e-06  
 [[PIRKW]] calcium binding 7e-06  
 [[PIRKW]] EF hand 7e-06  
 [[PIRKW]] cell division 7e-06  
 [[SUPFAM]] unassigned calmodulin-related proteins 3e-47  
 15 [[SUPFAM]] calmodulin 7e-06  
 [[SUPFAM]] calmodulin repeat homology 3e-47  
 [[KW]] All\_Alpha  
 [[KW]] 3D

20 SEQ MSGELSNRFQGGKAFGLLKARQERRLA EINREFLCDQKYSDEENLPEKLTAFKEKYMED  
 lctr- .....HHHHHHHHHHHHHT  
 25 SEQ LNNEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVL  
 lctr- TTTTTCBCHHHHHHHHHHTTTCCCHHHHHHHHHCTTTTCCCBCHHHHHHHHCCTTTHHH  
 SEQ KLVMMEGKANESSPKPVGPPPERDIASLP  
 30 lctr- HHHHHHTTTTC.....

(No Prosite data available for DKFZphamy2\_1j19.2)

35 (No Pfam data available for DKFZphamy2\_1j19.2)

DKFZphamy2\_24b4

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5 group: cell cyle

DKFZphamy2\_24b4 encodes a novel 698 amino acid protein with similarity to human STIM1.

10 The stromal interaction molecular 1 gene (STIM1) encodes a type I trans-membrane protein of unknown function, which induces growth arrest and degeneration of the human tumor cell lines G401 and RD but not HBL100 and CaLu-6, suggesting a role in the pathogenesis of rhabdomyosarcomas and rhabdoid tumors. There is also strong  
15 similarity to a Mus musculus stromal cell protein, which selectively increases interleukin 7-dependent proliferation of pre-B cells. The novel protein contains 1 transmembrane domain.

20 The new protein can find application in modulation of tumour growth.

similarity to STIM1 (Homo sapiens)

25 probably differential polyadenylation: cf. EST-BLAST file.  
perhaps complete cds.  
Pedant: SIGNAL\_PEPTIDE and TRANSMEMBRANE 1

Sequenced by GBF

30

Locus: /map="139.2 cR from top of Chr4 linkage group"

Insert length: 3305 bp

35

Poly A stretch at pos. 3274, polyadenylation signal at pos. 3260

```

1  GGC GCCCTTCA TCCCGCCTCG ACTCCTGGCC CAGCGTGGGG CTGGCTGCTG
51 CGGCGGCGGC GCTGGGCTGC GTTGCTGGTG CTCGGGCTGC TGGTACCCGG
101 AGCGGCGGAC GGATGCGAGC TTGTGCCCCG GCACCTCCGC GGGCGGCGGG
40 151 CGACTGGCTC TGCCGCAACT GCCGCCTCCT CTCCCGCCGC GGGCGGCCGC
201 GATAGCCCGG CGCTCATGAC AGATCCCTGC ATGTCACTGA GTCCACCATG
251 CTTTACAGAA GAAGACAGAT TTAGTCTGGA AGCTCTTCAA ACAATACATA
301 AACAAATGGA TGATGACAAA GATGGTGGAA TTGAAGTAGA GGAAAGTGAT
351 GAATTCATCA GAGAAGATAT GAAATATAAA GATGCTACTA ATAAACACAG
45 401 CCATCTGCAC AGAGAAGATA AACATATAAC GATTGAGGAT TTATGGAAAC
451 GATGGAAAAC ATCAGAAGTT CATAATTGGA CCCTTGAAGA CACTCTTCAG
501 TGGTTGATAG AGTTTGTTGA ACTACCCCAA TATGAGAAGA ATTTTAGAGA
551 CAACAATGTC AAAGGAACGA CACTTCCCAG GATAGCAGTG CACGAACCTT
601 CATTTATGAT CTCCAGTTG AAAATCAGTG ACCGGAGTCA CAGACAAAAA
50 651 CTTAGCTCA AGGCATTGGA TGTGGTTTTG TTTGGACCTC TAACACGCCC
701 ACCTCATAAC TGGATGAAAG ATTTTATCCT CACAGTTTCT ATAGTAATTG
751 GTGTTGGAGG CTGCTGGTTT GCTTATACGC AGAATAAGAC ATCAAAAGAA
801 CATGTTGCAA AAATGATGAA AGATTTAGAG AGCTTACAAA CTGCAGAGCA
851 AAGTCTAATG GACTTACAAG AGAGGCTTGA AAAGGCACAG GAAGAAAACA
55 901 GAAATGTTGC TGTAGAAAAG CAAAATTTAG AGCGCAAAAT GATGGATGAA
951 ATCAATTATG CAAAGGAGGA GGCTTGTCGG CTGAGAGAGC TAAGGGAGGG
1001 AGCTGAATGT GAATTGAGTA GACGTCAGTA TGCAGAACAG GAATTGGAAC
1051 AGGTTTCGCAT GGCTCTGAAA AAGGCCGAAA AAGAATTTGA ACTGAGAAGC

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1101 AGTTGGTCTG TTCCAGATGC ACTTCAGAAA TGGCTTCAGT TAACACATGA
1151 AGTAGAAGTG CAATACTACA ATATTA AAAAG ACAAACGCT GAAATGCAGC
1201 TAGCTATTGC TAAAGATGAG GCAGAAAAAA TTA AAAAGAA GAGAAGCACA
1251 GTCTTTGGGA CTCTGCACGT TGCACACAGC TCCTCCCTAG ATGAGGTAGA
5 1301 CCACAAAATT CTGGAAGCAA AGAAAGCTCT CTCTGAGTTG ACAACTTGTT
1351 TACGAGAACG ACTTTTTTCGC TGGCAACAAA TTGAGAAGAT CTGTGGCTTT
1401 CAGATAGCCC ATA ACTCAGG ACTCCCAGC CTGACCTCTT CCCTTTATTC
1451 TGATCACAGC TGGGTGGTGA TGCCCAGAGT CTCCATTCCA CCCTATCCAA
1501 TTGCTGGAGG AGTTGATGAC TTAGATGAAG ACACACCCCC AATAGTGTCA
10 1551 CAATTTCCCG GGACCATGGC TAAACCTCCT GGATCATTAG CCAGAAGCAG
1601 AGCCCTGTGC CGTTCACGCC GCAGCATTGT GCCGTCTCTG CCTCAGCCTC
1651 AGCGAGCTCA GCTTGCTCCA CACGCCCCCC ACCCGTCACA CCCTCGGCAC
1701 CCTCAACCACC CGCAACACAC ACCACACTCC TTGCCTTCCC CTGATCCAGA
1751 TATCCTCTCA GTGTCAAGTT GCCCTGCGCT TTATCGAAAT GAAGAGGAGG
15 1801 AAGAGGCCAT TTACTTCTCT GCTGAAAAGC AATGGGAAGT GCCAGACACA
1851 GCTTCAGAAT GTGACTCCTT AAATTCTTCC ATTGGAAGGA AACAGTCTCC
1901 TCCTTTAAGC CTCGAGATAT ACCAAACATT ATCTCCGCGA AAGATATCAA
1951 GAGATGAGGT GTCCCTAGAG GATTCTCTCC GAGGGGATTG GCCTGTAAC
2001 GTGGATGTGT CTTGGGGTTC TCCCGACTGT GTAGGTCTGA CAGAACTAA
20 2051 GAGTATGATC TTCAGTCCTG CAAGCAAAGT GTACAATGGC ATTTTGGAGA
2101 AATCCTGTAG CATGAACCAG CTTTCCAGTG GCATCCCGGT GCCTAAACCT
2151 CGCCACACAT CATGTTCTCT AGCTGGCAAC GACAGTAAAC CAGTTCAGGA
2201 AGCCCCAAGT GTTGCCAGAA TAAGCAGCAT CCCACATGAC CTTTGTCTATA
2251 ATGGAGAGAA AAGCAAAAAG CCATCAAAAA TCAAAAGCCT TTTTAAGAAG
25 2301 AAATCTAAGT GAACTGGCTG ACTTGATGGA ATCATGTTCA AGTGGCATCT
2351 GTAAACTATT ATCCCCCACC CTCCACTCCC CACCTTTTTT TTGGTTTAAT
2401 TTTAGGAATG TAACTCCATT GGGGCTTTCC AGGCCGGATG CCATAGTGGA
2451 ACATCCAGAA GGGCAACTGT CTACTGTCTG CTTATTTAAG TGA CTATATA
2501 TAATCAATTC ATCAAGCCAG TTATTACTGA AAAATCATTG AAATGAGACA
30 2551 GTTTACAGTC ATTTCTGCCT ATTTATTTCT GCTTTGTTCT CAGTGATGTA
2601 TATGCAACAT TTTGTTGAAA GCCACGATGG ACTTACAAGC TTTAATGGAC
2651 TCGTAAGCCA GCATGGGCTT GCAAAAATTT CTTGTTTACC AGAGCATCTT
2701 CTTATCTTTC CACAGAGCTA TTTACATCCT GGACTATATA ACTTAAAAGA
2751 AGTAAAACGT AATTGCACTA CTGTTTTCCA GACTGGAAAA AAAAAAAAT
35 2801 CTCTGCAAGT GAAACTGTAT AGAGTTTATA AAATGACTAT GGATAGGGGA
2851 CTGTTTTTAC TTTTAGATCA AAATGGGTTT TTAAGTAGAA CCTAGGGTTT
2901 CTAATTGACT TGATTTCTGG AAATGAAAAC CCGCGCTTTT ATTATGGGAA
2951 GCTTCTTGAA CTGCATTTAC TATTGTGAAG TTTCAAGTCC CGCTGTAAAG
3001 ATCATGTTGT TTTGTTTTCC CCAGGGCTTT CACTGTGATT TACTGCATTG
40 3051 CAGGCTGTAT GATAAAACAC ACATAATTTA AAGAGAGAAG GCTCTTGATT
3101 CCTTATGCAA GTGGAAGAGT TGAACTTGA TTGAAGGACT TAAACATTTC
3151 ACAACCTTAA GCCGAGGTGG GGGGATATGG GGATTCAGGC AGTTGTTTAC
3201 ACACTTTGAA TAACTGCAAA GGATTTACGG TTTGTGAAAA ATGTGTACTG
3251 TGGAAAAGAT AATAAATTGA AGACATTAAA AAAAAGAAAA AAAAAAAAAA
45 3301 AAAAA

```

## BLAST Results

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50

Entry HS5242610\_1 from database TREMBL:  
 gene: "STIM1"; product: "G0K"; Homo sapiens G0K (STIM1) mRNA,  
 complete  
 cds.

55

Score = 1397, P = 4.2e-142, identities = 275/447, positives =  
 336/447,  
 frame +3

Entry MMU47323\_1 from database TREMBL:

product: "stromal cell protein"; Mus musculus stromal cell protein

mRNA, complete cds.

5 Score = 1394, P = 8.8e-142, identities = 274/447, positives = 336/447, frame +3

Entry HS917349 from database EMBL:

10 human STS EST167479.

Score = 1390, P = 9.1e-57, identities = 284/287

15 Medline entries

-----

97079692:

20 Parker NJ, Begley CG, Smith PJ, Fox RM.; Molecular cloning of a novel

human gene (D11S4896E) at chromosomal region 11p15.5. Genomics 1996 Oct 15;37(2):253-6

96326680:

25 Oritani K, Kincade PW.; Identification of stromal cell products that interact

with pre-B cells. J Cell Biol 1996 Aug;134(3):771-82

30

Peptide information for frame 3

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35

ORF from 216 bp to 2309 bp; peptide length: 698

Category: similarity to known protein

Classification: Cell signaling/communication

Prosites motifs: RGD (589-591)

40

1 MTDPCMSLSP PCFTEEDRFS LEALQTIHKQ MDDDKDGGIE VEESDEFIRE  
 51 DMKYKDATNK HSHLHREDKH ITIEDLWKRW KTSEVHNWTL EDTLQWLIEF  
 101 VELPQYEKNF RDNNVKGTTL PRIAVHEPSF MISQLKISDR SHRQKLQLKA  
 45 151 LDVVLFGLPT RPPHNWMKDF ILTVSIVIGV GGCWFAYTQN KTSKEHVAKM  
 201 MKDLESQTAE EQSLMDLQER LEKAQEEENRN VAVEKQNLER KMMDEINYAK  
 251 EEACRLRELK EGAECESLRR QYAEQELEQV RMALKKAEKE FELRSSWSVP  
 301 DALQKWLQLT HEVEVQYYNI KRQNAEMQLA IAKDEAEKIK KKRSTVFGTL  
 351 HVAHSSSLDE VDHKILEAKK ALSELTTCLE ERLFRWQQIE KICGFQIAHN  
 50 401 SGLPSLTSSL YSDHSWVVMV RVSIPPYPPIA GGVDDLDEDT PPIVSQFPQT  
 451 MAKPPGSLAR SSSLCRSRRS IVPSSPQPQR AQLAPHAPHP SHPRHPHPQ  
 501 HTPHSLPSPD PDILSVSSCP ALYRNEEEEE AIYFSAEKQW EVPTASECD  
 551 SLNSSIGRKQ SPPLSLEIYQ TSPRKISRQ EVSLEDSSRG DSPVTVDVSW  
 601 GSPDCVGLTE TKSMIFSPAS KVYNGILEKS CSMNQLSSGI PVPKPRHTSC  
 55 651 SSAGNDSKPV QEAPSVARIS SIPHDLCHNG EKSKKPSKIK SLFKKSK

No BLASTP hits available

No Alert BLASTP hits found

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10 Pedant information for DKFZphamy2_24b4, frame 3
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15  [LENGTH] 769
    [MW]      86673.49
    [pI]      6.69
    [HOMOL]   TREMBL:HS5242610_1 gene: "STIM1"; product: "GOK";
    Homo sapiens GOK (STIM1) mRNA, complete cds. 1e-154
20  [BLOCKS]  BL00886C Dihydroxy-acid and b-phosphogluconate
    dehydratases proteins
    [BLOCKS]  PR00021D
    [BLOCKS]  PR01053F
    [BLOCKS]  BL00726B AP endonucleases family 1 proteins
25  [PROSITE] RGD 1
    [KW]      SIGNAL_PEPTIDE 38
    [KW]      TRANSMEMBRANE 1
    [KW]      LOW_COMPLEXITY 15.86 %
    [KW]      COILED_COIL 8.45 %

```

	SEQ	RLHPASTPGPAWGULLRRRRWAALLVLGLLVPGAADGCELVPRHLRGRRATGSAATAASS
	SEG	. . . . . xxx . . . . . xxxxxxxxxxxxxx
	PRD	ccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhccccccccccccchhhhhhcccccccccccccc
35	COILS	
	MEM	. . . . . . . . . .
	SEQ	PAAAAGDSPALMTDPMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEESDEFIR
40	SEG	xxxxxxxxxxx. . . . .
	PRD	ccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhccccceeeecchhhhh
	COILS	
	MEM	. . . . . . . . . .
45	SEQ	EDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNWTLEDTLQWLIEFVELPQYEKN
	SEG	. . . . .
	PRD	hhccccccccccccccccccccceeeehhhhhhhhhhhcccchhhhhhhhhhhhhhhcccchhh
	COILS	
50	MEM	. . . . . . . . . .
	SEQ	FRDNNVKGTTLPRIAVHEPSFMISQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKD
	SEG	. . . . .
55	PRD	hhhhhccccccccceeeeeccccceeeeecccchhhhhhhhhhhheeeccccccccccccccchh
	COILS	
	MEM	. . . . . . . . . .

SEQ FILTVSIVIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQERLEKAQEENR  
SEG .....  
PRD hhheeeeeeeccccceeeccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcc  
5 COILS .....CC  
MEM MMMMMMMMMMMMMMMMM.....

10 SEQ NVAVEKQNLERKMMDEINYAKEEACRLRELREGAECELSRRQYAEQELEQVRMALKKA EK  
SEG .....  
PRD ceeeee hhh  
COILS .....CC.....  
MEM .....  
15 SEQ EFELRSSWSVPDALQKWLQLTHEVEVQYYNIKRQNAEMQLAIADAEKIKKKRSTVFGT  
SEG .....xxxxxxxxxxxxxxxx.....  
PRD hhhh hccccccchhhhhhhhhhhhhheeeecchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccce  
COILS .....  
20 MEM .....  
25 SEQ LHVHSSSLDEV D HKILEAKKALSELTTCLRERLFRWQIEKICGFQIAHNSGLPSLTSS  
SEG .....  
PRD eeeeeeccccchhh  
COILS .....  
MEM .....  
30 SEQ LYS D HSWVVM PRVSIPPYPIAGGVDDLDEDT PPIVSQFP GTMAKPPGSLARSSSLCRSRR  
SEG .....xxxxxxxxxxxxxxxx.....  
PRD ccc  
COILS .....  
35 MEM .....  
40 SEQ SIVPSSPQ P QRAQLAPHAPHP SHPRHPHPQHTPHSLPSPDPDILSVSSCPALYRNEEEE  
SEG x.....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.....xxxx  
PRD eeccceeeeeeccccchhhhhhh  
COILS .....  
MEM .....  
45 SEQ EAIYFSAEKQWEVPDTASECDSLNSSIGRKQSPPLSLEIYQTLSPRKISRDEVSLEDSSR  
SEG x.....  
PRD hhhhhhhhhhhccccccccccccccccccccccccceeeeeecccccccccccccccccccccc  
COILS .....  
MEM .....  
50 SEQ GDSPVTVDVSWGSPDCVGLTETKSMIFSPASKVYNGILEKSCSMNQLSSGIPVPKPRHTS  
SEG .....  
PRD cccccceeeccccccccccccceeeccccccccccccceeeeeecccccccccccccccccccccc  
COILS .....  
55 MEM .....  
SEQ CSSAGNDSKPVQ EAPSVARISSIPHDLCHNGEKS K KPSKIKSLFKKSK



SEG .....xxxxxxxxxxxxxxxxxxxx  
PRD ccc  
COILS .....  
MEM .....

5

## Prosites for DKFZphamy2\_24b4.3

10 PS00016      660->663    RGD      PD0C00016

(No Pfam data available for DKFZphamy2\_24b4.3)

DKFZphamy2\_24c8

-----

5 group: transmembrane protein

DKFZphamy2\_24c8 encodes a novel 454 amino acid protein without similarity to known proteins.

10 The novel protein contains 1 transmembrane region.  
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

15 The new protein can find application in studying the expression profile of amygdala-specific genes and as a new marker for amygdala cells.

20 putative protein

EST of GEN-426HD7 is 141 Bp longer at 5'-end  
perhaps complete cds.

Pedant: TRANSMEMBRANE 1

25

Sequenced by GBF

Locus: /map="609.7 cR from top of Chr3 linkage group"

30 Insert length: 3200 bp

Poly A stretch at pos. 3177, polyadenylation signal at pos. 3156

```

      1 CCTGTCCACA GGGCCCGCTC CAGCAGCCAT GGCAACCACA TCCTCCAAGC
35    51 CAGAGGGCCG CCCTCGAGGG CAGGCTGCCC CCACCATCCT GCTGACAAAG
      101 CCACCGGGGG CCACCAGCCG CCCCACCACA GCGCCCCCCC GCACTACCAC
      151 ACGCAGGCCC CCCAGGCCCC CAGGCTCTTC CCGAAAAGGG GCTGGTAATT
      201 CATCAGCCCC TGTCCCGCCT GCACCTGGTG GCCACTCCAG GAGTAAAGAA
      251 GGACAGCGAG GACGAAATCC AAGCTCCACA CCTCTGGGGC AGAAGCGGCC
40    301 CCTGGGGAAA ATCTTTCAGA TCTACAAGGG CAACTTCACA GGGTCTGTGG
      351 AACC GGAGCC CTCTACCCTC ACCCCAGGA CCCCCTCTG GGGCTACTCC
      401 TCTTCAACCAC AGCCCCAGAC AGTGGCTGCG ACCACAGTGC CCAGCAATAC
      451 CTCATGGGCA CCCACCACCA CCTCCCTGGG GCCTGCAAAG GACAAGCCAG
      501 GCCTTCGCAG AGCAGCCAG GGGGGTGGTT CTACCTTCAC CAGCCAAGGA
45    551 GGGACACCAG ATGCCACAGC AGCCTCAGGT GCCCCGTGTA GTCCACAAGC
      601 TGCCCCAGTG CTTTCTCAGC GCCCCACCA CGGTGACCCA CAGGATGGCC
      651 CCAGCCATAG TGA CTCTTGG CTTACTGTTA CCCCTGGCAC CAGCAGACCT
      701 CTGTCTACCA GCTCTGGGGT CTTACGGCT GCCACGGGGC CCACCCAGC
      751 TGCCTTCGAT ACCAGTGTCT CAGCCCCTTC CCAGGGGATT CCTCAGGGAG
50    801 CATCCACAAC CCCACAAGCT CCAACCCATC CCTCCAGGGT CTCAGAAAGC
      851 ACTATTTCTG GAGCCAAGGA GGAGACTGTG GCCACCCTCA CCATGACCGA
      901 CCGGGTGCCC AGTCCTCTCT CCACAGTGGT ATCCACAGCC ACAGGCAATT
      951 TCCTCAACCG CCTGGTCCCC GCCGGGACCT GGAAGCCTGG GACAGCAGGG
55   1001 AACATCTCCC ATGTGGCCGA GGGGGACAAA CCGCAGCACA GAGCCACCAT
      1051 CTGCCTGAGC AAGATGGATA TCGCCTGGGT GATCCTGGCC ATCAGCGTGC
      1101 CCATCTCTCT CTGCTCTGTC CTGCTGACGG TGTGCTGCAT GAAGAGGAAG
      1151 AAGAAGACCG CCAACCCGGA GAACAACCTG AGCTACTGGA ACAACACCAT
      1201 CACCATGGAC TACTTCAACA GGCATGCTGT GGAGCTGCCC AGGGAGATCC
```

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1251 AGTCCCTTGA AACCTCTGAG GACCAGCTCT CAGAGCCCCG CTCCCCAGCC
1301 AATGGCGACT ATAGAGACAC TGGGATGGTC CTTGTTAACC CCTTCTGTCA
1351 AGAAACACTG TTTGTGGGAA ACGATCAAGT ATCTGAGATC TAACTACAGC
1401 AGGCATCACT TTGCCATTCC GTATTTTTCG TCTCTAAATT ATAAATATAC
5 1451 AAATATATAT ATTATAAATA TAACCTTTGT GTAACCCTGA CTTAATGAGA
1501 AACATTTTCA GCTTTTTTTC CTATGAATTG TCAACATCTT TTTTACAAGT
1551 GTGGTTTAAA AAAAAAAAAA CTTTACAGAA TGATCTGTGG CTTTATAAAA
1601 TAAAGGTATT TCTAAGCAAA GCAGTTGCAT TGATTGCTTC TCTTAATAAC
1651 TATTCTTGAG CACCTGGGGA TCCCAGGAAC CCTGGTCAGG TGAGGTAAGA
10 1701 GACTGACCTC CTGTAGAAGC TGAATGTTAC AGTGGTCAAG CGCACGATTC
1751 TTTGAGTGAT TCTTAAAGCT CTGGTTCCTC TTGATTTGGT GTGACCCCAT
1801 TTCCTCCCTT CTCATACGCA CACCTGTAAA GGGAACTGGA CCGCCTCAGG
1851 GGAAGACGGC AGACTCATGC ACAGAGAAGG AAAAGGGAAC ATCTCATCAC
1901 CTCTGAGGAT GAGTACCCTG GAGCCTTATG ACGGCACCAT TGGATGTCTAT
15 1951 GTTTAATTCC ATCCAAGTTG TGGATGGCAG GCAGGAGCAT GGAGCCCTCA
2001 GGAATCCATG GAGGACATCA AGGCATCCCA AGGCCATATT CCCCTAACAT
2051 TACTTCCACT GCTAACAACA GGACTGCCTT TCCCTGGTGG GAAAATGCTC
2101 CCTTTATGCC CATTCTGTGA TCCCCTCCAA CACCCACATC TGCATTAAAC
2151 ACCCGTGCCT TTCTCTTGGG GAGGGTTTAG ATGCAGATCC CGGCCCTGGA
20 2201 GCTTTAAAAT GCTTGCCCTT CTTTCTTCAA GGATCAAATG TTTATTGGGG
2251 TTCAGCTTTG TTTTCTCAAA AGGCCATGGT ATCGTGCCCC TGAGGAACAT
2301 GTTTATCTAA GAAGCTTTGA GGTAGTAGAG CGATAATTTT TGAAACCTTC
2351 CTCCTGCAAT CTTTAAAAAA GAAAAAAAAG ATTGCCCAA CAAATCATTT
2401 GGGAGAAGAC ATCATTATAC TCCTACTTGG CACTGCAAAC CTGCTCGCAG
25 2451 CACCAGCCGG TGGACTTGCC ATCCAGCTCT CAGCTTCCAC TGCTCCCTT
2501 GTTCCCGGCC GGCTGGCTGC CTCCCCGTGC TGTGTCCAGC ACGGCCAACA
2551 ACGTCAGACC CTCAGAGACG CCCAAGGGGC TTCCAGAGGT GGCCGCTTCT
2601 CTATTTTTTC CTGATTGTGG CTGAGAGAGA TGATTACTGC TTTGACACTT
2651 CCTTTCTCTA AAAGAAAAAT AGTTTGATAG TATATTTTGA ATATAGATGC
30 2701 TCTTATAGTC AGATTGGGAA TTGAACCTGA ATATTGGGTC ATATGTTTGT
2751 GTTGTTGCTG TAGTCTATCA TGACTTTTTT CTTTCTGCAT TTTCTTAAA
2801 AAAAAAAAAA AGATGGCCTT CAAAAGTGTG TTCTCAATGT TGTATGAACC
2851 TCCTTCACAT GAGTTCGGTT GTTGTCTCTC TTCAAAGACT CTTCAACCCA
2901 CAAAGAAGCA ACTAAATGTT TCTCTAAGTT TAATTTTCTA GCGTGTTGTT
35 2951 GTCTTACCTT TTTAACCTTA CCATAATATT TCTGTAACT GTTACATTTA
3001 ATATACCAAT GTGTGTAAGT ATACAGAGAA AAATCTGTTT GTAAAGTAAA
3051 ATTTATATAT AATATATGTA ATCAAAGATA CATATGTTAT ATATACATAT
3101 GTGGATGTAT GACTTATTTT TCCTTATCCA CAGATTTTCA CTACCATGTA
3151 TATATAAATA AACTTATTTT ATTAGCCAGA GAAAAAAAAA AAAAAAAAAA
40

```

## BLAST Results

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45 No BLAST result

## Medline entries

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50

No Medline entry

55

## Peptide information for frame 2

-----

ORF from 29 bp to 1390 bp; peptide length: 454

Category: putative protein

Classification: Transmembrane proteins unclassified

```

      1 MATTSSKPEG RPRGQAAPTI LLTKPPGATS RPTTAPPRTT TRRPPRPPGS
5      51 SRKGAGNSSR PVPPAPGGHS RSKEGQGRGN PSSTPLGQKR PLGKIFQIYK
      101 GNFTGSVEPE PSTLTPRTPL WGYSSSPQPPQ TVAATTVPSN TSWAPTTTSL
      151 GPAKDKPGLR RAAQGGGSTF TSQGGTPDAT AASGAPVSPQ AAPVPSQRP
      201 HGDPODGP SH SDSWLTVTPG TSRPLSTSSG VFTAATGPTP AAFDTSVSAP
      251 SQGIPQGGAST TPQAPTHPSR VSESTISGAK EETVATLTMT DRVPSPLSTV
10     301 VSTATGNFLN RLVPA GTWKP GTAGNISHVA EGDKPQHRAT ICLSKMDIAW
      351 VILAISVPIS SCSVLLTVCC MKRKKKTANP ENNLSYWNNT ITMDYFNRHA
      401 VELPREIQSL ETSEDQLSEP RSPANGDYRD TGMVLVNPFC QETLFVGNDA
      451 VSEI

```

15

## BLASTP hits

No BLASTP hits available

20

Alert BLASTP hits for DKFZphamy2\_24c8, frame 2

No Alert BLASTP hits found

25

Pedant information for DKFZphamy2\_24c8, frame 2

## Report for DKFZphamy2\_24c8.2

30

```

[LENGTH] 463
[MW]      48277.84
[pI]      9.80
[FUNCAT]  98 classification not yet clear-cut    [S. cerevisiae,
35 YJR151c] 2e-04
[BLOCKS]  PRO0912F
[BLOCKS]  BP03696F
[KW]      TRANSMEMBRANE 1
[KW]      LOW_COMPLEXITY 15.55 %
40

```

```

SEQ  LSTGPAPAA MATTSSKPEGRPRGQAAPTILLTKPPGATSRPTTAPPRTTTRRPPRPPGSS
SEG  .....
PRD  cccccchhhhhhhcccccccccccccccccccccccccccccccccccccccccccccc
45 MEM  .....

```

```

SEQ  RKGAGNSSR PVPPAPGGHSRSKEGQGRNPSSSTPLGQKRPLGKIFQIYKGNFTGSVEPEP
SEG  x.....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
50 MEM  .....

```

```

SEQ  STLTPRTPLWGYSSSPQPPQTVAATTVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGGSTFT
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
55 MEM  .....

```

```

SEQ  SQGGTPDATAAASGAPVSPQAAAPVPSQRP HHGDPQDGP SHSDSWLTVTPGTSRPLSTSSGV
SEG  xxxxx.....

```

[illegible][illegible]

25 (No Prosite data available for DKFZphamy2\_24c8.2)

(No Pfam data available for DKFZphamy2\_24c8.2)

DKFZphamy2\_24k15

-----

5 group: amygdala derived

DKFZphamy2\_24k15 encodes a novel 279 amino acid protein with weak similarity to pecanex of *Drosophila melanogaster*.

10 Pecanex is a maternal-effect neurogenic gene, involved in differentiation processes in the developing central nervous system. DKFZphamy2\_24k15.p3 seems to be expressed ubiquitiously.

15 The new protein can find application in studying the expression profile of amygdala-specific genes and as a new marker for amygdala cells.

similarity to pecanex (*Drosophila melanogaster*)

20 probably complete cds.

Sequenced by GBF

25 Locus: unknown

Insert length: 1464 bp

Poly A stretch at pos. 1445, polyadenylation signal at pos. 1421

30

```

      1 AAGGAAAACA AGAGGACATG CCATATATTC CTCTCATGGA GTTCAGTTGT
    51 TCACATTCTC ACTTAGTATG CTTACCCGCA GAGTGGAGGA CTAGCTGTAT
   101 GCCCAGTTCC AAAATGAAGG AGATGAGCTC GTTATTTCCA GAAGACTGGT
   151 ACCAATTTGT TCTAAGGCAG TTGGAATGTT ATCATTCAGA AGAGAAGGCC
   35 201 TCAAATGTAC TGGAAGAAAT TGCCAAGGAC AAAGTTTTAA AAGACTTTTA
      251 TGTTTCATACA GTAATGACTT GTTATTTTAG TTTATTTGGA ATAGACAATA
   301 TGGCTCCTAG TCCTGGTCAT ATATTGAGAG TTTACGGTGG TGTTTTGCCT
   351 TGGTCTGTTG CTTTGGACTG GCTCACAGAA AAGCCAGAAC TGTTTCAACT
   401 AGCACTGAAA GCATTCAAGT ATACTCTGAA ACTAATGATT GATAAAGCAA
   40 451 GTTTAGGTCC AATAGAAGAC TTTAGAGAAC TGATTAAGTA CCTTGAAGAA
      501 TATGAACGTG ACTGGTACAT TGGTTTGGTA TCTGATGAAA AGTGGGAAGGA
      551 AGCAATTTTA CAAGAAAAGC CATACTTGTT TTCTCTGGGG TATGATTCTA
   601 ATATGGGAAT TTACACTGGG AGAGTGCTTA GCCTTCAAGA ATTATTGATC
   651 CAAGTGGGAA AGTTAAATCC TGAAGCTGTT AGAGGTCAGT GGGCCAATCT
   45 701 TTCATGGGAA TTACTTTATG CCACAAACGA TGATGAAGAA CGTTATAGTA
      751 TACAAGCTCA TCCACTACTT TTAAGAAATC TTACGGTACA AGCAGCAGAA
   801 CCTCCCCTGG GATATCCGAT TTATTCTTCA AAACCTCTCC ACATACATTT
   851 GTATTAGAGC TCATTTTGAC TGTAATGTCA TCAAATGCAA TGTTTTTATT
   901 TTTTCATCCT AAAAAAGTAA CTGTGATTCT TGTAACCTGA GGA CTCTCC
   50 951 ACACCCCAT TCAGATGCCT GAGAACAGCT AAGCTCCGTA AAGTTGGTTC
   1001 TCTTAGCCAT CTTAATGGTT CTA AAAAACA GCAAAAACAT CTTTATGTCT
   1051 AAGATAAAAG AACTATTTGG CCAATATTTG TGCCCTCTGG ACTTTAGTAG
   1101 GCTTTGGTAA ATGTGAGAAA ACTTTTGTAG AATTATCATA TAATGAATTT
   1151 TGTAATGCTT TCTTAAATGT GTTATAGGTG AATTGCCATA CAAAGTTAAC
   55 1201 AGCTATGTAA TTTTACATA CTTAAGAGAT AAACATATCA GTGTTCTAAG
      1251 TAGTGATAAT GGATCCTGTT GAAGGTTAAC ATAATGTGTA TATATTTGTT
      1301 TGAAATATAA TTTATAGTAT TTTCAAATGT GCTGATTTAT TTTGACATCT
      1351 AATATCTGAA TGTTTTTGTA TCAAGTAGTT TGTTTTATA GACTTCAATT

```

1401 CATAAACTTT AAAAAAAGTTT TAATAAAATA TTTTCCTTCC TTTTCAAAAA  
 1451 AAAAAAAAAA AAAA

5

## BLAST Results

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Entry AC007939 from database EMBLNEW:

10 Homo sapiens clone 422\_H\_5, WORKING DRAFT SEQUENCE, 5 unordered  
 pieces.

Score = 4116, P = 0.0e+00, identities = 840/858  
 3 exons

15

## Medline entries

-----

No Medline entry

20

## Peptide information for frame 3

-----

25

ORF from 18 bp to 854 bp; peptide length: 279  
 Category: similarity to known protein  
 Classification: unclassified

30

1 MPYIPLMEFS CSHSHLVCLP AEWRTSCMPS SKMKEMSSLF PEDWYQFVLR  
 51 QLECYHSEEK ASNVLEEIAK DKVLKDFYVH TVMTCYFSLF GIDNMAPSPG  
 101 HILRVYGGVL PWSVALDWLT EKPELFQAL KAFRYTLKLM IDKASLGPIE  
 151 DFRELIKYLE EYERDWWYIGL VSDEKWKEL LQEKPYLFSL GYDSNMGIYT  
 201 GRVLSLQELL IQVGKLNPEA VRGQWANLSW ELLYATNDDE ERYSIQAHPL  
 35 251 LLRNLTVAQA EPPLGYPIYS SKPLHIHLY

## BLASTP hits

40

No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_24k15, frame 3

45

No Alert BLASTP hits found

Pedant information for DKFZphamy2\_24k15, frame 3

-----

50

## Report for DKFZphamy2\_24k15.3

[[LENGTH]] 284

[[MW]] 33066.31

55

[[pI]] 5.17

[[HOMOL]] TREMBL:AF067608\_11 gene: "B0511.12";

Caenorhabditis elegans cosmid B0511. 2e-13

[[KW]] Alpha\_Beta

5 SEQ GKQEDMPYIPLMEFSCSHSLVCLPAEWRTSCMPSSKMKEMSSLFPEDWYQFVLRQLECY  
PRD cccccccccceeeceeeceeececcccccccccccccccccccccccchhhhhhhhhhhhh

10 SEQ HSEKASNVLEEIAKDKVLKDFYVHTVMTCYFSLFGIDNMAPSPGHILRVYGGVLPWSVA  
PRD hhhhhhhhhhhhhhhhhhhhhhhhhheeeeeeeeeeeccccccccceeececccccccc

SEQ LDWLTEKPELFQALAKAFRYTLKLMIDKASLGPIEDFRELIKYLEEYERDWYIGLVSEK  
PRD cchhhhhchhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhheeececccc

15 SEQ WKEAILQEKPYLFSLGYDSNMGIYTGRVLSLQELLIQVGKLNPEAVRGQWANLSWELLYA  
PRD hhhhhhhhcchhhhhhhccccchhhhhhhhhhhhhheeecehhhhhhhhhhhhheeee

20 SEQ TNDDEERYSIQAHPLLLRNLTVQAAEPPLGYPIYSSKPLHIHLY  
PRD cccccccccchhhhhhhhhhhcccccccccccccccccccccccc

(No Prosite data available for DKFZphamy2\_24k15.3)

(No Pfam data available for DKFZphamy2\_24k15.3)



DKFZphamy2\_2a13

-----

5 group: amygdala derived

DKFZphamy2\_2a13 encodes a novel 440 amino acid protein without similarity to known proteins.

10 No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of amygdala-specific genes.

15

putative protein

perhaps complete cds.

20

Sequenced by MediGenomix

Locus: /map="16p13.3"

25

Insert length: 2584 bp

Poly A stretch at pos. 2562, polyadenylation signal at pos. 2545

```

30      1 GTTCCTGAGG ACGTGCTACG GGGGCAGCTT CCTGGTACAC GAGTCGTTCC
      51 TCTACAAGCG GGAGAAGGCT GTCGGGGACA AGGTGTATTG GACCTGCCGG
     101 GACCACGCGC TGCACGGCTG CCGGAGCCGG GCCATCACCC AGGGACAGCG
     151 GGTGACTGTG ATGCGTGGGC ACTGCCACCA GCCCGATATG GAGGGCCTGG
     201 AAGCCCGGCG GCAGCAGGAG AAGGCCGTGG AGACGCTGCA GGCTGGGCAG
     251 GACGGCCCTG GGAGCCAAGT GGACACGCTG CTCCGAGGCG TGGATAGTTT
35     301 GCTCTACCGC AGGGGTCCGG GTCCCCTGAC TCTCACCAGG CCTCGGCCCA
     351 GAAAGCGAGC AAAGGTGAA GACCAGGAGC TGCCAACCCA GCCCGAGGCC
     401 CCAGACGAGC ACCAGGACAT GGACGCAGAC CCGGGAGGCC CTGAGTTCTT
     451 GAAGACGCCC CTGGGGGGCA GCTTCCTGGT GTACGAGTCC TTCCTCTACC
     501 GGCGGGAGAA GGCGGCTGGG GAGAAGGTGT ATTGGACCTG CCGGGACCAG
40     551 GCCCGCATGG GCTGCCGACG CCGGCCATC ACCCAGGGCC GACGGGTGAC
     601 TGTCAATGCGT GGTCACTGCC ACCCGCCCGA CCTGGGAGGC CTGGAGGCCC
     651 TGAGGCAGCG GGAGAAACGC CCAACACGG CGCAGCGGGG GAGCCCAGGC
     701 GCTGGCCTCT CTTTCCAGTG GCTCTTCCGG ATCCTGCAGC TTTTGGGTCA
     751 TGCTCCTGTG CTGCTGTGCC CCTCAGGGTC CTCCTGCCTC CCGAGCCTCC
45     801 CTGCTCCACA TGGCCCTTGC CCAGCCCTCT CCATCCCTCT TGAAGGAGGC
     851 CCCGAGTTCC TGAAGACGCC CCTGGGGGGC AGCTTCCTGG TGTACGAGTC
     901 CTTCTCTTAC CGGCGGGAGA AGGCGGCCGG GGAGAAGGTG TATTGGACCT
     951 GCCGGGACCA GGCCCGCATG GGCTGCCGCA GCCGCGCCAT CACCCAGGGC
50    1001 CGGCGGGTCA TGGTCATGCG CAGGCACTGC CACCCACCGG ACCTGGGCGG
     1051 CCTGGAGGCC CTGCGGCAGC GGGAGCACTT CCCCACCTG GCGCAGTGGG
     1101 ACAGCCCAGA TCCTCTCCGG CCCCTGGAGT TCCTGAGGAC TTCCCTGGGG
     1151 GGCAGGTTC TGGTGCACGA GTCCTTCCTC TACAGGAAGG AGAAGGCGGC
     1201 TGGGGAGAAG GTGTACTGGA TGTGCCGGA CCAGGCTCGG CTGGGCTGCC
     1251 GCAGCCGCGC CATAACCCAG GGCCACCGCA TCATGGTCAT GCGCAGCCAC
55    1301 TGCCATCAGC CTGACCTGGC AGGCCTGGAG GCCTTGAGGC AACGGGAGCG
     1351 GCTCCCCACC ACGGCCCAGC AGGAGGACCC AGAAAAGATT CAAGTTCAGC
     1401 TGTGCTTCAA GACGTGTTCT CCTGAAAGCC AGCAGATTTA TGGGGACATC
     1451 AAAGACGTCA GACTGGATGG CGAGTCCAG TGAGGCGATG TGGGCAGAGG

```

```

1501 AGCTCCGAGC CGCCACCCCA AGGTGGCTTC ACATCCACAC AGGCACTTCC
1551 CATCCACCTA GGTTTGGCTT AGCAGAAACT TCTTTTCATT CTCCAAAGC
1601 ATCGATGGTC TTCGCGTCTC CTCAGGAGGT CTCCCAGGAG GAATTCTTGG
1651 ATGGTGTCTT CATGTCGGCG GAGAACAGTG CTCAGAGCTG GCGCTTGCAG
5 1701 ACGCAGCTGT CGTGGGGCAG GCGGGTGGCG CCTTCCTGAC CTTTGGGAAGA
1751 CATGACAAAG CTGCCTGGAC ACGGACGCCC CTGCTGTACG GCCACAGCAC
1801 CCCTGGGTTT GCAGAGCACG CAGCCTTCCT AGGGCTTTCC ACCTGGCGAG
1851 GCCCCGCTCT GCTCAGCACG GTGCAAAGTG AATGCTGCTG TCTTGGAGCC
1901 TGGGCACGTT TGGGGAAGTT CCTGCTTCAA ACTGAGCTGC CCCGCATAGG
10 1951 CCAGGTCAAC CCACACCAAT CTTTTCTGGA CAGGTGCTGG GTAGGCCTTC
2001 CTGGTCTCTG GCCGCCTGCT GCCAGGGTGT GGCCATCCCC AGCAACCGGA
2051 GCCGGCCAAA CCAGAGGCCT CGCTCCGCAC TCCACACTTT CCTTTCTGTG
2101 CTCCTTCCAA GTTAAATTAA ACCCCCTCTC CACGATTCCC ACGGCAGGCG
2151 TCATTCCCGA GATGGGAGCC AGTCCAGGGG TCAGCAGGAG CCAGCGCTGG
15 2201 GCACACGTGC CCTGGCTGAG GCCAGCGGCA TCCTGGGTGG CCCAGGTCCA
2251 TCCTGGGCAG CAAAGGCGTG TCCCCTTCTG TCAGACAGCT TCACAGAGTG
2301 TGGCTTCACC AGTCAGAGGG AGCAGTCCGG AGAGGCAAGA TGACCCACC
2351 GGGACTGCAG AGCCTCCTCC TTAATAACAA GGACCTGTCC GCAGCCGCGA
2401 GGTCTTCAC TCCACCCCTG TAATTGTGGG GGGAGTGCCA GCAACAGGCC
20 2451 TGTCCCCTGG CAAGTTGGCC ACGGAACCCA CCATGCACTG CAAGGCTGTG
2501 ACAGCCTGGG CACCCCTGCT TCTCCTCTGC TTGTACGGTT CCCCCAATAA
2551 ATCCTATTTT CCATCAAAAA AAAAAAAAAA AAAA

```

25

## BLAST Results

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No BLAST result

30

## Medline entries

-----

No Medline entry

35

## Peptide information for frame 2

-----

40

ORF from 161 bp to 1480 bp; peptide length: 440  
 Category: putative protein  
 Classification: no clue

45

```

1 MRGHCHQPD M EGLEARRQDE KAVETLQAGQ DGPQSQVDTL LRGVDSLLYR
51 RGPGLTLTR PRPRKRAKVE DQELPTQPEA PDEHQDMDAD PGGPEFLKTP
101 LGGSFLVYES FLYRREKAAG EKVYWTCTRDQ ARMGCRSRAI TQRRVTVMR
151 GHCHPPDLGG LEALRQREKR PNTAQRGSPG AGLSFQWLFR ILQLLGHPV
201 LLCPSGSSCL PSLPAPHGPC PALSIPLGG PEFLKTPLGG SFLVYESFLY
50 251 RREKAAGEKV YWTCRDQARM GCRSRAITQG RRVMMRRHC HPPDLGGLEA
301 LRQREHFPNL AQWDSPLR PLEFLRTSLG GRFLVHESFL YRKEKAAGEK
351 VYWMCRDQAR LGCRSRAITQ GHRIMVMRSH CHQPDLAGLE ALRQRRERLPT
401 TAQQEDPEKI QVQLCFKTC S PESQDIYGDI KDVRLDGESQ

```

55

## BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_2a13, frame 2

5 No Alert BLASTP hits found

Pedant information for DKFZphamy2\_2a13, frame 2

-----

10 Report for DKFZphamy2\_2a13.2

```

15  [LENGTH]  493
    [MW]      55840.13
    [pI]      9.33
    [KW]      Alpha_Beta
    [KW]      LOW_COMPLEXITY      6.29 %

20  SEQ  FLRTCYGGSFVLVHESFLYKREKAVGDKVYWTCRDHALHGCRSRAITQGQRTVVMRGHCHQ
    SEG  .....
    PRD  cccccccccceeeccchhhhhhhhhccceeecccccccccccccccccccccccccccccc

25  SEQ  PDMEGLEARRQQEKAVETLQAGQDGPQSQVDTLLRGVDSELLYRRGPGPLTLTRPRPRKRA
    SEG  .....xxxxxxxxxxxxxxxxxxxxx...
    PRD  cccchhhhhhhhhhhhhhhhhhhccceeeccccccccccccccccccccccccccccchh

    SEQ  KVEDQELPTQPEAPDEHQDMDADPGGPEFLKTPLGGSFVLVYESFLYRREKAAGEKVYWTC
    SEG  .....
    PRD  hhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccc

30  SEQ  RDQARMGCRSRAITQGRRTVVMRGHCHPPDLGGLEALRQREKRPNTAQRGSPGAGLSFQW
    SEG  .....
    PRD  cchhhhhccceeeccccccccccccccccccccccccccccccccccccccccchhhhh.

35  SEQ  LFRILQLLGHAPVLLCPSGSSCLPSLPAPHGPCPALSIPLEGGPEFLKTPLGGSFVLVYES
    SEG  .....xxxxxxxxxxxxxxxxxxxxx...
    PRD  hhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccc

40  SEQ  FLYRREKAAGEKVYWTCRDQARMGCRSRAITQGRRTVVMRRHCHPPDLGGLEALRQREHF
    SEG  .....
    PRD  hhhhccccccccccccccccccccccccccccccccccccccccccccccccccccchh

45  SEQ  PNLAQWDSPDPLRPLEFLRTSLGGRFLVHESFLYRKEKAAGEKVYWMCRDQARLGCRSRA
    SEG  .....
    PRD  cccccccccccccchhhhhhhccceeeecchhhhhhhccceeeecchhhhhhhccccc

    SEQ  ITQGHRIMVMRSHCHQPDLAGLEALRQRELRPTTAQQEDPEKIQVQLCFKTCSPESQQIY
    SEG  .....
    PRD  cccccccccccccccccccccchhhhhhhhhhhhhhhcccccccccccccccccccccc

50  SEQ  GDIKDVRLDGESQ
    SEG  .....
    PRD  ccccccccccccc

55

```

(No Prosite data available for DKFZphamy2\_2a13.2)

WO 01/98454

PCT/IB01/02050

(No Pfam data available for DKFZphamy2\_2a13.2)

DKFZphamy2\_2b19

-----

5 group: differentiation/development

DKFZphamy2\_2b19 encodes a novel 789 amino acid protein which originates from TXBP151 mRNA by alternative splicing.

10 It is ubiquitously expressed. The mRNA is also subject to alternative polyadenylation. Overexpression of TXBP151 in NIH3T3 cells causes inhibition of apoptosis induced by tumour necrosis factor (TNF). It binds to  
15 A20, which is also an inhibitor of cell death by a yet unknown mechanism.

The new protein can find application in modifying/blocking apoptotic pathways and therefore serve as a tool in diagnosis of  
20 cancer predisposition and as a tool in cell culture.

TXBP151, differentially spliced

25 differential splicing  
differential polyadenylation

Sequenced by MediGenomix

30 Locus: /map="7p15"

Insert length: 3028 bp

Poly A stretch at pos. 2885, polyadenylation signal at pos. 2868

35  
1 GAAGAGGTTT GCGGGCTGAT GCGGGATCAG GATCGGAAGC CTGCGTAACT  
51 TTCTCCCTTG ATCCGGGAGT CTTTCCACTG GATTCACAAT GACATCCTTT  
101 CAAGAAGTCC CATTGCAGAC TTCCAACCTT GCCCATGTCA TCTTTCAAAA  
151 TGTGGCCAAG AGTTACCTTC CTAATGCACA CCTGGAATGT CATTACACCT  
40 201 TAACTCCATA TATTCATCCA CATCCAAAAG ATTGGGTTGG TATATTCAAG  
251 GTTGGATGGA GTACTGCTCG TGATTATTAC ACGTTTTTAT GGTCCCCTAT  
301 GCCTGAACAT TATGTGGAAG GATCAACAGT CAATTGTGTA CTAGCATTCC  
351 AAGGATATTA CCTTCCAAAT GATGATGGAG AATTTTATCA GTTCTGTTAC  
401 GTTACCCATA AGGGTGAAAT TCGTGGAGCA AGTACACCTT TCCAGTTTCG  
45 451 AGCTTCTTCT CCAGTTGAAG AGCTGCTTAC TATGGAAGAT GAAGGAAATT  
501 CTGACATGTT AGTGGTGACC ACAAAGCAG GCCTTCTTGA GTTGAAATT  
551 GAGAAAACCA TGAAAGAAAA AGAAGAACTG TTAAAGTTAA TTGCCGTTCT  
601 GGAAAAAGAA ACAGCACAAAC TTCGAGAACA AGTTGGGAGA ATGGAAAGAG  
651 AACTTAAACCA TGAGAAAGAA AGATGTGACC AACTGCAAGC AGAACAAAAG  
50 701 GGTCTTACTG AAGTAACACA AAGCTTAAAA ATGGAAAATG AAGAGTTTAA  
751 GAAGAGGTTT AGTGATGCTA CATCCAAAGC CCATCAGCTT GAGGAAGATA  
801 TTGTGTCAGT AACACATAAA GCAATTGAAA AAGAAACCGA ATTAGACAGT  
851 TTAAAGGACA AACTCAAGAA GGCACAACAT GAAAGAGAAC AACTTGAATG  
901 TCAGTTGAAG ACAGAGAAGG ATGAAAAGGA ACTTTATAAG GTACATTTGA  
55 951 AGAATACAGA AATAGAAAAT ACCAAGCTTA TGTGAGAGGT CCAGACTTTA  
1001 AAAAATTTAG ATGGGAACAA AGAAAGCGTG ATTACTCATT TCAAAGAAGA  
1051 GATTGGCAGG CTGCAGTTAT GTTTGGCTGA AAAGGAAAAT CTGCAAAGAA  
1101 CTTTCCTGCT TACAACCTCA AGTAAAGAAG ATACTTGTTT TTTAAAGGAG

```

1151 CAACTTCGTA AAGCAGAGGA ACAGGTTTCAG GCAACTCGGC AAGAAGTTGT
1201 CTTTCTGGCT AAAGAACTCA GTGATGCTGT CAACGTACGA GACAGAACGA
1251 TGGCAGACCT GCATACTGCA CGCTTGGAAG ACGAGAAAGT GAAAAAGCAG
1301 TTAGCTGATG CAGTGGCAGA ACTTAAACTA AATGCTATGA AAAAAGATCA
5 1351 GGACAAGACT GATACACTGG AACACGAACT AAGAAGAGAA GTTGAAGATC
1401 TGAAACTCCG TCTTCAGATG GCTGCAGACC ATTATAAAGA AAAATTTAAG
1451 GAATGCCAAA GGCTCCAAAA ACAATAAAC AAACTTTCAG ATCAATCAGC
1501 TAATAATAAT AATGTCTTCA CAAAGAAAAAC GGGGAATCAG CAGAAAGTGA
1551 ATGATGCTTC AGTAAACACA GACCCAGCCA CTTCTGCCTC TACTGTAGAT
10 1601 GTAAAGCCAT CACCTTCTGC AGCAGAGGCA GATTTTGACA TAGTAACAAA
1651 GGGGCAAGTC TGTGAAATGA CCAAAGAAAT TGCTGACAAA ACAGAAAAAGT
1701 ATAATAAATG TAAACAACCTC TTGCAGGATG AGAAAGCAAA ATGCAATAAA
1751 TATGCTGATG AACTTGCAAA AATGGAGCTG AAATGGAAAG AACAAAGTGA
1801 AATTGCTGAA AATGTAAAAAC TTGAAGTAGC TGAAGTACAG GACAATTATA
15 1851 AAGAACTTAA AAGGAGTCTA GAAAATCCAG CAGAAAGGAA AATGGAAGGT
1901 CAGAATTCCC AGAGTCCTCA ATGTTTCAAA ACATGCTCAG AGCAAAATGG
1951 TTATGTTCTC ACATTGTCAA ATGCACAACC AGTTCTGCAA TATGGTAATC
2001 CTTATGCATC TCAGGAAACA AGAGATGGAG CAGATGGTGC TTTTACCCA
2051 GATGAAATAC AAAGGCCACC TGTGAGAGTC CCTCTTGGG GACTGGAAGA
20 2101 CAATGTTGTC TGCAGCCAGC CTGCTCGAAA CTTTAGTCGG CCTGATGGCT
2151 TAGAGGACTC TGAGGATAGC AAAGAAGATG AGAATGTGCC TACTGCTCCT
2201 GATCCTCCAA GTCAACATTT ACGTGGGCAT GGGACAGGCT TTTGCTTTGA
2251 TTCCAGCTTT GATGTTTACA AGAAGTGTCC CCTCTGTGAG TTAATGTTTC
2301 CTCCTAACTA TGATCAGAGC AAATTTGAAG AACATGTTGA AAGTCACTGG
25 2351 AAGGTGTGCC CGATGTGCAG CGAGCAGTTC CCTCCTGACT ATGACCAGCA
2401 GGTGTTTGAA AGGCATGTGC AGACCCATTT TGATCAGAAT GTTCTAAATT
2451 TTGACTAGTT ACTTTTTATT ATGAGTTAAT ATAGTTTAGC AGTAAAAAAA
2501 AAAAAAAAAA ACCACACCTA AAATAGACCA CTGAGGAGAC CATAGAGCGG
2551 ATGCTTTCAT GCACCTTTTA CTGCACTTTC TGACCAGGAG CTACTTTGAG
30 2601 TTTGGTGTTA CTAGGATCAG GGTCAGTCTT TGGCTTATCA ATAAATTTTA
2651 ATCTCTGTTA ATCTTACCTG CTTTAAAAAA AAGTTCTTGT GTGTTTCGTAT
2701 CTTTATTTAT TCCCTAGTTT GCAGAACTGT CTGAATAAAG GATACAAGGA
2751 TTATTTCAAT GTTACTGCAC TGAAAAACGT GTATGTATTA GTGTGCTAGA
2801 TTATTTAGCA GAATATTCAC AAGTTTCTGT TGACCTTGTT GATTGAGCAT
35 2851 GACTACTAAA TATTATGTAA TAAAAAGCAT TTGTCATAAC AAAAAAAAAA
2901 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2951 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3001 AAAAAAAAAA AAAAAAAAAA AAAAAAAA

```

40

## BLAST Results

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No BLAST result

45

## Medline entries

-----

50

99361984:

De Valck D, Jin DY, Heyninck K, Van de Craen M, Contreras R, Fiers W,

Jeang KT, Beyaert R.; The zinc finger protein A20 interacts with a

55

novel

anti-apoptotic protein which is cleaved by specific caspases. Oncogene

1999 Jul 22;18(29):4182-90

5

## Peptide information for frame 2

-----

ORF from 89 bp to 2455 bp; peptide length: 789

Category: known protein

10 Classification: Cell division

1 MTSFQEVPLQ TSNFAHVIFQ NVAKSYLPNA HLECHYTLTP YIHPHPKDWV  
 51 GIFKVGWSTA RDYYTFLWSP MPEHYVEGST VNCVLAFAQY YLPNDGGEFY  
 101 QFCYVTHKGE IRGASTPFQF RASSPVEELL TMEDEGNSDM LVVTTKAGLL  
 15 151 ELKIEKTMKE KEELLKLIIV LEKETAQLRE QVGRMERELN HEKERCDQLQ  
 201 AEQKGLTEVT QSLKMENEEF KKRFSDATSK AHQLEEDIVS VTHKAIEKET  
 251 ELDSLKDKLK KAQHEREQLE CQLKTEKDEK ELYKVHLKNT EIENTKLMSE  
 301 VQTLKNLDGN KESVITHFKE EIGRLQLCLA EKENLQRTFL LTTSSKEDTC  
 351 FLKEQLRKAE EQVQATRQEV VFLAKELSDA VNVDRDTMAD LHTARLENEK  
 20 401 VKKQLADAVA ELKLNAMKKD QDKTDLEHE LRREVEDLKL RLQMAADHYK  
 451 EKFKECQRLQ KQINKLSQSQ ANNNNVFTKK TGNQQKVNDQ SVNTDPATSA  
 501 STVDVKPSPS AAADFQDIVT KGQVCEMTKE IADKTEKYNK CKQLLQDEKA  
 551 KCNKYADELA KMELKWKEQV KIAENVKLEL AEVQDNYKEL KRSLENPAER  
 601 KMEGQNSQSP QCFKTCSEQN GYVLTLSNAQ PVLQYGNPYA SQETRDGADG  
 25 651 AFYPDEIQRP PVRVPSWGLE DNVVCSQPAR NFSRPDGLD SEDSKEDENV  
 701 PTAPDPPSQH LRGHGTGFCF DSSFQVHKKC PLCELMFPPN YDQSKFEEHV  
 751 ESHWKVCPMC SEQFPPDYDQ QVFERHVQTH FDQNVLNFD

30

## BLASTP hits

No BLASTP hits available

35

## Alert BLASTP hits for DKFZphamy2\_2b19, frame 2

TREMBL:HS338211\_1 product: "tax1-binding protein TXBP151"; Homo  
 sapiens tax1-binding protein TXBP151 mRNA, complete cds., N = 2,  
 Score

40 = 2948, P = 0

>TREMBL:HS338211\_1 product: "tax1-binding protein TXBP151"; Homo  
 sapiens

45 tax1-binding protein TXBP151 mRNA, complete cds.  
 Length = 747

## HSPs:

50 Score = 2948 (442.3 bits), Expect = 0.0e+00, Sum P(2) = 0.0e+00  
 Identities = 575/603 (95%), Positives = 576/603 (95%)

Query: 1

MTSFQEVPLQTSNFAHVIFQNVAKSYLPNAHLECHYTLTPYIHPHPKDWVGIFKVGWSTA 60

55

MTSFQEVPLQTSNFAHVIFQNVAKSYLPNAHLECHYTLTPYIHPHPKDWVGIFKVGWSTA

Sbjct: 1

MTSFQEVPLQTSNFAHVIFQNVAKSYLPNAHLECHYTLTPYIHPHPKDWVGIFKVGWSTA 60

Query: 61  
RDYYTFLWSPMPEHYVEGSTVNCVLAFQGYL PND DGEFYQFCYVTHKGEIRGASTPFQF 120

5 RDYYTFLWSPMPEHYVEGSTVNCVLAFQGYL PND DGEFYQFCYVTHKGEIRGASTPFQF  
Sbjct: 61  
RDYYTFLWSPMPEHYVEGSTVNCVLAFQGYL PND DGEFYQFCYVTHKGEIRGASTPFQF 120

Query: 121  
10 RASSPVEELLTMEDEGNSDMLVVTTKAGXXXXXXXXXXXXXXXXXXXXXXXXXTAQLRE 180  
RASSPVEELLTMEDEGNSDMLVVTTKAG  
TAQLRE  
Sbjct: 121  
RASSPVEELLTMEDEGNSDMLVVTTKAGLLELKIEKTMKEKEELLKLIIVLEKETAQLRE 180

15 Query: 181  
QVGRMERELNHEKERCDQLQAEQKGLTEVTQSLKMENEEFKRFS DATSKAHQLEEDIVS 240  
QVGRMERELNHEKERCDQLQAEQKGLTEVTQSLKMENEEFKRFS DATSKAH  
+EEDIVS  
20 Sbjct: 181  
QVGRMERELNHEKERCDQLQAEQKGLTEVTQSLKMENEEFKRFS DATSKAHVVEEDIVS 240

Query: 241  
25 VTHKAIEKETELDSLKDKLKAQHEREQLEQKTEKDEKELYKVHLKNTEIENTKLMSE 300  
VTHKAIEKETELDSLKDKLKAQHEREQLEQKTEKDEKELYKVHLKNTEIENTKLMSE  
Sbjct: 241  
VTHKAIEKETELDSLKDKLKAQHEREQLEQKTEKDEKELYKVHLKNTEIENTKLMSE 300

30 Query: 301  
VQTLKNLDGNKESVITHFKEEIGRLQLCLAEKENLQRTFLLTTSSKEDTCFLKEQLRKAE 360  
VQTLKNLDGNKESVITHFKEEIGRLQLCLAEKENLQRTFLLTTSSKEDTCFLKEQLRKAE  
Sbjct: 301  
35 VQTLKNLDGNKESVITHFKEEIGRLQLCLAEKENLQRTFLLTTSSKEDTCFLKEQLRKAE 360

Query: 361  
EQVQATRQEVVFLAKELSDAVNVRDRTMADLHTARLENEKVKKQLADAVAELKLNAMKKD 420  
40 EQVQATRQEVVFLAKELSDAVNVRDRTMADLHTARLENEKVKKQLADAVAELKLNAMKKD  
Sbjct: 361  
EQVQATRQEVVFLAKELSDAVNVRDRTMADLHTARLENEKVKKQLADAVAELKLNAMKKD 420

Query: 421  
45 QDKTDTLEHELRRREVEDLKLRLQMAADHYKEKFKECQRLQKQINKLSDQSANNNNVFTKK 480  
QDKTDTLEHELRRREVEDLKLRLQMAADHYKEKFKECQRLQKQINKLSDQSANNNNVFTKK  
Sbjct: 421  
QDKTDTLEHELRRREVEDLKLRLQMAADHYKEKFKECQRLQKQINKLSDQSANNNNVFTKK 480

50 Query: 481  
TGNQKQVNDASVNTDPATSASTVDVKPSPSAAEADF DIVTKGQVCEMTKEIADKTEKYNK 540  
TGNQKQVNDASVNTDPATSASTVDVKPSPSAAEADF DIVTKGQVCEMTKEIADKTEKYNK  
55 Sbjct: 481  
TGNQKQVNDASVNTDPATSASTVDVKPSPSAAEADF DIVTKGQVCEMTKEIADKTEKYNK 540



Query: 541  
CKQLLQDEKAKCNKYADELAKMELKWKEQVKIAENVKLELAEVQDNYKELKRSLENPAER 600

5 CKQLLQDEKAKCNKYADELAKMELKWKEQVKIAENVKLELAEVQDNYKELKRSLENPAER  
Sbjct: 541  
CKQLLQDEKAKCNKYADELAKMELKWKEQVKIAENVKLELAEVQDNYKELKRSLENPAER 600

Query: 601 KME 603  
KME  
10 Sbjct: 601 KME 603

Score = 831 (124.7 bits), Expect = 0.0e+00, Sum P(2) = 0.0e+00  
Identities = 147/153 (96%), Positives = 149/153 (97%)

15 Query: 637  
NPYASQETRDGADGAFYPDEIQRPVVRVPSWGLEDNVVCSPARNFSRPDGLDSEDSKE 696  
NP A ++  
DGADGAFYPDEIQRPVVRVPSWGLEDNVVCSPARNFSRPDGLDSEDSKE  
Sbjct: 596 NP-  
20 AERKMEDGADGAFYPDEIQRPVVRVPSWGLEDNVVCSPARNFSRPDGLDSEDSKE 654

Query: 697  
DENVPTAPDPPSQHLRGHGTGFCFDSSFDVHKKCPLCELMFPPNYDQSKFEEHVESHWKV 756  
25 DENVPTAPDPPSQHLRGHGTGFCFDSSFDVHKKCPLCELMFPPNYDQSKFEEHVESHWKV  
Sbjct: 655  
DENVPTAPDPPSQHLRGHGTGFCFDSSFDVHKKCPLCELMFPPNYDQSKFEEHVESHWKV 714

Query: 757 CPMCSEQFPPDYDQVFERHVQTHFDQNVLNFD 789  
30 CPMCSEQFPPDYDQVFERHVQTHFDQNVLNFD  
Sbjct: 715 CPMCSEQFPPDYDQVFERHVQTHFDQNVLNFD 747

Score = 104 (15.6 bits), Expect = 9.2e-02, Sum P(2) = 8.8e-02  
Identities = 80/351 (22%), Positives = 157/351 (44%)

35 Query: 177 QLR---EQVGRMERELNH-  
EKERCQQLQAEQKGLTEVTQSLKMENEEFKRFSDATSKAH 232  
QLR EQV +E+ KE D + + + + + + + ENE+ KK+  
+DA  
40 Sbjct: 355 QLRKAAEQVQATRQEVVFLAKELSDAVNVRDRTMADL-  
HTARLENEKVKKQLADA----- 408

Query: 233 QLEEDIVSVTHKAIEKETE-  
45 LDSLKDKLKAQHEREQLECKTEKDEKELYKVHLKNT 291  
+ + A++K+ + D+L+ +L++ E E L+ +L+ D  
YK K +  
Sbjct: 409 -----VAELKLNAMKKDQDKTDLEHELRR---EVEDLKLRLQMAADH---  
YKEKFKECQ 457

50 Query: 292  
IENTKLMSEVQTLKNLDGNKESVITHFKEEIGRLQLCLAEKENLQRTFLLTTSSKEDTCF 351  
+L ++ L + N +V T ++ G Q N T  
T++S D  
Sbjct: 458 ----RLQKQINKLSDQSANNNNVFT---KKTGNQQKVNDASVN---  
55 TDPATSASTVD--- 504

Query: 352 LKEQLRKAAEQVQ-  
ATRQEVVFLAKELSDAVNVRDRTMADLHTARLENEKVKKQLADAVA 410

+K AE T+ +V + KE++D ++ L + + K  
+LA  
Sbjct: 505  
VKPSPSAAEADF DIVTKGQVCEMTKEIADKTEKYNKCKQLLQDEKAKCNKYADELAKMEL 564  
5  
Query: 411 ELKLNAMKKDQDKTDTLE-----HELRREVED-LKLRLQMAAD--  
HYKEKFKECQ-RLQK 461  
+ K + K + E EL+R +E+ + +++ AD Y ++ +  
R+  
10 Sbjct: 565  
KWKEQVKIAENVKLELAEVQDNYKELKRSLENPAERKMEDGADGAFYPDEIQRPVVRVPS 624  
Query: 462 ---QINKLSDQSANNNNVFTKKTG---  
NQQKVNDASVNTDPATSASTVDVKPSPSAAEAD 515  
15 + N + Q A N F++ G ++ D +V T P + +  
+ ++  
Sbjct: 625 WGLEDNVVCSPARN---  
FSRPDGLEDSKEDENVPTAPDPPSQHLRGHGTGFCFDSS 681  
20 Query: 516 FDIVTKGQVCEM 527  
FD+ K +CE+  
Sbjct: 682 FDVHKKCPLCEL 693

25 Pedant information for DKFZphamy2\_2b19, frame 2  
-----

# Report for DKFZphamy2\_2b19.2

30 [LENGTH] 789  
[MW] 90877.47  
[pI] 5.30  
[MOLE] TREMBL:HS338211\_1 product: "tax1-binding protein  
35 TXBP151"; Homo sapiens tax1-binding protein TXBP151 mRNA,  
complete cds. 0.0  
[FUNCAT] 99 unclassified proteins [S. cerevisiae, Y0R216c]  
3e-14  
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S.  
40 cerevisiae, YDLO58w] 2e-13  
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae,  
YDLO58w] 2e-13  
[FUNCAT] 09.10 nuclear biogenesis [S. cerevisiae, YDR356w]  
4e-13  
45 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae,  
YDR356w] 4e-13  
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae,  
YDR356w] 4e-13  
[FUNCAT] 11.04 dna repair (direct repair, base excision repair  
50 and nucleotide excision repair) [S. cerevisiae, YKR095w] 7e-12  
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKR095w]  
7e-12  
[FUNCAT] 03.25 cytokinesis [S. cerevisiae, YHR023w MY01 -  
myosin-1 isoform] 6e-11  
55 [FUNCAT] 08.22 cytoskeleton-dependent transport [S. cerevisiae,  
YHR023w MY01 - myosin-1 isoform] 6e-11  
[FUNCAT] 03.04 budding, cell polarity and filament formation  
[S. cerevisiae, YHR023w MY01 - myosin-1 isoform] 6e-11

- 1 genome replication, transcription, recombination and repair [M. jannaschii, MJ1322] 3e-08  
 1 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YJR134c] 4e-08  
 5 [FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YNL250w] 2e-07  
 [FUNCAT] 03.13 meiosis [S. cerevisiae, YNL250w] 2e-07  
 [FUNCAT] 03.01 cell growth [S. cerevisiae, YNL079c] 2e-06  
 10 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YNL079c] 2e-06  
 [FUNCAT] 08.99 other intracellular-transport activities [S. cerevisiae, YNL079c] 2e-06  
 [FUNCAT] 09.13 biogenesis of chromosome structure [S. cerevisiae, YLR086w] 5e-06  
 15 [FUNCAT] 11.01 stress response [S. cerevisiae, YPR141c] 2e-05  
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YPR141c] 2e-05  
 [FUNCAT] 03.22.01 cell cycle check point proteins [S. cerevisiae, YGL086w] 2e-05  
 20 [FUNCAT] 30.05 organization of centrosome [S. cerevisiae, YPR141c] 2e-05  
 [FUNCAT] 08.16 extracellular transport [S. cerevisiae, YOR326w] 1e-04  
 [FUNCAT] 09.25 vacuolar and lysosomal biogenesis [S. cerevisiae, YOR326w] 1e-04  
 25 [FUNCAT] 30.16 mitochondrial organization [S. cerevisiae, YAL011w] 2e-04  
 [FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation, palmitylation, farnesylation and processing) [S. cerevisiae, YKL201c] 2e-04  
 30 [FUNCAT] e amino acid metabolism and transport [M. genitalium, MG042] 4e-04  
 [FUNCAT] 30.13 organization of chromosome structure [S. cerevisiae, YDR285w] 7e-04  
 35 [FUNCAT] n secretion and adhesion [M. jannaschii, MJ0291] 0.001  
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YAL035w] 0.001  
 40 [BLOCKS] BL00326 Tropomyosins proteins  
 [BLOCKS] PR00545E  
 [BLOCKS] PR00041F  
 [SCOP] d2tmab\_1.105.4.1.1 Tropomyosin [rabbit (Oryctolagus cuniculus)] 5e-05  
 [EC] 3.6.1.32 Myosin ATPase 5e-16  
 45 [PIRKW] nucleus 2e-35  
 [PIRKW] phosphotransferase 5e-10  
 [PIRKW] duplication 2e-09  
 [PIRKW] citrulline 7e-09  
 [PIRKW] tandem repeat 2e-13  
 50 [PIRKW] heterodimer 2e-08  
 [PIRKW] heart 2e-11  
 [PIRKW] endocytosis 3e-10  
 [PIRKW] polymorphism 1e-09  
 [PIRKW] transmembrane protein 6e-12  
 55 [PIRKW] serine/threonine-specific protein kinase 5e-10  
 [PIRKW] cell wall 7e-09  
 [PIRKW] zinc finger 3e-10  
 [PIRKW] surface antigen 6e-08

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	[[PIRKW]]	metal binding 3e-10
	[[PIRKW]]	muscle contraction 2e-13
	[[PIRKW]]	brain 8e-08
5	[[PIRKW]]	acetylated amino end 4e-09
	[[PIRKW]]	actin binding 5e-16
	[[PIRKW]]	endoplasmic reticulum 4e-09
	[[PIRKW]]	mitosis 3e-15
	[[PIRKW]]	microtubule binding 3e-15
10	[[PIRKW]]	ATP 5e-16
	[[PIRKW]]	chromosomal protein 2e-08
	[[PIRKW]]	receptor 4e-10
	[[PIRKW]]	thick filament 2e-13
	[[PIRKW]]	phosphoprotein 5e-16
15	[[PIRKW]]	glycoprotein 4e-10
	[[PIRKW]]	skeletal muscle 7e-11
	[[PIRKW]]	calcium binding 7e-09
	[[PIRKW]]	alternative splicing 3e-13
	[[PIRKW]]	DNA condensation 2e-08
20	[[PIRKW]]	coiled coil 5e-16
	[[PIRKW]]	P-loop 5e-16
	[[PIRKW]]	heptad repeat 3e-13
	[[PIRKW]]	methylated amino acid 2e-13
	[[PIRKW]]	basement membrane 1e-09
25	[[PIRKW]]	immunoglobulin receptor 2e-09
	[[PIRKW]]	peripheral membrane protein 3e-10
	[[PIRKW]]	cardiac muscle 2e-11
	[[PIRKW]]	extracellular matrix 1e-09
	[[PIRKW]]	hydrolase 5e-16
30	[[PIRKW]]	microtubule 1e-11
	[[PIRKW]]	muscle 1e-09
	[[PIRKW]]	membrane protein 1e-09
	[[PIRKW]]	EF hand 7e-09
	[[PIRKW]]	protein biosynthesis 4e-09
35	[[PIRKW]]	cytoskeleton 3e-13
	[[PIRKW]]	hair 7e-09
	[[PIRKW]]	Golgi apparatus 1e-11
	[[PIRKW]]	calmodulin binding 3e-10
40	[[SUPFAM]]	myosin heavy chain 5e-16
	[[SUPFAM]]	conserved hypothetical P115 protein 4e-10
	[[SUPFAM]]	IgA Fc receptor 7e-09
	[[SUPFAM]]	centromere protein E 3e-15
	[[SUPFAM]]	unassigned Ser/Thr or Tyr-specific protein kinases 5e-10
45	[[SUPFAM]]	calmodulin repeat homology 7e-09
	[[SUPFAM]]	myosin motor domain homology 5e-16
	[[SUPFAM]]	alpha-actinin actin-binding domain homology 5e-10
	[[SUPFAM]]	hypothetical protein MJ0914 4e-08
	[[SUPFAM]]	tropomyosin 6e-09
50	[[SUPFAM]]	plectin 5e-10
	[[SUPFAM]]	trichohyalin 7e-09
	[[SUPFAM]]	pleckstrin repeat homology 1e-08
	[[SUPFAM]]	ribosomal protein S10 homology 5e-10
	[[SUPFAM]]	giantin 4e-13
55	[[SUPFAM]]	protein kinase homology 5e-10
	[[SUPFAM]]	protein kinase C zinc-binding repeat homology 1e-08
	[[SUPFAM]]	kinesin motor domain homology 3e-15
	[[SUPFAM]]	human early endosome antigen 1 3e-10

[SUPFAM] myosin MY02 8e-08  
 [SUPFAM] unassigned kinesin-related proteins 1e-10  
 [SUPFAM] M5 protein 3e-10  
 [SUPFAM] cytoskeletal keratin 4e-07  
 5 [KW] All\_Alpha  
 [KW] LOW\_COMPLEXITY 3.30 %  
 [KW] COILED\_COIL 22.18 %

10 SEQ MTSFQEVPLQTSNFAHVIFQNVAKSYLPNAHLECHYTLTPYIHPHPKDWVGIFKVGWSTA  
 SEG .....  
 PRD ccc  
 COILS .....

15 SEQ RDYYTFLWSPMPEHYVEGSTVNCVLAFAQGYLPNDGGEFYQFCYVTHKGEIRGASTPFQF  
 SEG .....  
 PRD eeeeeeeeecc  
 COILS .....

20 SEQ RASSPVEELLTMEDEGNSDMLVVTTKAGLLELKIEKTMKEKEELLKLIIVLEKETAQLRE  
 SEG .....xx.....  
 PRD hhh  
 25 COILS .....cc

SEQ QVGRMERELNHEKERCDQLQAEQKGLTEVTQSLKMENEEFKKRFSDATSKAHQLEEDIVS  
 SEG .....  
 30 PRD hhh  
 COILS .....cc

SEQ VTHKAIEKETELDSLKDKLKAQHEREQLEQKTEKDEKELYKVHLKNTIEIENTKLMSE  
 SEG .....  
 PRD hhh  
 35 COILS .....cc

SEQ VQTLKNLDGNKESVITHFKEEIGRLQLCLAEKENLQRTFLLTTSSKEDTCFLKEQLRKA  
 SEG .....  
 PRD hhh  
 40 COILS .....cc

SEQ EQVQATRQEVVFLAKELSDAVNVDRDTMADLHTARLENEKVKKQLADAVAELKLNAMKKD  
 SEG .....  
 PRD hhh  
 45 COILS .....cc

SEQ QDKTDLEHELRRVEDLKLRLQMAADHYKEKFKECQRLQKQINKLSDQSANNNNVFTKK  
 SEG .....  
 PRD hhh  
 50 COILS .....cc

SEQ TGNQQKVNDASVNTDPATSASTVDVKPSPSAAEADFQIVTKGQVCEMTKEIADKTEKYNK

5

SEQ CKQLLQDEKAKCNKYADELAKMELKWKEQVKIAENVKLELAEVQDNYKELKRSLENPAER

```

SEG .....

```

PRD hhhhhhhhhhhh

COILS

```

10      .....CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.....

```

SEQ KMEG@NS@SP@CFKTCSE@NGYVLTLSNA@PVL@YGNPYAS@ETRDGADGAFYPDEI@RP

```

SEG .....

```

[illegible]

15 COILS

.....

SE0 PVRVPSWGLFDNVVCSQPARNESRPDGI EDSFDSKEDENVPTAPDPPSØHI RGHGTGECF

```

SER 1 VRV1 SWCEEDNVVCS&T ARNT SRI DCEEDSEDSKEDENV1 TAT 011 S&HEROHO10101 CI
SFG .....

```

```

20 PRD ccccccccccccccEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

```

COILS

.....

SEQ DSSFDVHKKCPLCELMFPPNYDQSKFEEHVESHWKVCPMCSEQFPPDYDQQVFERHVQTH

25 SEG .....  
.....

```
PRD cccccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhcfffffffffffffchhhhhhhhhhhhhhhh
```

COPIES

.....

30 SEQ FDQNVLFNF

SEG .....

PRD hccccccc

COILS . . . . .

35

(No Prosite data available for DKFZphamy2\_2b19.2)

(No Pfam data available for DKFZphamy2\_2b19.2)

DKFZphamy2\_2c22

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5 group: metabolism

DKFZphamy2\_2c22 encodes a novel 364 amino acid protein with similarity to the 1-acyl-glycerol-3-phosphate acyltransferase of Zea mais.

10 It contains one leucine zipper. The protein is believed to play a role in fatty acid metabolism. It is ubiquitous expressed, with a slight predominance in uterus, placenta and foreskin.

15 The new protein can find application in modulation of fatty acid metabolism and as a new enzyme for biotechnological production processes.

20 weak similarity to 1-acyl-glycerol-3-phosphate acyltransferase (Zea mais)

perhaps complete cds.

25 Sequenced by MediGenomix

Locus: /map="8"

30 Insert length: 3403 bp  
Poly A stretch at pos. 3373, polyadenylation signal at pos. 3351

```

1  AGATGCTGCT GTCCCTGGTG CTCCACACGT ACTCCATGCG CTACCTGCTG
35  51 CCCAGCGTCG TGCTCCTGGG CACGGCGCCC ACCTACGTGT TGGCCTGGGG
101 GGTCTGGCGG CTGCTCTCCG CCTTCCTGCC CGCCCGCTTC TACCAAGCGC
151 TGGACGACCG GCTCTACTGC GTCTACCAGA GCATGGTGCT CTTCTTCTTC
201 GAGAATTACA CCGGGGTCCA GATATTGCTA TATGGAGATT TGCCAAAAAA
251 TAAAGAAAAT ATAATATATT TAGCAAATCA TCAAAGCACA GTTGACTGGA
40  301 TTGTTGCTGA CATCTTGGCC ATCAGGCAGA ATGCGCTAGG ACATGTGCGC
351 TACGTGCTGA AAGAAGGGTT AAAATTGGCTG CCATTGTATG GGTGTTACTT
401 TGCTCAGCAT GGAGGAATCT ATGTAAAGCG CAGTGCCAAA TTTAACGAGA
451 AAGAGATGCG AAACAAGTTG CAGAGCTACG TGGACGCAGG AACTCCAATG
501 TATCTTGTTGA TTTTTCAGAG AGGTACAAGG TATAATCCAG AGCAAACAAA
45  551 AGTCCTTTCA GCTAGTCAGG CATTTGCTGC CCAACGTGGC CTTGCAGTAT
601 TAAAACATGT GCTAACACCA CGAATAAAGG CAACTCACGT TGCTTTTGAT
651 TGCATGAAGA ATTATTTAGA TGCAATTTAT GATGTTACGG TGGTTTATGA
701 AGGGAAAGAC GATGGAGGGC AGCGAAGAGA GTCACCGACC ATGACGGAAT
751 TTCTCTGCAA AGAATGTCCA AAAATTCTTA TTCACATTGA TCGTATCGAC
50  801 AAAAAAGATG TCCCAGAAGA ACAAGAACAT ATGAGAAGAT GGCTGCATGA
851 ACGTTTCGAA ATCAAAGATA AGATGCTTAT AGAATTTTAT GAGTCACCAG
901 ATCCAGAAAG AAGAAAAAGA TTTCTGGGGA AAAGTGTTAA TTCCAAATTA
951 AGTATCAAGA AGACTTTACC ATCAATGTTG ATCTTAAGTG GTTTGACTGC
1001 AGGCATGCTT ATGACCGATG CTGGAAGGAA GCTGTATGTG AACACCTGGA
55  1051 TATATGGAAC CCTACTTGGC TGCCTGTGGG TTAATAATTA AGCATAGACA
1101 AGTAGCTGTC TCCAGACAGT GGGATGTGCT ACATTGTCTA TTTTGGCGG
1151 CTGCACATGA CATCAAATTG TTTCTGAAT TTATTAAGGA GTGTAAATAA
1201 AGCCTTGTTG ATTGAAGATT GGATAATAGA ATTTGTGACG AAAGCTGATA

```

1251 TGCAATGGTC TTGGGCAAAAC ATACCTGGTT GTACAACTTT AGCATCGGGG  
1301 CTGCTGGAAG GGTAAGAGCT AAATGGAGTT TCTCCTGCTC TGTCATTTC  
1351 CTATGAACTA ATGACAACCTT GAGAAGGCTG GGAGGATTGT GTATTTTGCA  
1401 AGTCAGATGG CTGCATTTTTT GAGCATTAAT TTGCAGCGTA TTTCACTTTT  
5 1451 TCTGTTATTT TCAATTTATT ACAACTTGAC AGCTCCAAGC TCTTATTACT  
1501 AAAGTATTTA GTATCTTGCA GCTAGTTAAT ATTTTCATCTT TTGCTTATTT  
1551 CTACAAGTCA GTGAAATAAA TTGTATTTAG GAAGTGTGAG GATGTTCAAA  
1601 GGAAAGGGTA AAAAGTGTTT ATGGGGAAAA AGCTCTGTTT AGCACATGAT  
1651 TTTATTGTAT TGC GTTATTA GCTGATTTTA CTCATTTTAT ATTTGCAAAA  
10 1701 TAAATTTCTA ATATTTATTG AAATTGCTTA ATTTGCACAC CCTGTACACA  
1751 CAGAAAATGG TATAAAATAT GAGAACGAAG TTTAAAATTG TGACTCTGAT  
1801 TCATTATAGC AGAACTTTAA ATTTCCCAGC TTTTGAAGA TTTAAGCTAC  
1851 GCTATTAGTA CTTCCTTTTG TCTGTGCCAT AAGTGCTTGA AAACGTTAAG  
1901 GTTTTCTGTT TTGTTTTGTT TTTTAAATAT CAAAAGAGTC GGTGTGAACC  
15 1951 TTGGTTGGAC CCCAAGTTCA CAAGATTTT AAGGTGATGA GAGCCTGCAG  
2001 ACATTTGCTC TAGATTTACT AGCGTGTGCC TTTTGCCTGC TTCTCTTTGA  
2051 TTTACAGAA TATTCATTCA GAAGTCGCGT TTCTGTAGTG TGGTGGATTG  
2101 CCACTGGGCT CTGGTCCTTC CTTGGATCC CGTCAGTGGT GCTGCTCAGC  
2151 GGCTTGACG CAGACTTGCT AGGAAGAAAT GCAGAGCCAG CCTGTGCTGC  
20 2201 CCACTTTCAG AGTTGAACTC TTTAAGCCCT TGTGAGTGGG CTTCAACCAGC  
2251 TACTGCAGAG GCATTTTGCA TTTGTCTGTG TCAAGAAGTT CACCTTCTCA  
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2351 TTCCCATTAG GTTTAGTGGA GCTACACATT AATATGTATC GCCTTAGAGC  
2401 AAGAGCTGTG TTCCAGGAAC CAGATCACGA TTTTGTAGCA TGGAAACAATA  
25 2451 TATCCCATGG GAGAAGACCT TTCAGTGTGA ACTGTTCTAT TTTTGTGTTA  
2501 TAATTTAAAC TTCGATTTCC TCATAGTCCT TTAAGTTGAC ATTTCTGCTT  
2551 ACTGCTACTG GATTTTTGCT GCAGAAATAT ATCAGTGGCC CACATTAAAC  
2601 ATACCAAGTTG GATCATGATA AGCAAAATGA AAGAAATAAT GATTAAGGGA  
2651 AAATTAAGTG ACTGTGTTAC ACTGCTTCTC CCATGCCAGA GAATAAACTC  
30 2701 TTTCAAGCAT CATCTTTGAA GAGTCGTGTG GTGTGAATTG GTTTGTGTAC  
2751 ATTAGAATGT ATGCACACAT CCATGGACAC TCAGGATATA GTTGGCCTAA  
2801 TAATCGGGGC ATGGGTAAAA CTTATGAAAA TTTCCTCATG CTGAATTGTA  
2851 ATTTTCTCTT ACCTGTAAAG TAAATTTAG ATCAATTCCA TGTCTTTGTT  
2901 AAGTACAGGG ATTTAATATA TTTTGAATAT AATGGGTATG TTCTAAATTT  
35 2951 GAACTTTGAG AGGCAATACT GTTGGAAATTA TGTGGATTCT AACTCATTTT  
3001 AACAAGGTAG CCTGACCTGC ATAAGATCAC TTGAATGTTA GGTTCATAG  
3051 AACTATACTA ATCTTCTCAC AAAAGGTCTA TAAATACAG TCGTTGAAAA  
3101 AAATTTTGTA TCAAAATGTT TGGAAATTA GAAGCTTCTC CTTAACCTGT  
3151 ATTGATACTG ACTTGAATTA TTTTCTAAAA TTAAGAGCCG TATACCTACC  
40 3201 TGTAAGTCTT TTCACATATC ATTTAACTT TTGTTTGTAT TATTACTGAT  
3251 TTACAGCTTA GTTATTAATT TTTCTTTATA AGAATGCCGT CGATGTGCAT  
3301 GCTTTTATGT TTTTCAGAAA AGGGTGTGTT TGGATGAAAG TAAAAAAA  
3351 AAATAAAATC TTTCACTGTC TCTAAAAAAA AAAGAAAAAAA AAAAAAAA  
45 3401 AAA

## BLAST Results

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50 No BLAST result

## Medline entries

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55 No Medline entry



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10

15

20

No BLASTP hits available

25

No Alert BLASTP hits found

30

Pedant information for DKFZphamy2\_2c22, frame 3

## 35

40

45

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-172-

```

5  SEQ  MVLFFFENYTGVDILLYGDLPKNKENIIYLANHQSTVDWIVADILAIRQNALGHVRYVLK
   SEG  .....
   PRD  hhhhhhheeeeeeeeeccccccccceeeeeccccchhhhhhhhhhhhhccccchhhhhh

10  SEQ  EGLKWLPYGCYFAQHGGIYVKRSKFNKEMRNKLQSYVDAGTPMYLVIFPEGTRYNPE
   SEG  .....
   PRD  hhhccccceeeccccceeeccccccchhhhhhhhhhhccccceeeccccchhh

15  SEQ  RRESPTMTEFLCKECPKIHIDRIDKKDVPEEQEHMRRWLHERFEIKDKMLIEFYESP
   SEG  .....xxxxxxxxxxxx.....
   PRD  cccccchhhhccccceeeccccccccccccchhhhhhhhhhhhhhhhhhhhhccc

20  SEQ  PERRKRFPKSVNSKLSIKKTLPSMLILSGLTAGMLMTDAGRKLYVNTWIYGTLLGCLWV
   SEG  .....
   PRD  cccccccccchhhhhhhhhchhhhhchhhhhhhhhhhccccceeeeeecehhhhhhhh

   SEQ  TIKA
   SEG  ....
   PRD  hccc
25

```

## Prosites for DKFZphamy2\_2c22.3

```

30  PS00029      105->127  LEUCINE_ZIPPER      PD0000029

```

(No Pfam data available for DKFZphamy2\_2c22.3)

DKFZphamy2\_2f18

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5 group: signal transduction

DKFZphamy2\_2f18 encodes a novel 215 amino acid protein with similarity to sodium channel protein beta1 of *Rattus norvegicus*.

10 The sodium channel protein beta 1 of *Rattus norvegicus* is crucial in the assembly, expression, and functional modulation of the heterotrimeric complex of the rat brain sodium channel. The expression of the new protein seems to be restricted to brain, all matching ESTs isolated so far, derive from there.

15 The new protein can find application in modulating the sodium channel beta 1, studying the expression profile in neurodegenerative diseases and of amygdala-specific genes.

20 similarity to sodium channel protein beta1 (*Rattus norvegicus*)

Pedant: SIGNAL\_PEPTIDE

25 Sequenced by MediGenomix

Locus: unknown

30 Insert length: 4052 bp  
Poly A stretch at pos. 4035, no polyadenylation signal found

```

      1 CAGGGCTGAC AGCACACACG GCCTGGGGGC CTAGAGAAGG ATTGCTGATC
35    51 ACCTGCCACC CAGGGTCGGG GCCCCGCACC ATCCGGGGGC GAGCTCCCGG
      101 GAAGGGGCTC CCCCTCTACA CCCACCCCCC AACCTCTGAC ATCGCCGGCC
      151 GAACGGGAGC TGCCGCTTCC TTCCCGGCCC CGCTGCACCT CCCCAGGGAG
      201 CCGAGGGCGG GCGTGGGACG GACCGACGTG GAACGCATTG TGTAGCCCAG
      251 ACGGGCGGGC CCGCGGGCTT CGGGAGTGCG GTACGCCCCA GCTGGAGAAG
40    301 CAGTTAGGGC GGACGAAGCA GAGCGCGCGG GGCTGGGAGG ATTCCAGTCG
      351 GAACGCAACC GATCCTGGGG AGGCGAGAGG TGAATCAACC TGGACCCCTC
      401 CACAGCCTGG CTGCTAGGCC AGCAGTGCGA CTCCCTTCCG AGCTGAGCTT
      451 ACCCTGGGCG CAAACGAGCG AGGCAGGGGC GCGAGTGGAA GCTGGAGTTC
      501 CGGGGTGGGC GGGGAGGCGA CTGTCCGTGG TGCTGAGCGC CGGCGAGAGC
45    551 GGGCGCGGAG CGGCTGATCA GCTCCCTCGA ACTGGGGAGG TCCAGTGGGG
      601 TCGCTTAGGG CCCAAAGCCC CCGCCCGGCT CCAAAGCTC CCAGGGCCTC
      651 CCCAGGCACC GGTGCTCGGC CCTTCCTTCG GTCAGAAAGT CGCCCCCTGG
      701 GGGCAGTTCG TCCCAAAGGG TTTCCTCGAA AGAATCTGAG AGGGCGCAGT
      751 CCTTGACCGA GGAATCTCT CTGTGTAGCC TTGGAAGCCG CCAGCCCCAG
50    801 AAGATGCCTG CCTTCAATAG ATTGTTTCCC CTGGCTTCTC TCGTGCTTAT
      851 CTA CTGGGTC AGTGTCTGCT TCCCTGTGTG TGTGGAAGTG CCCTCGGAGA
      901 CGGAGGCCGT GCAGGGCAAC CCCATGAAGC TCGCTGCAT CTCCTGCATG
      951 AAGAGAGAGG AGGTGGAGGC CACCACGGTG GTGGAATGGT TCTACAGGCC
      1001 CGAGGGCGGT AAAGATTTCC TTATTTACGA GTATCGGAAT GGCCACCAGG
55    1051 AGGTGGAGAG CCCCTTTTCA GGGCGCCTGC AGTGGGAATGG CAGCAAGGAC
      1101 CTGCAGGACG TGTCCATCAC TGTGCTCAAC GTCACCTCTGA ACGACTCTGG
      1151 CCTCTACACC TGCAATGTGT CCCGGGAGTT TGAGTTTGAG GCGCATCGGC
      1201 CCTTTGTGAA GACGACGCGG CTGATCCCCC TAAGAGTCAC CGAGGAGGCT

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	1251	GGAGAGGACT	TCACCTCTGT	GGTCTCAGAA	ATCATGATGT	ACATCCTTCT
	1301	GGTCTTCCTC	ACCTTGTGGC	TGCTCATCGA	GATGATATAT	TGCTACAGAA
	1351	AGGTCTCAAA	AGCCGAAGAG	GCAGCCCAAG	AAAACGCGTC	TGACTACCTT
5	1401	GCCATCCCAT	CTGAGAACAA	GGAGAACTCT	GCGGTACCAG	TGGAGGAATA
	1451	GAACAGGAGC	AGTGTGACAT	GAGGTGGCCT	GAACACCTGA	GGGACTGGAC
	1501	ATCCCATGTT	CAGCAATGTC	AATGGCATCA	GGAGGGCGCC	CCAAGGGCCC
	1551	CATCGCTTCC	CTTCATGCA	CCATTGTTCT	GTTCAATTCAT	TCATCCATAC
	1601	ATCCACCTGC	CTCTGAGCTT	TCACCTCTGA	CTCCCTAACT	CCATCAGACC
	1651	TCTACGCACC	ATAAGACTCT	GCCAGAACTG	AGAAGCCAAC	ATTTCTACAT
10	1701	AGACTCAACC	TCACCTCTC	CTAGTTTTCC	AACAAGACAC	TCCAAAGCCA
	1751	ACTGGATTTT	TCCCTGTGTC	TCCAAATGAC	TTTGTACAAG	TGCTGGAGTT
	1801	AGCACCTCCC	TCTGCCCTTA	ACTGGCTGGA	ACTGGTTTCAT	TCTCCATTAC
	1851	TGCAAGAGAA	TGGAAGTCTT	AATAGAAGGA	AGCAGGAGTG	ATTAGTTCGG
	1901	GTTAAAGCAA	AAGTGTGTCA	TGAACCTGGA	TTCCCTGAAG	TCAGTTTTGT
15	1951	CAGGTTTCATG	GCCCACTTTG	CTACAGCATC	AGAGTGAAGC	ACGCCTGTCT
	2001	AGGTTCTCCA	GTGACAGAAA	GATCCTGAAG	CATGGACTAA	CATGCTCTCT
	2051	GGAGCTTAGT	ACTCCAGAGC	TAGATCCTGA	TGGGTCTCTA	AGGTTCCCTC
	2101	CAAGAAGACA	AGGACAGGAG	ACTTGGGAAG	GACCAATGGT	AATTTAAGTG
	2151	GCTCTTAAAA	AGTCATGCAA	CATGTTTCTG	GACACGTTCC	TGATCCTATT
20	2201	GCGATAATGT	ATGTGTGCCC	TCCCTGTGGG	CACACCACCT	GGGCATTAGG
	2251	ACTGAAATTC	CTGAGTTCTT	CCTCTCAAAA	TTTCTGTGCA	CCAGTATTAT
	2301	TCCTCATTTT	ACATACAGGA	GGCAACTAAG	ACTCATACAG	GGCTCAACTG
	2351	AATAAGAGGC	TAAAGAGGAT	AACTGGAGC	AGAAATAAGC	CTTAGGTGCT
	2401	GCCCAGTTTA	CACTTCCTGG	GATGGATGTT	TTTGTGTTGT	TTGTTTTTTG
25	2451	TTTTTTTTGT	TTGAGATGGA	GTCTCACTCT	GTCACCTAGG	CTAGAGTGCA
	2501	GTGGTGTGAT	CTCGGCTCAC	TGCAACCTCT	GCCTCTTGGG	TTCAAGCAAT
	2551	TCTCATGCCT	CGGCCTCTCC	AGTAGCTGGG	ATTACAGGTG	TGCACCACCA
	2601	CGCCTGGCTA	AATTTTGTAT	TTTTAGTACA	GACAGGGTTT	GACTATGTTG
	2651	GCCAGGCTAG	TCTTGAACCTC	CTGACCTCAA	ATGACCCACC	CACCTCAGCC
30	2701	TCCCAAAGTG	CTGAGATTAC	AGGCGTGAGG	CACTGCGCCC	GGTGGATAAC
	2751	TTTGTTTCTG	AAAAGACTGA	CATTGAACTT	GTCTATGGCA	ATGCTTCTTT
	2801	CACAAGCACG	GACTGGGCTG	AGGTCAACTC	TGATAGATTC	AGATGACTAG
	2851	AAATTGGCCA	AAAAAGCAGG	GAGAAGAACA	TGAGGTAGAC	TTAAAGAACT
	2901	TCCTTTATGT	AAAGATCTGT	GACTCTGAAA	TATCCTCCAA	AAGGAGAGTG
35	2951	CATCTGAGAC	TGATATTTAA	ACTAAGAAAA	ATGTTTAGTC	TGAGATGGAT
	3001	CATAAGTAAA	TGAGCAGTGT	GAGAGGGGAG	GGATGGGTAG	GTGCTTTCCA
	3051	AATACTTCGC	CTATGAATGC	ATAATTTTCA	GATTTTTTTC	CCCTAGATTT
	3101	TGAGGGAGCA	GAGAACTGG	AAAAAACTTT	AGTCAATATC	TCGTGTTTCA
	3151	TTTTAATTAA	GTGACAGGTC	CAAGTGTCAG	ATCCTTCAGC	ACCCAGGGAC
40	3201	AAGAGAGGGG	AAAGATGCTT	TATGGAATGT	AAGAAGATGA	AGGTGACTGG
	3251	GATTCAGCGA	GAGAGAGGTC	CCTCAGACCT	GGGACCTCCC	TTTATAGGGA
	3301	AAGACCATAT	TCCATAGGTT	TAGGGCTTTA	CCTTAAAAGC	TCATTTTTTT
	3351	CATTCTTCCA	TCCCTAGGAA	AGTACTTAAA	ACCAGACTTT	TAAATTTTTTA
	3401	TTTATTTATT	ATTATTTTTT	TGAGACAGAT	TCTCACTCTG	TCTCCCAGGC
45	3451	TAGAGTGCA	TGGTGCAATC	TCAGCTCACT	GCAGCCTCAA	CTGCCCCAGG
	3501	TTTAAGCAAT	CCTCCACCT	CAGCCCCCAG	GTAACCTGGG	CTACAGGCAT
	3551	GCACCACCAT	GCCTGGCTAA	TTTTTGTATT	TTATGTAGAG	ACAGGGGTCT
	3601	TGCCATGTG	CCCAGGCTGA	TCTTGAACCTC	CTGGGCTCAA	GCAATCTGCC
	3651	AGCCTCAGCC	TCTCAAAGTG	CTGGGATTAC	AGGCCTGAGC	AACTGTGCCT
50	3701	GGCCCCAAAC	CAGACCGTTA	ACACATTAAA	GAGTCTGATT	TTGTTGAAGA
	3751	AAATATTTGC	AATAAATTC	AGACTCTTCT	TATTGGTAAT	TTTCCACACA
	3801	ATCCCTCTGA	AATAAGGGAG	AGGATATAGA	CCTTTTAAAC	TTTATAGTTA
	3851	GAAAAATTGG	CCTCAGTGTG	AAATTTTTCC	AGTCCCATAG	CTCATGGATG
	3901	CCACCAGCTT	GCGGTAGTAG	CAAGATGCTT	ACTACCACAC	CGTTTTCTCT
55	3951	GGTGGCCCCA	TAGCTCGTGT	ATCTAAGTTG	AACCCGGCAG	TATGCATGAT
	4001	TGCCTTTTTT	TCTTCTTTTT	AAAAAAACCC	AACTCAAAAA	AAAAAATAAA
	4051	AA				

## BLAST Results

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5 No BLAST result

## Medline entries

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10

92271207:

Isom LL, De Jongh KS, Patton DE, Reber BF, Offord J, Charbonneau H,

Walsh K, Goldin AL, Catterall

15 WA.; Primary structure and functional expression of the beta 1 subunit of

the rat brain sodium channel. Science 1992 May 8;256(5058):839-42

20

96235151:

Belcher SM, Howe JR.; Cloning of the cDNA encoding the sodium channel

beta 1 subunit from rabbit. Gene 1996 May 8;170(2):285-6

25

93357746:

McClatchey AI, Cannon SC, Slaughter SA, Gusella JF.; The cloning and

expression of a sodium channel beta

1-subunit cDNA from human brain. Hum Mol Genet 1993 Jun;2(6):745-

30 9

35

## Peptide information for frame 3

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ORF from 804 bp to 1448 bp; peptide length: 215

Category: similarity to known protein

40

Classification: Transmembrane proteins unclassified

1 MPAFNRLFPL ASLVLIYWVS VCFPVCVEVP SETEAVQGNP MKLRCISCMK

51 REEVEATTVV EWFYRPEGGK DFLIYEYRNG HQEVESPFQG RLQWNGSKDL

101 QDVSITVLNV TLNDSGLYTC NVSREFEFEA HRPFVKTTTL IPLRVTEEAG

45

151 EDFTSVVSEI MMYILLVFLT LWLLIEMIYC YRKVSKAEEA AQENASDYLA

201 IPSENKENSA VPVEE

50

## BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_2f18, frame 3

55

PIR:JC4788 sodium channel protein beta1 chain - rabbit, N = 1,

Score =

434, P = 8.3e-41

PIR:A55734 sodium channel, voltage-gated, beta-1 chain precursor  
human, N = 1, Score = 428, P = 3.6e-40

PIR:A42737 sodium channel beta 1 subunit - rat, N = 1, Score =  
429, P =  
2.8e-40

>PIR:JC4788 sodium channel protein beta1 chain - rabbit  
Length = 218

HSPs:

Score = 434 (65.1 bits), Expect = 8.3e-41, P = 8.3e-41  
Identities = 100/214 (46%), Positives = 129/214 (60%)

Query: 10

LASLVLIYWVSVCFPVCVEVPSETEAVQGNPMKLRISC MKREEVEATTVVEWFYRPEGG 69  
LA +V VS + C VEV SETEAV G K+ CISC +R E A T

EW +R +G

Sbjct: 5

LAFVVGAAALVSSAWGGCVEVDSETEAVYGMTFKILCISCKRRSETTAETFTETWFRQKGT 64

Query: 70 KDFL-IYEYRNGHQEVESP--FQGR LQWNGS---

KDLQDV SITVLNVTLNDSGLYTCNVS 123

++F+ I Y N ++E F+GR+ WNGS KDLQD+SI + NVT N

SG Y C+V

Sbjct: 65

EEFVKILRYENEVLQLEEDERFEGRVVWNGSRGTD LQDLSIFITNVTYNHSGDYQCHVY 124

Query: 124

REFEFEAHRPFVKTTTRLIPLRVTEEAGEDFTSVVSEIMMYIXXXXXXXXXXXIEMIYCYRK 183

R FE + + I L V ++A D S+VSEIMMY+

EM+YCY+K

Sbjct: 125

RLLSFENYEHNTSVVKKIHLEVVDKANRDMASIVSEIMMYVLIVVLTIIWLVAEMVYCYKK 184

Query: 184 VSKAEAAA-QENASDYLAIPSENKEN-SAVPVEE 215

++ A EAA QENAS+YLAI SE+KEN + V V E

Sbjct: 185 IAAATEAAAQENASEYLAITSESKENCTGVQVAE 218

Pedant information for DKFZphamy2\_2f18, frame 3

Report for DKFZphamy2\_2f18.3

[[LENGTH]] 215

[[MW]] 24702.40

[[pI]] 4.69

[[HOMOL]] PIR:JC4788 sodium channel protein beta1 chain -  
rabbit 3e-41

[[BLOCKS]] BL004010 Prokaryotic sulfate-binding proteins

[[BLOCKS]] BP00570

```

[SCOP]      d]neu__ 2.1.1.1.1 Myelin membrane adhesion
molecule PD [ra 2e-43
[PIRKW]      Schwann cell 2e-07
[PIRKW]      transmembrane protein 1e-40
5 [PIRKW]      myelin 2e-07
[PIRKW]      phosphoprotein 5e-07
[PIRKW]      glycoprotein 1e-40
[PIRKW]      structural protein 2e-07
[PIRKW]      muscle 1e-40
10 [PIRKW]      membrane protein 5e-07
[USPFAM]     immunoglobulin homology 2e-07
[USPFAM]     myelin PD protein 2e-07
[PFAM]       IG (immunoglobulin) superfamily
[KW]         All_Beta
15 [KW]         3D
[KW]         SIGNAL_PEPTIDE 23
[KW]         LOW_COMPLEXITY      4.65 %

20 SEQ  MPAFNRLFPLASLVLIYWVSVCFPVCEVPSETEAVQGNPMKLCISCMKREEVEATTVV
SEG  .....
]neu- .....CEEEECCEEETTTbCEEECE-
EEEECCCCCCCCCEE

25 SEQ  EWFYRPEGGKDFLIYEYRNGHQEVESPFQGRLOWNGSKDLQDV SITVLNVTLNDSGLYTC
SEG  .....
]neu- .....
EEEEEEETTTCCCEEEEEETTEEEETTTTTTTEEECCBGGGCBCEEECCbTTTTTEEEEE

30 SEQ  NVSREFEFEAHRPFVKTTRLIPLRVTEEAGEDFTSVVSEIMMYILLVFLTLWLLIEMIYC
SEG  .....xxxxxxxxxxxx.....
]neu- .....
EE.....

35 SEQ  YRKVSKAEAAQENASDYLAIPSENKENSAPVVEE
SEG  .....
]neu- .....

40 (No Prosite data available for DKFZphamy2_2f18.3)

```

## Pfam for DKFZphamy2\_2f18.3

```

45 HMM_NAME  IG (immunoglobulin) superfamily

HMM
*yrNgqpipssegyWytRweqqgRYsisifqLtIisWepeDsGtYWCMV*
50 YRNG ++ E+ ++ R++++G ++ +++T+ +++ +DSG
Y+C+V
Query      77 YRNGHQEV--
ESPFQGRLOWNGSKDLQDV SITVLNVTLNDSGLYTCNV      122

55

```

DKFZphamy2\_2f22

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5 group: nucleic acid management

DKFZphamy2\_2f22 encodes a novel 479 amino acid protein with similarity to YDL153c of *Saccharomyces cerevisia*.

10 The novel protein is ubiquitously expressed. YDL153c is involved in transcriptional silencing.

The new protein can find application in modulation of transcription, e.g. transcriptional silencing.

15

putative protein

probably complete cds.

20 perhaps differential polyadenylation  
YDL153c is involved in transcriptional silencing

Sequenced by MediGenomix

25 Locus: /map="4"

Insert length: 2019 bp

Poly A stretch at pos. 2000, polyadenylation signal at pos. 1981

30

```

1  GGAGTCTGCA  AACTCCGGTG  GTAGGGGAGC  GCGCTGCTGT  TTAGAGCCAC
51  GAGTTACCGG  AGCGCCTGAT  TCCTGCGCCG  AAGTCAGTGG  TGGCCGAAAG
101  TCCGGAGTCC  CTGTAAAACC  TGAGATTGTG  AGCCATGGTG  GGGAGATCCC
151  GGC GGCGCGG  AGCAGCTAAG  TGGGCAGCTG  TGC GAGCCAA  GGCAGGTCCC
35  201  ACGCTCACC  ACGAAAATGG  AGATGATTTA  GGATTGCCAC  CCTCACCAGG
251  GGACACCAGC  TACTACCAAG  ATCAGGTAGA  TGACTTTCAT  GAGGCACGAT
301  CCCGGGCCGC  CTTAGCTAAG  GGCTGGAATG  AAGTACAGAG  TGGAGACGAG
351  GAGGATGGCG  AGGAGGAGGA  GGAGGAGGTG  CTAGCCCTAG  ATATGGACGA
401  TGAGGACGAC  GAAGATGGAG  GGAATGCGGG  GGAGGAGGAG  GAGGCAGAGA
40  451  ATGCCGATGA  TGATGGTGGG  AGCTCCGTGC  AAAGTGAAGC  TGAGGCCTCT
501  GTGGATCCCA  GTTTGTCGTG  GGGTCAGAGG  AAAAACTTT  ACTATGACAC
551  GGA CTATGGT  TCCAAGTCCC  GAGGCCGGCA  GAGTCAACAG  GAGGCAGAGG
601  AGGAGGAAAG  AGAGGAGGAG  GAGGAGGCAC  AGATCATTCA  GCGGCGCCTA
651  GCCCAAGCGC  TGCAAGAGGA  TGATTTTGGT  GTCGCCTGGG  TTGAGGCCTT
45  701  TGCAAAACCA  GTGCCTCAGG  TAGATGAGGC  TGAGACACGG  GTCGTGAAGG
751  ATTTGGCTAA  AGTTTCAGTG  AAAGAGAAGC  TGAAAATGTT  GCGAAAGGAA
801  TCACCAGAAC  TCTTGGAGCT  GATAGAAGAC  CTGAAAGTCA  AGTTGACAGA
851  GGT TAAGGAT  GAGCTGGAGC  CATTGTTAGA  GTTGGTGGAA  CAAGGGATCA
901  TTCCACCCGG  AAAAGGAAGC  CAATACTTGA  GGACCAAGTA  CAACCTCTAC
50  951  TTGAATTATT  GCTCGAACAT  CAGTTTTTAT  TTGATCCTGA  AAGCTAGGAG
1001  AGTCCCAGCA  CATGGACATC  CTGTCATAGA  AAGGCTTGTT  ACCTACCGAA
1051  ATTTGATCAA  CAAGCTGTCC  GTTGTGGATC  AGAAGCTGTC  CTCAGAAATT
1101  CGTCATCTGT  TGACACTTAA  GGATGATGCT  GTAAAGAAAG  AACTGATTCC
1151  AAAAGCAAAA  TCCACCAAGC  CCAAACCAAA  GTCTGTTTCA  AAGACTTCTG
55  1201  CTGCTGCCTG  TGCTGTTACA  GATCTTTCTG  ATGATTCTGA  TTTTGTATGAA
1251  AAAGCAAAAC  TGAAGTACTA  TAAAGAAATA  GAAGACAGGC  AAAAGCTAAA
1301  GAGAAAGAAA  GAAGAAAATA  GCACTGAAGA  ACAGGCTCTT  GAAGATCAAA
1351  ATGCAAAGAG  AGCTATTACC  TATCAAATTG  CTA AAAATAG  GGGACTTACT

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1401 CCTAGGAGAA AGAAGATTGA TCGCAATCCC AGAGTGAAAC ACAGAGAGAA
1451 GTTCAGAAGA GCCAAAATTA GAAGAAGAGG CCAGGTTTCGT GAAGTTCGTA
1501 AAGAAGAGCA ACGTTATAGT GGTGAATTAT CTGGCATTCTG TGCAGGAGTT
1551 AAAAAGAGCA TTAAGCTTAA ATGAAGTTTT TGCTTAGCAT AAGGTTTTTG
5 1601 GCAGTTTTGG ATCAATAAAT TTTTACTTTT AACTAAAGTC ATTGTATTAA
1651 TATATAATAC TTTAAATTTT AAAAATTCTT GTCCACAAGG AAATTTGTCT
1701 GGGTTATTGG ACAATTTATA AGAACTATGG GAGCAATATG AAGGTGCTTG
1751 AGAAAAGAGA TGATGTTGAA GTTTTCCAAT ATTCTGTTGA AGTTTTCCAA
1801 TATTAAGTAT TAGCTTAGGG AAATTTTACA GTTCATTGTG GAGTGTTAAA
10 1851 CTTAGAACAT GTGTAACCTT TCACATAAAG AGAATGCATC TTTGACAGTT
1901 ATCTTATTTG TAAGGCAGCC TATAAAATAG TTCTGAAGTA TTTTATTTAC
1951 CTAACATAAA TTATTGGGCC AGATACTTGT TAATAAATGG GCTTAATGTC
2001 AAAAAAAAAA AAAAAAAAAA

```

15

## BLAST Results

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No BLAST result

20

## Medline entries

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25 No Medline entry

## Peptide information for frame 3

30

ORF from 135 bp to 1571 bp; peptide length: 479

Category: similarity to unknown protein

Classification: Nucleic acid management

35

```

1 MVGRSRRRGÁ AKWAAVRAKA GPTLTDENGÐ DLGLPPSPGÐ TSYYQÐQVDD
51 FHEARSRAAL AKGWNEVQSG DEEDGEEEE EVLALDMÐDE DDEDGGNAGE
101 EEEEEENADDD GGSSVQSEAE ASVDPSLSWG QRKKLYYÐTD YGSKSRGRQÐS
151 QQEAEEEEERE EEEEAQIIQR RLAQALQEDD FGVAVVEAFA KPVPQVDEAE
40 201 TRVVKÐLAKV SVKEKLMRLR KESPELLELI EDLKVKLTEV KÐELEPLLEL
251 VEQGIIPPCK GSQYLRTKYN LYLNYCSNIS FYLILKARRV PAHGHPVIER
301 LVTYRNLINK LSVVDQKLSS EIRHLLTLKD ÐAVKKELIPK AKSTKPKPKS
351 VSKTSAAACA VTDLSÐÐSDF ÐEKAKLKYYK EIEDRQKLKR KKEENSTEEQ
401 ALEDQNAKRA ITYQIAKNRG LTPRRKKIDR NPRVKHREKF RRAKIRRRGQ
45 451 VREVRKEEQR YSGELSGIRA GVKKSIKIK

```

## BLASTP hits

50

No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_2f22, frame 3

55 PIR:S67701 hypothetical protein YDL153c - yeast (*Saccharomyces cerevisiae*), N = 4, Score = 134, P = 1.8e-08

PIR:T08694 hypothetical protein DKFZp5640092.1 - human  
(fragment), N =  
1, Score = 141, P = 5.8e-07

5 TREMBL:SPBC3B8\_9 gene: "SPBC3B8.09"; product: "hypothetical  
protein";  
S.pombe chromosome II cosmid c3B8., N = 2, Score = 164, P = 6.2e-  
13

10 >TREMBL:SPBC3B8\_9 gene: "SPBC3B8.09"; product: "hypothetical  
protein";  
S.pombe chromosome II cosmid c3B8.  
Length = 597

15 HSPs:

Score = 164 (24.6 bits), Expect = 6.2e-13, Sum P(2) = 6.2e-13  
Identities = 44/126 (34%), Positives = 68/126 (53%)

20 Query: 367 DSDFDKAKLKYYKEIEDRQKLKRK-KEEN-----STEEQALE-  
DQNAKRAITYQ 414  
D + +++ L YY+ ++ + K+ +K ++EN S + +E +

KR IT  
25 Sbjct: 472  
DREVEDQDDLDDYYESLDKSKMAKKLRKENHDLERDLIRASRHP ELIELGEGDKRGITLD 531

Query: 415 IAKNRGLTPRRKKIDRNPRVKHXXXXXXXXXXXXGQVREVRKEEQR-  
YSGELSGIRAGVK 473  
30 IAKNRGLTPRR K +RNPR+K + + Q Y+GE  
+GI+AG+  
Sbjct: 532  
IAKNRGLTPRRPKENRNPRLLKRMRYEKAKKKLASKKAIYKGAPQGGYAGEQTGIKAGLV 591

35 Query: 474 KSIKLL 479  
KSIKL+  
Sbjct: 592 KSIKLL 597

Score = 80 (12.0 bits), Expect = 6.2e-13, Sum P(2) = 6.2e-13  
40 Identities = 29/129 (22%), Positives = 66/129 (51%)

Query: 197 DEAE TRVVK-DLAKVSVKEKLLKMLRKESP--ELLELIE----  
DLKVKL TEVKDELEPLLE 249  
D ++ + +K D + +++E ++ + + P ELL+++E + ++ L E+  
45 ++L+P L  
Sbjct: 173 DNSDLKSIKQDSSAAAIEELVQQISPDLPRTTELLKILEAKHPEFQLFLDEL-  
NQLKPQLN 231

Query: 250 LVEQGIIPP GKG S QYLR TKYNLYLNYCSNISFYL-  
50 ILKARRVPAHGHPVIERLV TYRNL I 308  
+++ + SQ L+ + Y S ++FY +LK HP++  
LV +  
Sbjct: 232 EIKEKL-  
KTPSSQLLQAACTALSTYISFLTIFYFALLKDGEEDLKNHPIMVDLVRCKQ TW 290

55 Query: 309 NKLSVVDQKLS 319  
+D+ L+  
Sbjct: 291 ESYCGLDEVLT 301

Score = 59 (8.9 bits), Expect = 9.2e-11, Sum P(2) = 9.2e-11  
Identities = 18/59 (30%), Positives = 35/59 (59%)

5 Query: 196 VDEAETRVVKDLAKVSVKEKLMRLKESPEL---  
LELIEDLKVKLTEVKDELE--PLLEL 250  
++E ++ DL + E LK+L + PE L+ + LK +L  
E+K++L+ P +L

Sbjct: 189 IEELVQQISPDLPR---  
10 ELLKILEAKHPEFQFLDELNQLKPQLNEIKEKLTYPSSQL 245

Query: 251 VE 252

++

Sbjct: 246 LQ 247

15 Score = 57 (8.6 bits), Expect = 3.0e-01, Sum P(2) = 2.6e-01  
Identities = 13/58 (22%), Positives = 26/58 (44%)

20 Query: 367 DSDFDKAKLKYYKEIEDRQKLKRK--  
KEENSTEEQALEQNAKRAITYQIAKNRGLT 422  
D + +++ L YY+ ++ + K+ +K KE + E + I  
RG+T  
Sbjct: 472  
DREVEDQDDLDDYYESLDKKSMAKKLRKENHDLERDLIRASRHPLELIEGEGDKRGIT 529

25 Score = 42 (6.3 bits), Expect = 5.2e-09, Sum P(2) = 5.2e-09  
Identities = 13/51 (25%), Positives = 29/51 (56%)

30 Query: 199 AETRVVKDLAKVSVKEKLMRLKESPE--  
LLELIEDLKVKLTEVKDELEPLLE 249  
+ET + D+++ + LK ++++S + EL++ + L + EL  
+LE

Sbjct: 160 SETDAIDDISQWADNSDLKSIKQDSSAAAIEELVQQISPDLP--  
35 RTELLKILE 210

Score = 39 (5.9 bits), Expect = 1.1e-08, Sum P(2) = 1.1e-08  
Identities = 8/18 (44%), Positives = 11/18 (61%)

40 Query: 43 YYQDQVDDFHEARSRAAL 60  
+Y +Q+D RSRA L  
Sbjct: 402 FYANQIDQKAAKRSRAVL 419

45 Pedant information for DKFZphamy2\_2f22, frame 3  
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### Report for DKFZphamy2\_2f22.3

50 [LENGTH] 479  
[MW] 54558.00  
[pI] 5.50  
[HOMOL] TREMBL:SPBC388\_9 gene: "SPBC388.09"; product:  
"hypothetical protein"; S.pombe chromosome II cosmid c388. 1e-10  
55 [FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae,  
YDL153c] 1e-08  
[BLOCKS] PRO0528  
[BLOCKS] BL00360C Ribosomal protein S9 proteins

55

(No Prosite data available for DKFZphamy2\_2f22.3)

(No Pfam data available for DKFZphamy2\_2f22.3)

5

5 group: nucleic acid management

DKFZphamy2\_2g12 encodes a novel 191 amino acid protein with similarity to NVL-2 of *Rattus norvegicus*.

10 The novel protein contains 3 EF-hand calcium-binding domains. The related human VILIP Ca-dependent protein specifically binds the 3'-untranslated region of the neurotrophin receptor, trkB, an mRNA localized to hippocampal dendrites in an activity-dependent manner. The new protein exhibits elevated expression in brain  
15 and testis.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

20

strong similarity to NVL-2 (*Rattus norvegicus*)

Comment for P35332:

25 FUNCTION: MAY BE INVOLVED IN THE CALCIUM-DEPENDENT REGULATION OF RHODOPSIN PHOSPHORYLATION.  
TISSUE SPECIFICITY: NEURON-SPECIFIC IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEM.  
MISCELLANEOUS: PROBABLY BINDS TWO OR THREE CALCIUM IONS (BY  
30 SIMILARITY)  
SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BELONGS TO THE RECOVERIN SUBFAMILY.

35 Sequenced by MediGenomix

Locus: /chromosome="1"

Insert length: 4285 bp

40 Poly A stretch at pos. 4258, polyadenylation signal at pos. 4247

```

      1 GCGGGCTCCG GCGCAGACCT TGGAGAGCAC AGCTGCCGGC CCGCGAGCCA
      51 GCCTCGGTTC CCGCGGCCCG CCGAGGCTCG GAGCCATCCA GCGACCCGGC
45    101 GACCGGCCTC AGGCCCCGCC ATGGGGAAGA CCAACAGCAA GCTGGCCCCC
      151 GAGGTGCTGG AGGACCTTGT TCAGAACACT GAGTTCAGCG AGCAGGAGCT
      201 GAAGCAGTGG TACAAGGGCT TCCTGAAGGA CTGCCCCAGC GGCATCCTCA
      251 ACCTGGAGGA GTTTCAGCAG CTCTACATCA AGTTCTTCCC CTACGGCGAC
      301 GCCTCCAAGT TCGCGCAGCA CGCTTTCGCG ACCTTCGACA AGAACGGCGA
50    351 CGGCACCATC GACTTCCGGG AGTTCATCTG CGCCCTGTCT GTCACCTCCC
      401 GCGGCAGCTT CGAGCAGAAG CTCAACTGGG CCTTTGAGAT GTACGACCTG
      451 GACGGCGACG GCGGAATCAC GCGCCTGGAG ATGCTGGAGA TCATCGAGGC
      501 AATCTACAAG ATGGTGGGCA CCGTGATCAT GATGCGCATG AACCAGGACG
      551 GGCTCACGCC CCAGCAGCGT GTGGACAAGA TCTTCAAGAA GATGGACCAG
55    601 GATAAGGACG ACCAGATTAC ATTGGAGGAG TTCAAGGAGG CAGCCAAGAG
      651 TGACCCATCC ATTGTGTTGC TGCTGCAGTG TGACATGCAG AAGTAGAAGC
      701 TGGTGAGGGG CAGGGTCCCT GGCCAGAAGG GGCATGGCCA CCTCCCAACC
      751 TGATGACCTC TCTGGCTGGC CTCCCAGGAG GAGGGACACT CCAGCCCCCC
```

	801	TCTCTGGCCC	ACCCAGTCCT	CTGCCCAAGC	CCTTCCTCCC	CTCCATCAAG
	851	ATCTTTGAGG	GACCACCTCA	CCCTGCAAAA	GAGACAGGTC	CTCCAGTACC
	901	CTGTCTTCTA	GCCCCACCTC	CCACTTGGCC	AGAACCAATG	TCCATTGGGC
	951	ATAGGGGAGT	TGGCTTTTGC	CCCAGGAGGT	GAGGTAAAGG	AGTTGGGGGC
5	1001	CTGGGGTTCT	GGTTAGGAAT	TCTCTTGATC	CTGGGATTAT	GCTTTATAGG
	1051	ATGTGGTCCC	ACAGGCCTGT	CACAGGGCCA	AATTGGGTCT	GTCCATTCTT
	1101	GAGGCTCCAG	ATCCCATAAA	GGGGGTCTCT	TCCCCATCCC	TTCTACTCTA
	1151	CCTGGCCCTT	CCAGCCCCAG	CCTTTGGAGC	GTTCAATTCAG	TCCTTTCTTC
	1201	AGCTAATGAT	TACTGAGCAC	CTGTTTGGTG	CTAAGGATAT	GGTCATTTAC
10	1251	AAGACACATC	TTGTGCCCTC	TGAAGCTCA	TAGGGTTGTG	AGGCAAACCT
	1301	CCAGCCGTCA	GGGTCTCAGC	TAGCAGAAG	GTGCTGGAAG	GCTGGTTAGT
	1351	CTGGGAGGAG	CTATTTTCATC	TTCCAGCTCA	GCTCCACACA	AAGCTGCAGA
	1401	AGGACGAAAT	GAAAAGCATT	TGGAAGTTTA	GGAGCCACGT	GAGTGAAAGT
	1451	TTTAAGAAAA	ATGAAATTTA	TGTCATACTT	ATTTTTTTAG	TACCCTTTAA
15	1501	AGGAGCTACA	GTCATTTTAT	TATTTTCAGGA	GGTTAAAATA	TACTCTATAT
	1551	TACTTGGTTT	ATTATAAAAT	GATTAAATGA	ATAGAGAAAA	TATTAATTTT
	1601	CAAGGGGAAA	AAACCTGAGA	AGAAAGGGAG	AAAAGACCAT	GAAATTTACC
	1651	AGATAACACT	TTTTAAGACT	AAGTCCTGAG	CTGCCACTCT	CAGCAGTTTT
	1701	TGCTGCTTCA	GCTCTTCTCT	TTTATTACCT	TTTTCAATTC	AACAAGCAAC
20	1751	TTTCTGCTAC	ATACTTACTC	CGGTGGGTG	CTGACTTCAG	GGACAGGAAA
	1801	AAGCAAGGTT	TGCAAAGAGT	GAAACTAGTG	TATATTCCGT	ATCTTGGTAG
	1851	TTCTGTTCTG	GATTGGGTTT	AGTTTCAGAA	CTGGACTTGT	TCCTTCACTG
	1901	CCACAGAATC	AGAAAGAGCT	AGAAGAAAAG	GCTCACCTGG	CCACTGTTTA
	1951	GGCACCCAGA	CATAATTTAT	GGACGAAATG	CCTAAAAATG	TGCCAGGCAT
25	2001	GCTCTGTTTG	AGAGGCTTTT	TCTAACCCCA	AATCTTAGAT	CTGCCAGGTA
	2051	GTTCAACATC	TTCCAAGTGT	GCTGGTTCTG	CTTTCCAATG	CCTGCTTCCC
	2101	AATTTTGGAT	CCATGAGCTA	TACAGCTGCA	TGCTTTGACT	GCCGGAAAAA
	2151	TTAATCTTGC	TTCTTCATCA	GGTCTTTCTC	CTGTACTTGT	GATCAGAAAT
	2201	TACCTTTGAC	GTGCAGTGAC	AGTTGATTTT	CTCTTGAAC	GCCGGTGAAA
30	2251	ACAGTCTAGT	ACACAGGTGC	TGTCAGCCCA	GGGTGGGAGC	AGGAAATGAT
	2301	TGCTGAGCCC	GGGGCAGGGG	AATTGCATCT	GCAGGAAAGA	GATGCAGCAT
	2351	GCTCCTCACT	CCTGAGTGCC	CACCTGTCTT	GCTTCTCTGC	AGGTGAAAAC
	2401	TCTGGGGGAT	GCTGATCAAT	AGAGCTTGGT	CCCAAGCTCT	ACTGGGCCCT
	2451	TGGAGGTAGC	AAGGCCACTG	GGTTGCTATC	CTCTTGATGG	GGATAGCAAC
35	2501	CACTGGTTTG	CAACCCTGCT	GTTGCTATCC	TTTTGCTATC	CTCTTGCTCA
	2551	TGACCAGCCA	TATGGTGAGG	CTGGGGAGTT	CACATCCTCA	GGCAGGAACT
	2601	AGCAGTTGTT	TATCCAGCAA	TGCCTCAAGG	ATGTTGCATT	GCTCCCAGGA
	2651	GCTGGCTATT	AGGTATGTCT	TGTGCGGTCA	GTCAGCATCA	CAGACACATA
	2701	GATGCTCACC	AGCCTGGCTT	AGCTGGGACC	TAAATCTTCT	GGTGAAAAGC
40	2751	TTTTCACTAA	GTGAGGTTCC	TTCCCTGCAA	ATGCTGAATC	TAGCCTAATT
	2801	CGCAACCACA	CAGAATTTCA	TGGCTTTCAA	AGGCTTGCCA	TGTGCCCCAT
	2851	CTCATTTCTAT	ACTCACATCC	CATGGAGGTG	AGGATTTTCA	CTTCTTTTCT
	2901	CTAGACTTGG	AAGCTGAGAT	TCAGAGAGGA	AGCATCCCTT	GTGCAAGATC
	2951	ACATAGTCAG	GAGGTGACAC	AGGGCTAAGA	CTTGAACCAA	GGCTCTAAGA
45	3001	GGATTTCTTC	TTTTTCAGAGT	CTCTTCCCTG	TCCATTTCTG	TGACTAAGCT
	3051	GTGCAGAGGT	TGACAGCAGG	GCAAGTTACA	TTGATATTCA	TCCTTTATAG
	3101	GCTTCTCTGT	AAAAAGCTTC	TGAGATTGTG	GTCTTCCAAA	AAAAATAGGA
	3151	GCTTGGTTGA	AGTCCCCACA	TTTTCAAGCA	CTCAGTGTTT	TGCCTCTGGC
	3201	AGCTGTGCTA	ACAGCTCAGT	GCTGTCTCTG	GAGTCTCTG	ACTCAGAAAC
50	3251	CTCGAAGCAT	CCTGCATTGT	CTTTACCCAC	CATCATCGTC	ACTAAGAGAA
	3301	ACATGCCTAC	CCATGAAGGC	GTGTTTGATT	ACTCCAGGCT	TCTGGACACA
	3351	CATACCCATG	GGTGATTTTT	GCTCCTCAGG	CCCAATATTC	TCAGACAGCC
	3401	CAGCAGTGTG	AACACACAAT	GCCAGGCCAG	GAAGTGGGAC	CACCATCTTG
	3451	CTGATGGAAG	GAACAACAGG	TGGCCCAGGA	CATGCTCCTG	CATACTCCTG
55	3501	GGTGTCCCAG	GGACTGTGTG	CTCAGGAGCA	CTGTGGTAGA	GCACTGGCCC
	3551	TGCCTTGAGA	AGAGACACAG	GTCTCCCGTC	CCTGCACCAG	CTGAGAGAGA
	3601	CTTGCCACAA	AGCACAAAGG	TGGCAGAGAT	TTATGTATGA	CTTGACACAGA
	3651	CACAAAAATA	TACAGACAAT	CAAAACATTG	ATATATTCAA	ACTCTCCTTT

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3701 AAATTCCAAT CTTATTGCAA CAACTCTGTG AATTGCAAGG TCCCAGAATC
3751 TGCCTTCTCA CATACTCTAC CCTCATTCAT CCTTTTGGGC TAATTGATGA
3801 GCATCTTATT TCTTATCTCT AAAAATTATC AGCAAAGGCT ACTTCAGATG
3851 GCCACTTTAG TCCTTTCAGC TGTAAGTCAGG ATTATTTAAC TTACCTGTAT
5 3901 ATCAAAAAGTG AAGAAAAAGT TAGTTCATAA GTAAAGGCAC TAAATCCTTT
3951 CCTGACAATG GCAGAGTCTC TAGAGGTAGA AATTTGCCCTT GCTGCAGAGA
4001 GAGAAGGAAT GCGGTGGGAT GGGGGAAAGA AAAGAAAGAG AAGAAGAGAA
4051 GAAGCTGGGG TCTCCAGGCA GGGTAGTAAG CTGACACTAA ATATTTTTTA
4101 CACAAAAATG TATTGAAGCA ACAAATATTT CCTGAAGATC CACCCTGGGT
10 4151 GAGGCTTTGA GCTGACTTTA GAGATCACTG TGGGGTCAAG AATGTCTTAC
4201 ATGTTTTTATT CATCATTCCTT GAAAAAAGAA ATAATTCAAA CCTTGGAATT
4251 AAAAAGTCAG AAAAACAAAA AAAAAAAAAA AAAAA

```

# 15 BLAST Results

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No BLAST result

# 20 Medline entries

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93367470:
25 Kajimoto Y, Shirai Y, Mukai H, Kuno T, Tanaka C.; Molecular
   cloning of
   two additional members of the neural
   visinin-like Ca(2+)-binding protein gene family. J Neurochem 1993
   Sep;61(3):1091-6
30 96079121:
   Polymeropoulos M.H., Ide S., Soares M.B., Lennon G.G.; Sequence
   characterization and genetic mapping of the human VSNL1 gene, a
   homologue of the rat visinin-like peptide RNVP1. Genomics
35 29(1):273-275(1995).

```

# 40 Peptide information for frame 1

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```

ORF from 121 bp to 693 bp; peptide length: 191
Category: strong similarity to known protein
45 Classification: Protein management
   Prosite motifs: EF_HAND (73-85)
   EF_HAND (109-121)
   EF_HAND (159-171)

```

```

50 1 MGKTNSKLAP EVLEDLVQNT EFSEQELKQW YKGFLKDCPS GILNLEEFQQ
   51 LYIKFFPYGD ASKFAQHAFR TFDKNGDGTI DFREFICALS VTSRGSFEQK
   101 LNWAFEMYDL DGDGRITRLE MLEIEAIYK MVGTVIMMRM NQDGLTPQQR
55 151 VDKIFKKMDQ DKDDQITLEE FKEAAKSDPS IVLLLQCDMQ K

```

BLASTP hits



No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_2g12, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphamy2\_2g12, frame 1

Report for DKFZphamy2\_2g12.1

15 [LENGTH] 231  
 [MW] 26277.92  
 [pI] 5.26  
 [HOMOL] PIR:JH0815 neural visinin-like Ca<sup>2+</sup>-binding  
 protein-type 2 - rat 1e-107  
 20 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae,  
 YDR373w] 3e-52  
 [FUNCAT] 03.01 cell growth [S. cerevisiae, YKL190w] 3e-18  
 [FUNCAT] 03.07 pheromone response, mating-type determination,  
 sex-specific proteins [S. cerevisiae, YKL190w] 3e-18  
 [FUNCAT] 13.04 homeostasis of other ions [S. cerevisiae,  
 25 YKL190w] 3e-18  
 [FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae,  
 YKL190w] 3e-18  
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae,  
 YKL190w] 3e-18  
 30 [FUNCAT] 11.01 stress response [S. cerevisiae, YGR100w] 7e-04  
 [BLOCKS] BL00303B S-100/ICaBP type calcium binding protein  
 [BLOCKS] BL00018  
 [BLOCKS] PR00450G  
 [BLOCKS] PR00450F  
 35 [BLOCKS] PR00450E  
 [BLOCKS] PR00450D  
 [BLOCKS] PR00450C  
 [BLOCKS] PR00450B  
 [BLOCKS] PR00450A  
 40 [SCOP] dlosa\_ 1.37.1.5.13 Calmodulin [(Paramecium  
 tetraurelia) 8e-25  
 [SCOP] dlrec\_ 1.37.1.5.21 Recoverin [bovine (Bos  
 taurus) 1e-72  
 [SCOP] dla4pa\_ 1.37.1.2.5 Calcyclin (S100) [Human (Homo  
 45 sapiens), P1 7e-05  
 [SCOP] dlrrro\_ 1.37.1.4.1 Oncomodulin [rat (Rattus  
 norvegicus) 2e-17  
 [SCOP] dlsyma\_ 1.37.1.2.2 Calcyclin (S100) [rat (Rattus  
 norvegicus) 9e-14  
 50 [SCOP] d4icb\_ 1.37.1.1.1 Calbindin D9K [bovine (Bos  
 taurus) 2e-18  
 [SCOP] dlauib\_ 1.37.1.5.19 Calcineurin regulatory subunit  
 (B-chain 1e-45  
 [PIRKW] blocked amino end 1e-99  
 55 [PIRKW] phosphotransferase 3e-08  
 [PIRKW] duplication 7e-17  
 [PIRKW] tandem repeat 7e-06  
 [PIRKW] heterodimer 7e-17

-189-

Query 104 FAQHAFRTFDKNGDGTIDFREFICALSVT 132

27.15 140 168 1 29 dkfzphamy2\_2g12.1 strong  
similarity to NVL-2 (Rattus norvegicus)

5 Alignment to HMM consensus:

Query \*EIqEMFrMMDkDGDGyIDFEEFmeMMkem\*  
++++F+M+D DGDG+I+ E++E++ ++

dkfzphamy2 140 KLNWAFEMYDLDDGRITRLEMLEIIIEAI 168

10 Query 218 1 29 dkfzphamy2\_2g12.1 strong  
similarity to NVL-2 (Rattus norvegicus)

Alignment to HMM consensus:

HMM \*EIqEMFrMMDkDGDGyIDFEEFmeMMkem\*  
++++F++MD+D+D +I+ EEf+E+ K+

15 Query 190 RVDKIFKKMDQDKDDQITLLEEFKEAAKSD 218

DKFZphamy2\_2i17

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5 group: amygdala derived

DKFZphamy2\_2i17 encodes a novel 462 amino acid protein without similarity to known proteins.

10 Most ESTs are derived from brain and pancreas.  
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

15 The new protein can find application in studying the expression profile of amygdala-specific genes.

unknown protein

20 perhaps complete cds.

Sequenced by MediGenomix

Locus: unknown

25

Insert length: 3473 bp

Poly A stretch at pos. 3454, polyadenylation signal at pos. 3436

```

30      1 GATATCCCAA TCTTTGGACT GCATCCTGGT TGCCTCTACT GTGGTCACCT
      51 TTGGGAAGAA ATGTCTTCTG TAAAAAGAAG TCTGAAGCAA GAAATAGTTA
     101 CTCAGTTTCA CTGTTTCAGCT GCTGAAGGAG ATATTGCCAA GTTAACAGGA
     151 ATACTCAGTC ATTCTCCATC TCTTCTCAAT GAAACTTCTG AAAATGGCTG
     201 GACTGCTTTA ATGTATGCGG CAAGGAATGG GCACCCAGAG ATAGTCCAAT
35     251 TTCTGCTTGA GAAAGGGTGT GACAGATCAA TTGTCAATAA ATCAAGGCAG
     301 ACTGCACTGG ATATTGCTGT ATTTTGGGGT TATAAGCATA TAGCTAATTT
     351 ACTAGCTACT GCTAAAGGTG GGAAGAAGCC TTGGTTCCTA ACGAATGAAG
     401 TGGAAGAATG TGAAAATTAT TTTAGCAAAA CACTACTGGA CCGGAAAAGT
     451 GAAAAGAGGA ATAATTCTGA CTGGCTGCTA GCTAAAGAAA GCCATCCAGC
40     501 CACAGTTTTT ATTCTTTTCT CAGATTTAAA TCCCTTGGTT ACTCTAGGTG
     551 GCAATAAAGA AAGTTTCCAA CAGCCAGAAG TTAGGCTTTG TCAGCTGAAC
     601 TACACAGATA TAAAGGATTA TTTGGCCCAG CCTGAGAAGA TCACCTTGAT
     651 TTTTCTTGGA GTAGAACTTG AAATAAAAGA CAAACTACTT AATTATGCTG
     701 GTGAAGTCCC GAGAGAGGAG GAAGATGGAT TGGTTGCCTG GTTTGCTCTA
45     751 GGTATAGATC CTATTGCTGC TGAAGAATTC AAGCAAAGAC ATGAAAATTG
     801 TTACTTTCTT CATCCTCCTA TGCCAGCCCT TCTGCAATTG AAAGAAAAAG
     851 AAGCTGGGGT TGTAGCTCAA GCAAGATCTG TTCTTGCCTG GCACAGTCGA
     901 TACAAGTTTT GCCCAACCTG TGGAAATGCA ACTAAAATTG AAGAAGGTGG
     951 CTATAAGAGA CTATGTTTAA AAGAAGACTG TCCTAGTCTC AATGGCGTCC
50    1001 ATAATACCTC ATACCCAAGA GTTGATCCAG TAGTAATCAT GCAAGTTATT
     1051 CATCCAGATG GGACCAAATG CCTTTTAGGC AGGCAGAAAA GATTTCCCCC
     1101 AGGCATGTTT ACTTGCTTGT CTGGATTTAT TGAGCCTGGA GAGACAATAG
     1151 AAGATGCTGT TAGGAGAGAA GTAGAAGAGG AAAGTGGAGT CAAAGTTGGC
     1201 CATGTTCAGT ATGTTGCTTG TCAACCATGG CCAATGCCTT CCTCCTTAAT
55    1251 GATTGGTTGC TTAGCTCTAG CAGTGTCTAC AGAAATTAAA GTTGACAAGA
     1301 ATGAAATAGA GGATGCCCGC TGGTTCACCTA GAGAACAGGT CCTGGATGTT
     1351 CTGACCAAAG GGAAGCAGCA GGCATTCTTT GTGCCACCAA GCCGAGCTAT
     1401 TGCACATCAA TTAATCAAAC ACTGGATTAG AATAAATCCT AATCTCTAAA

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1451 TCTAAGAACT AAGCTTTGAG TATTATTTAA TAATTTCTAA TAACACTCAT  
1501 TCCTCAAGTG ATATTAGAGA TTATTCAGTA CTCTTGAGAG TGTCAACA  
1551 CAAAATACGA TGTGGGGTTT TCGAAATATT TTCAAAGTGT TCTGTCTTAA  
1601 TCACAAATTC ATATTTTAC ACATTTTAC AATATTGCCT CAGATTATGT  
5 1651 TAAATTTGGG TCAGTCTTCT CTGAACTTTT TCTCTCTCGG TTTCTTTTCT  
1701 TCCTTCACAG TTTTATCTCA CAAAACCAT TTTCTAATAA GAGACATCAT  
1751 GTTGGAAAGA TGTGTAGAA ATGTGCATAA ATTTCAAGTGC CTCTTGTAAG  
1801 CATTAAACTG ATGATGAAGA AAGTTCCTGA TTTGAGAAAT GAATCAAAGT  
1851 AATTTTAATG AATTTTATAGC TTGTATTAGC TTGAGTTAGC TGGCATTGAT  
10 1901 TTTTTAGTCC TTTTGTACC TTTAAGTTGT CAATATATGG TTTTGTTC  
1951 TCTCCCCATT GTAGTCCAC TTGCTCTTTC CTGGGGGTTT CATTGTTCTA  
2001 GCAGTGGAGG TGTACAGTG TCGCCACTCG TCTAATTTGA CCAGTGTTAA  
2051 GAATTTTCTA ATTTAATAAT TTAATAGTGA TCTCAATACC ACACCTCAT  
2101 GGAAGGAGAA AAGCATACTA TTATATCTGG GACCTCTCTT TTAGACCTAA  
15 2151 AATTAATTA CATATCTACT TATATGTTAC TTATACCTAA AGCTGTTATT  
2201 AAGACAAACC AAGATTCTCT GCTTTTGCAC TGAAATTAAA CTTGAAAGGA  
2251 ATTCTCCTCA AAGGTCGGAT ATTAAATAAG TCCCAGGCAG ATTTACATAT  
2301 TTAATTTAAA ACATTGGCTT TATTTTCAAT TGTGATGAGT GATGTATCTG  
2351 TGTTAACAAA AAATTGTATA ATCATTACCA ATACTATTTA TTATGCTCAA  
20 2401 ATATATCTTG GCTTTGACCT TATTTCAACA CATTCTAAGA AGCCTTGACA  
2451 AAGTAAGTAT ATTTTAGAGC TGAATCAGTA AGATTCTAGA GAAAGCAAAA  
2501 CATAGTAGTT CACAATTTTG CAACATAGAA AGTCACATTT TGAAAGGCTA  
2551 TTTTGAAATT GATTTAATAG CTATTATAGT TTATGAATAT CAAAATTTGT  
2601 ATAATTTGCA TCTTTACTAA TGTATGCTAG AGCTACAAGA GACCTTAAGG  
25 2651 ATAATATATG AAATTAGCTT TCCTTATTTT ATAGATAAGG AAAAAGAAAT  
2701 TGTGAAAGGT GAATTTACCT AATTAGTGAA AGTTACATAA CTAATTACAA  
2751 CAGTCTGTAC TATATAATGC AGAGGACGAT TCTCCCTGTA AAAGGAACTA  
2801 GAAGCTATTA CTAAAAATAT ATATAGACAA AATTTAAAAGA AGGAATGATA  
2851 AGAATAAATT TAATTTACCA AATATTGTTA ATTTAAAATT TAGATACTTA  
30 2901 ACATTTATTT AACTTAAATA AAAGATAACT GTCAGATAAA ACTTTATTTT  
2951 ACTAATGAGC AGTGATTTTC TTAGGAATTG ATGAAGGCTT ATTGGTATCA  
3001 AGAATTTAAA CCAAATTAATA ACTGACAGAG GACATTTAGA TACATAATAA  
3051 AATTCGAGCT ACATAAGTAT ATGGAAAATA ATGTACCTTG ATTATTATGA  
3101 AATAGAGCAT CTTGAAATTC AGTTTTACTC TAAATGTACT TTTAATACTT  
35 3151 GCAGATTCTA AGATTACATT GTGAAATTCC AGGTTTTCAT AATGTTAAAA  
3201 TAGGAAAGTA GAATATAAAG TATCAACAAG TGATAGTTATA CATTTTGT  
3251 TGGATATTTA ATCCTTACTT GGGAAAAAAT CAGCATCTAG GTAAATTATT  
3301 ATTTTAATAA GAACTCTTAA ATTGCCAACC TCTGAGAGGT GAAAAGCTAT  
3351 GTAAATAGAA GGAATGGCCA GTTCAAAAAGA ATAGTAGAAG TGATAGTGCC  
40 3401 GTGAATGTAT TCTACTGGAA ATGAATGTAA TAATACATTA AATTTTAAA  
3451 ATCGAAAAAA AAAAAAAAAA AAA

## BLAST Results

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No BLAST result

## Medline entries

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No Medline entry

Peptide information for frame 1

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ORF from 61 bp to 1446 bp; peptide length: 462

Category: putative protein

Classification: unclassified

5 Prosite motifs: MUTT (355-374)

```

1  MSSVKRSLKQ EIVTQFHCSA AEGDIAKLTG ILSHSPSLLN ETSENGWTAL
51 MYAARNGHPE IVQFLLEKGC DRSIVNKSQR TALDIAVFWG YKHIANLLAT
10 101 AKGGKKPWFL TNEVEECENY FSKTLLDRKS EKRNSDWLL AKESHPATVF
151 ILFSDLNPLV TLGGNKESFQ QPEVRLCQLN YTDIKDYLAQ PEKITLIFLG
201 VELEIKDKLL NYAGEVPREE EDGLVAWFAL GIDPIAAEEF KQRHENCYFL
251 HPPMPALLQL KEKEAGVVAQ ARSVLAWSHR YKFCPTCGNA TKIEEGGYKR
301 LCLKEDCPSL NGVHNTSYPR VDPVVIMQVI HPDGTKCLLG RQKRFPFGMF
15 351 TLAGFIEPG ETIEDAVRRE VEEESGVKVG HVQYVACQPW PMPSSLMIGC
401 LALAVSTEIK VDKNEIEDAR WFTREQVLDV LTKGKQQAFF VPPSRAIAHQ
451 LIKHWRINP NL

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20

#### BLASTP hits

No BLASTP hits available

25

Alert BLASTP hits for DKFZphamy2\_2117, frame 1

No Alert BLASTP hits found

30

Pedant information for DKFZphamy2\_2117, frame 1

#### Report for DKFZphamy2\_2117.1

```

35 [LENGTH] 462
[MW] 52076.25
[pI] 6.38
[MOLE] TREMBL:SPBC1778_3 gene: "SPBC1778.03c"; product:
40 "conserved hypothetical protein"; S.pombe chromosome II cosmid
c1778. 1e-45
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YGL067w]
4e-34
[FUNCAT] r general function prediction [H. influenzae,
H10432 pyrophosphohydrolase] 4e-24
45 [FUNCAT] 1 genome replication, transcription, recombination and
repair [M. jannaschii, MJ1149 nucleotide pyrophosphohydrolase]
1e-04
[BLOCKS] BL00219F Anion exchangers family proteins
[BLOCKS] BL01293B
50 [BLOCKS] DM01909
[BLOCKS] PF00023A
[BLOCKS] BL00893 mutT domain proteins
[SCOP] dlawcb_ 1.91.3.1.2 GA binding protein (GABP) alpha
GA bindini 2e-35
55 [SUPFAM] hypothetical protein H10432 1e-22
[PROSITE] MUTT 1
[PFAM] Bacterial mutT protein
[PFAM] Ank repeat

```

[[KW]] Irregular  
[[KW]] 3D

5 SEQ MSSVKRSLKQEIIVTQFHCSAAEGDIAKLTGILSHSPSLLNETSENGWTALMYAARNGHPE  
lawcB .CCCTTTTCTTTCCHHHHHHHHHTTHHHHHHHHHCCCTT-  
TTEETTTTEHHHHHHHHHCCHH

10 SEQ IVQFLLEKGCDRSIVNKSRTALDIAVFUGYKHIANLLATAKGGKKPWFLTNEVEECENY  
lawcB HHHHHHHHCCTTTTCBTTTBCHHHHHHHHCCHHHHHHH.....

15 SEQ FSKTLLDRKSEKRNNSDWLLAKESH PATVFILFSDLNPLVTLGGNKESFQQPEVRLCQLN  
lawcB .....

20 SEQ YTDIKDYLAQPEKITLIFLGVELEIKDKLLNYAGEVPREEDGLVAWFALGIDPIAAEEF  
lawcB .....

25 SEQ LCLKEDCPSLNGVHNTSYPRVDPVVIMQVIHPDGTKLLGRQKRFPFGMFTCLAGFIEPG  
lawcB .....

30 SEQ ETIEDAVRREVEEESGVKVGHVQYVACQWPMPSSLMIGCLALAVSTEIKVDKNEIEDAR  
lawcB .....

35 SEQ WFTREQVLDVLTGKGQQAFFVPPSRAIAHQLIKHWIRINPNL  
lawcB .....

## Prosites for DKFZphamy2\_2117.1

40 PS00893 355->375 MUTT PD0C00695

## Pfam for DKFZphamy2\_2117.1

45

HMM\_NAME Ank repeat

50 HMM \*GyTPLHIAARyNNvEMVrILLQHGADIN\*  
G+T+L++AAR+++ E+V++LL++G D  
Query 46 GW TALMYAARNGHPEIVQFLLEKGCDS 73

55 HMM\_NAME Bacterial mutT protein

HMM  
\*ILMIqRedppnHYdtHhgdWIFPGGKIEeGETPEQCarREIWEETGI\*

```

                L++++++   +++   +
++G+IE+GET+E+++RRE++EE+G+
Query          337  CLLGRQKRF--PPG----
MFTCLAGFIEPGETIEDAVRREVEEEESGV    377

```

5



DKFZphamy2\_2013

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5 group: intracellular transport and trafficking

DKFZphamy2\_2013 encodes a novel 590 amino acid protein with high similarity to murine synaptotagmin 3.

10 The novel protein contains two C2 domains. The C2 domain is thought to be involved in calcium-dependent phospholipid binding. Synaptotagmins are essential for Ca(2+)-regulated exocytosis of neurosecretory vesicles.

15 The new protein can find application in modulating/blocking synaptic activity.

similarity to synaptotagmin 3 (Mus musculus)

20

Sequenced by MediGenomix

Locus: unknown

25 Insert length: 2731 bp

Poly A stretch at pos. 2712, polyadenylation signal at pos. 2884

```

30  1 ACTCTATGTC TCCTCTCGTT GGATTGTGAC ACCGGGAGGT CAGGGAACTC
    51 CAGGACCTTG TTCTCTGCTG GATTTCGAGC AACCAGCACA GCACGTAGGG
   101 CGTAGTTGGT GCTGGATGGA TGTTTGTGTA ATGAATGAAT GATGAATGGC
   151 TGGCACCTTG TCTGCTCATC CTAACCTCCT GTTCCTTCAT CTGTGCAGCC
   201 CTAATCTTTG TTTCTTCATC TGTCATCCCT TTTATTTGTG CATCCTCATT
   251 CTTAGCCCCCT TCACTGCCCT TCTCCATCTC TTCCTCCTTG TTCATTTGTC
   35  301 CCTGTTCTCT GTCTCTACT CCACTCATGC CCATCTCTGT CCCCTTGACT
    351 TACCCAGTCC CTGCTACTAT CTCCATCCCT AATTTCTGCC CTCTTGCTG
   401 TCTACTCCTA ATTCCTTTTC CTGTCCATC CTAATACCT GTCACCTTGT
   451 CTTTCTTCTT CGAATCTCCA TCCCTAATCC ATCTGCCCTT AATCTGTCT
   501 CCCTTTGCCC ATCTTCTCTT TTCTCGGTGT CTCTTTCCAC CTTATCTCC
   40  551 ACACCTGCCC ACCCTGCACT CCCATTCTGT TTCCCATCTG CACCCTTGCC
    601 CCATCCCTCC CACACACAGG ACCAGACGGC CACCATGTCA GGAGACTACG
    651 AGGATGACCT CTGCCGGCGG GCACTCATCC TGGTCTCGGA CCTCTGTGCG
    701 CGGGTCCGAG ATGCTGACAC CAACGACAGG TGCCAGGAGT TCAATGACCG
    751 AATCCGAGGC TATCCCCGGG GTCCAGATGC AGACATCTCC GTGAGCCTGC
   45  801 TGTGCGTCAT CGTGACATTC TGTGGCATTG TCCTTCTGGG TGTCTCTCTC
    851 TTCGTGTCCT GGAAGTTGTG CTGGGTGCCC TGGCGGGACA AGGGAGGCTC
    901 GGCAGTGGGC GGTGGCCCCC TGC GCAAAGA CTAGGCCCTT GGTGTCGGGC
    951 TGGCAGGCCCT GGTAGGCGGA GCGGGGCACC ACCTGGCGGC TGGCCTGGGT
   1001 GGCCATCCTC TGCTGGGCGG CCCACACCAC CATGCCCATG CCGCCCACCA
   50  1051 TCCACCCCTT GCTGAGCTGC TGGAGCCAGG CAGCCTGGGG GGTCTTGACA
   1101 CCCCTGAGCC CTCCTACTTG GACATGGACT CGTATCCAGA GGCTGCAGCA
   1151 GCAGCAGTGG CCGCTGGGGT CAAACCGAGC CAAACATCCC CTGAGCTGCC
   1201 CTCTGAGGGG GGAGCAGGCT CTGGGTGCTT CCTGCTGCCC CCCAGTGGTG
   1251 GGGGCTTGCC CAGTGCCCAAG TCACATCAGC AGGTCACAAG CCTGGCACCC
   55  1301 ACTACCAGGT ACCCAGCCCT GCCCCGACCC CTCACCCAGC AGACTCTGAC
   1351 CTCCAGCCG GACCCAGCA GTGAGGAGCG CCCACCTGCC CTGCCCTTAC
   1401 CCCTGCCTGG AGGCGAGGAA AAAGCCAAAC TCATTGGGCA GATTAAGCCA
   1451 GAGCTGTACC AGGGGACTGG CCCTGGTGGC CGGCGGAGCG GTGGGGGCCC

```

```

1501 AGGCTCTGGA GAGGCAGGCA CAGGGGCACC CTGTGGCCGT ATCAGCTTCG
1551 CCCTGCGGTA CCTCTATGGC TCGGACCAGC TGGTGGTGAG GATCCTGCAG
1601 GCCCTGGACC TCCCTGCCAA GGA CTCCAAC GGCTTCTCAG ACCCTACGT
1651 CAAGATCTAC CTGCTGCCTG ACCGCAAGAA AAAGTTTCAG ACCAAGGTGC
5 1701 ACAGGAAGAC CCTGAACCCC GTCTTCAATG AGACGTTTCA ATTCTCGGTG
1751 CCCCTGGCCG AGCTGGCCCA ACGCAAAC TG CACTTCAGCG TCTATGACTT
1801 TGACCGCTTC TCGCGGCACG ACCTCATCGG CCAGGTGGTG CTGGACAACC
1851 TCCTGGAGCT GGCCGAGCAG CCCCCTGACC GCGGCTCTG GAGGGACATC
1901 GTGGAGGGCG GCTCGGAAAA AGCAGATCTT GGGGAGCTCA ACTTCTCACT
10 1951 CTGCTACCTC CCCACGGCCG GCGGCTCAC CGTGACCATC ATCAAAGCCT
2001 CTAACCTCAA AGCGATGGAC CTCACTGGCT TCTCAGACCC CTACGTGAAG
2051 GCCTCCCTGA TCAGCGAGGG GCGGCTCTG AAGAAGCGGA AAACCTCCAT
2101 CAAGAAGAAC ACGCTGAACC CCACCTATAA TGAGGCGCTG GTGTTGACG
2151 TGGCCCCCGA GAGCGTGGAG AACGTGGGGC TCAGCATCGC CGTGGTGGAC
15 2201 TACGACTGCA TCGGGCACA ACGAGGTGATC GCGGTGTGCC GTGTGGGCC
2251 CGACGCTGCC GACCCGACG GCGCGAGCA CTGGGCAGAG ATGCTGGCCA
2301 ATCCCCGCAA GCGCGTGGAG CACTGGCATC AGCTAGTGGG GGAAGAACT
2351 GTGACCAGCT TCACAAAAGG CAGCAAAGGA CTATCAGAGA AAGAGAACTC
2401 CGAGTGAGGG GTCTGGCCTA GGCCCGGGAT CGGACCAGGC TCCCTCAGGA
20 2451 CCCCATCCTT TCCTGCCCCG ACCGTGAATT CATCTCCTTG AAGCCATAAC
2501 GTCCGAGCTG CTGGTGC GCGGCTGG CCCTAGGCTT CCTAACCTG
2551 GAAGCGAGAG GATGAGAGGA GGCCGCCCCA GCTCCTTCTT TCAGGGTGGG
2601 GGTCAATCAG CCTCCACTGT GTCTGTCTTT TCTTCCCTGG GGCTCCCCCT
2651 CGAGGCGAGG GGCCATGCAT GTCTGGGGGA CCCCTGCCCC CAAAAACCT
25 2701 CTGTCTGTCT CTGTCTCTTT GCTGTTTGT CAAGACTCAG TGTCCCGACC
2751 CTTGTTCTCG CCGTGAATGT CAATGGGCCA ATCCTCTCTG TCCTTTCAGA
2801 CACACACACA CCTGTGTCCA CCCCTTCTGT TCGCCACACC CTGCGTCTGG
2851 CCGGTCCCCC CACTGCTGCT GCTATCAACG CCAGAATAAA CACTCTGT
2901 GGGTCTCACT CCAAAAAAAAA AAAAAAAAAA A
30

```

## BLAST Results

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```

35 Entry MMAB893_1 from database TREMBL:
   product: "synaptotagmin 3"; Mus musculus mRNA for synaptotagmin
   3,
   complete cds.
   Score = 1814, P = 5.7e-239, identities = 362/450, positives =
40 369/450,
   frame +2

```

## Medline entries

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```

96064733:
50 Fukuda M, Kojima T, Aruga J, Niinobe M, Mikoshiba K.: Functional
   diversity of C2 domains of synaptotagmin family.
   Mutational analysis of inositol high polyphosphate binding
   domain. J
   Biol Chem 1995 Nov 3;270(44):26523-7

```

55

Peptide information for frame 2

ORF from 635 bp to 2404 bp; peptide length: 590  
 Category: strong similarity to known protein  
 5 Classification: Cell signaling/communication  
 Prosite motifs: C2\_DOMAIN\_1 (323-338)  
 C2\_DOMAIN\_1 (455-470)

```

10      1 MSGDYEDDLR RRALILVSDL CARVRDADTN DRCQEFNDRI RGYPRGPDAD
      51 ISVSLLSVIV TFCGIVLLGV SLFVSWKLCW VPWRDKGGS VGGGPLRKDL
     101 GPGVGLAGLV GGGGHHLAAG LGGHPLLGPP HHHAAHAHHP PFAELLEPGS
     151 LGGSDTPEPS YLDMDSYPEA AAAAVAAGVK PSQTSPELPS EGGAGSGLLL
     201 LPPSGGGLPS AQSHQQVTSI APTTRYPALP RPLTQQTLTS QPDPSSEERP
15     251 PALPLPLPGG EEKAKLIGQI KPELYQGTGP GGRRSGGGPG SGEAGTGAPC
     301 GRISFALRYL YGSDQLVURI LQALDLPKAD SNGFSDPYVK IYLLPDRKKK
     351 FQTKVHRKTL NPVFNETFQF SVPLAELAQR KLHFSVYDFD RFSRHDLIGQ
     401 VVLNLLLELA EQPPDRPLWR DIVEGGSEKA DLGELNFSLC YLPTAGRLTV
     451 TIIKASNLKA MDLTGFSDPY VKASLISEGR RLKKRKTSIK KNTLNPTYNE
20     501 ALVFDVAPES VENVGLSIAV VDYDCIGHNE VIGVCRVGPD AADPHGREHW
     551 AEMLANPRKP VEHWHQLVEE KTVTSFTKGS KGLSEKENSE
  
```

25 BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphamy2\_2013, frame 2

30 TREMBL:MMAB893\_1 product: "synaptotagmin 3"; Mus musculus mRNA  
 for  
 synaptotagmin 3, complete cds., N = 2, Score = 1814, P = 1.1e-239

35 >TREMBL:MMAB893\_1 product: "synaptotagmin 3"; Mus musculus mRNA  
 for  
 synaptotagmin 3, complete cds.  
 Length = 587

40 HSPs:

Score = 1814 (272.2 bits), Expect = 1.1e-239, Sum P(2) = 1.1e-239

45 Identities = 362/449 (80%), Positives = 369/449 (82%)

Query: 142 FAELLEPGSLGGSDTPEPSYLDMDSYPEXXXXXX-  
 XXGVKPSQXXXXXXXXXXXXXXXXXXXX 200

FAELLEPG LGGS+ PEPSYLDMDSYPE GVKPSQT

50 Sbjct: 143  
 FAELLEPGGLGGSELPEPSYLDMDSYPEAAVASVVAAGVKPSQTSPELPSEGGTGSGLLL 202

Query: 201  
 XXXXXXXXXXXXQSHQQVTSIAPTTRYPALPRPLTQQTLTSQPDXXXXXXXXXXXXXXXXXXXX 260  
 QSHQQVTSIAPTTRYPALPRPLTQQTLT+Q D

55 Sbjct: 203  
 LPPSGGGLPSAQSHQQVTSIAPTTRYPALPRPLTQQTLTTQADPSTEERPPALPLPLPGG 262

Query: 261  
XXKAKLIGQIKPELYQXXXXXXXXXXXXXXXXXXXXPCGRISFALRYLYGSDQLVVRI 320  
KAKLIGQIKPELYQ  
PCGRISFALRYLYGSDQLVVRI  
5 Sbjct: 263 EEKAKLIGQIKPELYQGTGPGGRRGGGSGEAGA-----  
PCGRISFALRYLYGSDQLVVRI 317

Query: 321  
10 LQALDLPKDSNGFSDPYVKIYLLPDRKKKFQTKVHRKTLNPVFNETFQFSVPLAELAQR 380  
LQALDLPKDSNGFSDPYVKIYLLPDRKKKFQTKVHRKTLNP+FNETFQFSVPLAELAQR  
Sbjct: 318  
LQALDLPKDSNGFSDPYVKIYLLPDRKKKFQTKVHRKTLNPIFNETFQFSVPLAELAQR 377

15 Query: 381  
KLHFSVYDFDRFSRHDLIGQVVLNLLLELAEQPPDRPLWRDIVEGGSEKADLGELNFSLC 440  
KLHFSVYDFDRFSRHDLIGQVVLNLLLELAEQPPDRPLWRDI+EGGSEKADLGELNFSLC  
Sbjct: 378  
20 KLHFSVYDFDRFSRHDLIGQVVLNLLLELAEQPPDRPLWRDILEGGSEKADLGELNFSLC 437

Query: 441  
YLPTAGRLTVTIKASNLKAMDLTGFSDPYVKASLISEGRRLKKRKTSIKKNTLNPTYNE 500  
25 YLPTAGRLTVTIKASNLKAMDLTGFSDPYVKASLISEGRRLKKRKTSIKKNTLNPTYNE  
Sbjct: 438  
YLPTAGRLTVTIKASNLKAMDLTGFSDPYVKASLISEGRRLKKRKTSIKKNTLNPTYNE 497

Query: 501  
30 ALVFDVAPESVENVGLSIAVVDYDCIGHNEVIGVCRVGPDAADPHGREHWAEMLANPRKP 560  
ALVFDVAPESVENVGLSIAVVDYDCIGHNEVIGVCRVGP+AADPHGREHWAEMLANPRKP  
Sbjct: 498  
35 ALVFDVAPESVENVGLSIAVVDYDCIGHNEVIGVCRVGPEAADPHGREHWAEMLANPRKP 557

Query: 561 VEHWHQLVEEKT VTSFTKGS KGLSEKENSE 590  
VEHWHQLVEEKT++SFTKG KGLSEKENSE  
Sbjct: 558 VEHWHQLVEEKT LSSFTKGG KGLSEKENSE 587

40 Score = 520 (78.0 bits), Expect = 1.1e-239, Sum P(2) = 1.1e-239  
Identities = 98/100 (98%), Positives = 99/100 (99%)

Query: 1 MSGDYEDDLCCRALILVSDLCARVRDADTNDRCQEFND-  
RIRGYPRGPDADISVSLLSVI 59  
45 MSGDYEDDLCCRALILVSDLCARVRDADTNDRCQEFN+  
RIRGYPRGPDADISVSLLSVI  
Sbjct: 1  
MSGDYEDDLCCRALILVSDLCARVRDADTNDRCQEFNELRIRGYPRGPDADISVSLLSVI 60

50 Query: 60 VTFCGIVLLGVSLFVSWKLCWVPWRDKGGSAVGGGPLRKD 99  
VTFCGIVLLGVSLFVSWKLCWVPWRDKGGSAVGGGPLRKD  
Sbjct: 61 VTFCGIVLLGVSLFVSWKLCWVPWRDKGGSAVGGGPLRKD 100

55 Pedant information for DKFZphamy2\_2013, frame 2  
-----

[LENGTH] 590  
 [MW] 63304.02  
 5 [PI] 6.16  
 [HOMOL] TREMBL:MMAB893\_1 product: "synaptotagmin 3"; Mus  
 musculus mRNA for synaptotagmin 3, complete cds. 0.0  
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YML072c]  
 6e-10  
 10 [FUNCAT] 01.06.01 lipid, fatty-acid and sterol biosynthesis  
 [S. cerevisiae, YGR170w] 7e-06  
 [FUNCAT] 30.08 organization of golgi [S. cerevisiae, YGR170w]  
 7e-06  
 [BLOCKS] BL01224A N-acetyl-gamma-glutamyl-phosphate reductase  
 15 proteins  
 [BLOCKS] BL010138 Oxysterol-binding protein family proteins  
 [BLOCKS] PF013688  
 [SCOP] d1a25a\_ 2.6.1.2.2 C2 domain from protein kinase c  
 (beta) [Ra 2e-27  
 20 [SCOP] d1rsy\_ 2.6.1.2.1 Synaptogamin I, first C2 domain  
 [Rat (Rattu 4e-43  
 [SCOP] d1rlw\_ 2.6.1.1.2 A domain from cytosolic  
 phospholipase A2 [Huma 5e-12  
 [SCOP] d1qasb2 2.6.1.1.1 Phosphoinositide-specific  
 25 phospholipase C 4e-27  
 [PIRKW] phosphotransferase 7e-15  
 [PIRKW] duplication 6e-76  
 [PIRKW] synaptic vesicle 1e-167  
 [PIRKW] phorbol ester binding 2e-14  
 30 [PIRKW] zinc 2e-14  
 [PIRKW] transmembrane protein 0.0  
 [PIRKW] serine/threonine-specific protein kinase 7e-15  
 [PIRKW] membrane trafficking 0.0  
 [PIRKW] phospholipid binding 6e-76  
 35 [PIRKW] autophosphorylation 7e-15  
 [PIRKW] ATP 7e-15  
 [PIRKW] phosphoprotein 7e-15  
 [PIRKW] glycoprotein 1e-167  
 [PIRKW] calcium binding 5e-34  
 40 [PIRKW] alternative splicing 1e-10  
 [PIRKW] dimer 1e-75  
 [PIRKW] membrane protein 1e-167  
 [PIRKW] calmodulin binding 2e-74  
 [SUPFAM] ras-specific GAP catalytic domain homology 1e-08  
 45 [SUPFAM] protein kinase C zinc-binding repeat homology 7e-15  
 [SUPFAM] protein kinase homology 7e-15  
 [SUPFAM] protein kinase C alpha 7e-15  
 [SUPFAM] HsC2 phosphatidylinositol 3-kinase 1e-09  
 [SUPFAM] synaptotagmin 0.0  
 50 [SUPFAM] PX domain homology 1e-09  
 [SUPFAM] pleckstrin repeat homology 1e-08  
 [SUPFAM] protein kinase C C2 region homology 0.0  
 [PROSITE] C2\_DOMAIN\_1 2  
 [PFAM] C2 domain  
 55 [KW] Irregular  
 [KW] 3D  
 [KW] LOW\_COMPLEXITY 20.00 %

SEQ MSGDYEDDL CRRALILVSDL CARVRDADTNDRCQEFNDRIRGYPRGPDADISVSLLSVIV  
SEG .....  
lrsy- .....  
5 .....  
  
SEQ TFCGIVLLGVSLFVSWKLCWVPWRDKGGS AVGGG PLRKDLGPGVGLAGLVGGGGHHLAAG  
SEG .....  
lrsy- .....  
10 .....  
  
SEQ LGGHP LLGGPHHHAHAHHPFAELLEPGSLGGSDTPEPSYLDMDSYPEAAAAAVAAGVK  
SEG .....  
lrsy- .....  
15 .....  
  
SEQ PSQTSPELPSEGGAGSGLLLLPPSGGGLPSAQSHQQTSLAPTTRYPALPRPLTQQTLS  
SEG .....  
lrsy- .....  
20 .....  
  
SEQ QPDPSSSEERPPALPLPLPGGEEKAKLIGQIKPELYQGTGPGGRRSGGGPGSGEAGTGAPC  
SEG .....  
lrsy- .....  
25 .....  
  
SEQ GRISFALRYLYGSDQLVVRILQALDLPKDSNGFSDPYVKIYLLPDRKKKFQTKVHRKTL  
SEG .....  
lrsy- .....  
30 CEEEEEEEEETTTTEEEEEEEEECCCCBTBBCEEEEEEEEEETTTTTECCCTTTBT  
  
SEQ NPVFNETFQFSVPLAELAQRKLHFSVYDFDRFSRHD LIGQVVL DNLELAEQPPDRPLWR  
SEG .....  
lrsy- .....  
35 TEEEEEEEEECCHHHHCCEEEEEEEECTTTTCCEEEEE.....  
  
SEQ DIVEGGSEKADLGELNFSLCYLPTAGRLTVTIKASNLKAMDLTGFSDPYVKASLISEGR  
SEG .....  
lrsy- .....  
40 .....  
  
SEQ RLKKRKTSIKKNTLNPTYNEALVFDVAPESVENVGLSIAVVDYDCIGHNEVIGVCRVGP  
SEG .....  
lrsy- .....  
45 .....  
  
SEQ AADPHGREHWAEMLANPRKPVEHWHQLVEEKT VTSFTKGSKGLSEKENSE  
SEG .....  
lrsy- .....  
50 .....

## Prosites for DKFZphamy2\_2013.2

55	PS00499	323->339	C2_DOMAIN_1	PD0C00380
	PS00499	455->471	C2_DOMAIN_1	PD0C00380

## Pfam for DKFZphamy2\_2013.2

5 HMM\_NAME C2 domain

HMM

\*LtVrIIeARNLWkMDMnGfSDPYVKVdMdPdPkDtkKWKTkTiWNNGLN  
L+VRI++A +L+++D+NGFSDPYVK++++PD+K

10 KK++TK++++ LN

Query 316 LVVRILQALDLPKDSNGFSDPYVKIYLLPDRK--  
KKFQTKVHRKT-LN 361

HMM

15 PVWNEEEFvFedIPyPdlqrkMLRFaVWDWDRFSRBDFIGHCi\*  
PV+N E+F+F +P+ +L+ + L+F+V+D+DRFSR+D+IG+++  
Query 362 PVFN-ETFQFS-VPLAELAQRKLHFSVYDFDRFSRHD LIGQVV  
402

HMM

20 \*LtVrIIeARNLWkMDMnGfSDPYVKVdMdPdPkDtkKWKTkTiWNNGLN  
LTV+II+A NL++MD +GFSDPYVK +++ +

+++KK+KT++++N+ LN

Query 448  
LTVTIKASNLKAMDLTGFSDPYVKASLISEGRRLKKRKT SIKKNT-LN 495

25

HMM

PVWNEEEFvFedIPyPdlqrkMLRFaVWDWDRFSRBDFIGHCi\*  
P++N E +VF+ ++ ++ +++ L +AV D+D++++++IG+C+  
Query 496 PTYN-EALVFD-VAPESVENVGLSIAVVDYDCIGHNEVIGVCR  
536

30

DKFZphamy2\_7j5

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group: differentiation/development

5

DKFZphamy2\_7j5 encodes a novel 693 amino acid protein with similarity to Tspyl1 testis-specific Y-encoded-like protein of *Mus musculus*.

10

TSPY genes are arranged in clusters on the Y chromosome of many mammalian species. TSPY is believed to function in early spermatogenesis and is a candidate for GBY, the putative gonadoblastoma-inducing gene on the Y. The TSPY family forms part of a superfamily, TTSN, with autosomal representatives, highly conserved in mammals and beyond.

15

The new protein can find application in studying the expression profile of testis- and brain-specific genes and diagnosis/therapy of malfunctioning male fertility.

20

HRIHFB221b

similarity to Y-linked Gene of *Mus musculus*

25

Sequenced by BMFZ

Locus: unknown

30

Insert length: 2819 bp

Poly A stretch at pos. 2800, polyadenylation signal at pos. 2779

35

45

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```

1  AGGAGAGCTG GTTGCCTGAG TCTCCTCAGC TCTGCTTACC GGTGCGACTA
51  GCGGCAGCGA CGCGGCTAAA AGCGAAGGGG CGAGTGCGAG TCCCCTGAGC
101  TGTACGAACG CCGTCGCCAT GGACCGCCCA GATGAGGGGC CTCCGGCCAA
151  GACCCGCCGC CTGAGCAGCT CCGAGTCTCC ACAGCGCGAC CCGCCCCCGC
201  GCGCGCCGCC GCGCGCGCTC CTCCGACTGC CGCTGCCTCC ACCCCAGCAG
251  CGCCCGAGGC TCCAGGAGGA AACGGAGGCG GCACAGGTGC TGGCCGATAT
40  301  GAGGGGGGTT GGAAGGGGAT CCGCGCTGCC CCGCGCGCCT CCCTATGTCA
351  TTCTCGAGGA GGGGGGGGAT CGCGCATACT TCACGCTCGG TGCTGAGTGT
401  CCGGCTGGG ATTCTACCAT CGAGTCGGGG TATGGGGAGG CGCCCCCGCC
451  CACGGAGAGC CTGGAAGCAC TCCCCACTCC TGAGGCCTCG GGGGGGAGCC
501  TGGAAATCGA TTTTCAGGTT GTACAGTCGA GCAGTTTTGG TGGAGAGGGG
45  551  GCCCTAGAAA CCTGTAGCGC AGTGGGGTGG GCGCCCCAGA GGTTAGTTGA
601  CCCGAAGAGC AAGGAAGAGG CGATCATCAT AGTGGAGGAT GAGGATGAGG
651  ATGAGCGGGA GAGTATGAGG AGCAGCAGGA GCGGCGGCG GCGGCGGAGG
701  AGGAAGCAGA GGAAGGTGAA GAGGGAAAGC AGAGAGAGAA ATGCCGAGAG
751  GATGGAGAGC ATCCTGCAGG CACTGGAGGA TATTCAGCTG GATCTGGAGG
50  801  CAGTGAACAT CAAGGCAGGC AAAGCCTTCC TCGGTCTCAA GCGCAAGTTC
851  ATCCAGATGC GAAGACCCTT CCTGGAGCGC AGAGACCTCA TCATCCAGCA
901  TATCCCAGGC TTCTGGGTCA AAGCATTCCT CAACCACCCC AGAATTTCAA
951  TTTTGATCAA CCGACGTGAT GAAGACATTT TCCGCTACTT GACCAATCTG
1001  CAGGTACAGG ATCTCAGACA TATCTCCATG GGCTACAAA TGAAGCTGTA
55  1051  CTTCCAGACT AACCCCTACT TCACAAACAT GGTGATTGTC AAGGAGTTCC
1101  AGCGCAACCG CTCAGGCCGG CTGGTGTCTC ACTCAACCCC AATCCGCTGG
1151  CACCGGGGCC AGGAACCCCA GGCCCGTCGT CACGGGAACC AGGATGCGAG
1201  CCACAGCTTT TTCAGCTGGT TCTCAAACCA TAGCCTCCCA GAGGCTGACA

```



```

1251 GGATTGCTGA GATTATCAAG AATGATCTGT GGGTTAACCC TCTACGCTAC
1301 TACCTGAGAG AAAGGGGCTC CAGGATAAAG AGAAAGAAGC AAGAAATGAA
1351 GAAACGTAAA ACCAGGGGCA GATGTGAGGT GGTGATCATG GAAGACGCCC
1401 CTGACTATTA TGCAGTGGAA GACATTTTCA GCGAGATCTC AGACATTGAT
5 1451 GAGACAATTC ATGACATCAA GATCTCTGAC TTCATGGAGA CCACCGACTA
1501 CTTGAGAGCC ACTGACAATG AGATAACTGA CATCAATGAG AACATCTGCG
1551 ACAGCGAGAA TCCTGACCAC AATGAGGTCC CCAACAACGA GACCACTGAT
1601 AACAACGAGA GTGCTGATGA CCACGAAACC ACTGACAACA ATGAGAGTGC
1651 AGATGACAAC AACGAGAATC CTGAAGACAA TAACAAGAAC ACTGATGACA
10 1701 ACGAAGAGAA CCTAACAAC AACGAGAACA CTTACGGCAA CAATTCTTC
1751 AAAGGTGGCT TCTGGGGCAG CCATGGCAAC AACCAGGACA GCAGCGACAG
1801 TGACAATGAA GCAGATGAGG CCAGTGATGA TGAAGATAAT GATGGCAACG
1851 AAGGTGACAA TGAGGGCAGT GATGATGATG GCAATGAAGG TGACAATGAA
1901 GGCAGCGATG ATGACGACAG AGACATTGAG TACTATGAGA AAGTTATTGA
15 1951 AGACTTTGAC AAGGATCAGG CTGACTACGA GGACGTGATA GAGATCATCT
2001 CAGACGAATC AGTGGAAGAA GAGGGCATTG AGGAAGGCAT CCAGCAAGAT
2051 GAGGACATCT ATGAGGAAGG AAACATATGAG GAGGAAGGAA GTGAAGATGT
2101 CTGGGAAGAA GGGGAAGATT CGGACGACTC TGACCTAGAG GATGTGCTTC
2151 AGGTCCCAA ACGTTGGGCC AATCCGGGGA AGAGGGGGAA AACCGGATAA
20 2201 GGGTTTTCCC CTTTGGGGGA TCACCTCTCT GTATCCCCCA CCCACTATCC
2251 CATTTGCCCT CCTCCTCAGC TAGGGCCACG CGGCCCCACA TTGCACTTCT
2301 GGGGGGTGAC CGACTTCGTA CACGGGTTTA AAGTTTATTT TTATGGTTTA
2351 GTCATTGCAG AGTTCTTATT TTGGGGGGAG GGAAGGGGG CTAGTCCCCT
2401 TCTTTTGGCC CTCCGCCCCC GCAGGCTTCT GTGTGCTGCT AACTGTATTT
25 2451 ATTGTGATGC CTTGGTCAGG GCCCCCTCTAC CCACTTCTCC CAGTCAGTTG
2501 TGGCCCCAGC CCTCTCCCT GTGCTGTGTG GAGTGGACAC CCTGACCCCC
2551 GAAGCGGGGA GGGCCGCTGT GGCCTTCGTC ACAGCCGCGC AGTGCCCATG
2601 GAGGCGCTGC TGCCACCTTC CTCTCCCAAG TTCTTTCTCC ATCCCTCTCC
2651 TCTTCCCGCC GCGCCGCTAG CCCGCCTCGG TGTCTATGCA AGGCCGCTTC
30 2701 GCCATTGCGG TATTCTTTGC GGTATTCTTG TCCCCGTCCC CCAGAAGGCT
2751 CGCCTCTCCC CGTGGACCT GTTAATCCCA ATAAAATTCT GAGCAAGTTT
2801 AAAAAAAAAA AAAAAAAAAA

```

35

## BLAST Results

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No BLAST result

40

## Medline entries

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98399864:

45

Vogel T, Dittrich O, Mehraein Y, Dechend F, Schnieders F,  
Schmidtke

J.: Murine and human TSPYL genes: novel members of the  
TSPY-SET-NAP1L1 family. Cytogenet Cell Genet 1998;81(3-4):265-70

50

## Peptide information for frame 2

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55

ORF from 119 bp to 2197 bp; peptide length: 693  
Category: similarity to known protein  
Classification: unclassified

```

      1 MDRPDEGPPA KTRRLSSSES PQRDPPPPPP PPPLLRLPLP PPQQRPRLQE
      51 ETEAAQVLAD MRGVGLGPAL PPPPPYVILE EGGIRAYFTL GAECPGWDST
    101 IESGYGEAPP PTESLEALPT PEASGGSLEI DFQVVQSSSF GGEGALETCS
    5 151 AVGWAPQRLV DPKSKEEAI IVEDEDEDER ESMRSSRRRR RRRRRKQRKV
    201 KRESRERNAE RMESILQALE DIQLDLEAVN IKAGKAFLRL KRKFIQMRRP
    251 FLERRDLIIQ HIPGFQVKAF LNHPRISILI NRRDEDIFRY LTNLQVQDLR
    301 HISMGYKMKL YFQTNPYFTN MVIVKEFQRN RSGRLVSHST PIRWHRGQEP
    351 QARRHGNQDA SHSFFSWFSN HSLPEADRIA EIIKNDLWVN PLRYYLRRER
    10 401 SRIKRKKQEM KKRKTRGRCE VVIMEDAPDY YAVEDIFSEI SDIDETIHDI
    451 KISDFMETTD YFETTDNEIT DINENICDSE NPDHNEVPNN ETTDNNESAD
    501 DHETTDNNES ADDNNENPED NNKNTDDNEE NPNNNENTYG NNFFKGGFWG
    551 SHGNNQDSSD SDNEADEASD DEDNDGNEGD NEGSDDDGNE GDNEGSDDDD
    601 RDIEYYEKVI EDFDKDQADY EDVIEIISDE SVEEEGIEEG IQQDEDIYEE
    15 651 GNYEEEGSED VWEEGEDSDD SDLEDVLQVP NGWANPGKRG KTG

```

## BLASTP hits

20

No BLASTP hits available

## Alert BLASTP hits for DKFZphamy2\_7j5, frame 2

```

    25 TREMBL:AB015345_1 gene: "HRIHFB221b"; Homo sapiens HRIHFB221b
      mRNA,
      partial cds., N = 4, Score = 1393, P = 2.1e-165

    30 TREMBL:HSDJ486I3_2 gene: "dJ486I3.2"; product: "dJ486I3.2
      (KIAA0721
      (NAP (Nucleosome Assembly Protein) domain containing protein))";
      Human
      DNA sequence from clone 486I3 on chromosome 6q22.1-22.3. Contains
      the
    35 part of a gene for a novel protein, the gene for KIAA0721 (NAP
      (Nucleosome Assembly Protein) domain containing protein), the TSPYL
      gene
      for TSPY-like (testis specific protein, Y-linked like), and an
      RPS5
    40 (40S Ribosomal Protein S5) pseudogene. Contains ESTs, STSs, GSSs
      and
      two putative CpG islands., N = 1, Score = 570, P = 3.4e-55

    45 >TREMBL:AB015345_1 gene: "HRIHFB221b"; Homo sapiens HRIHFB221b
      mRNA,
      partial cds.
      Length = 486

    50 HSPs:

      Score = 1393 (209.0 bits), Expect = 2.1e-165, Sum P(4) = 2.1e-
      165
      Identities = 268/295 (90%), Positives = 268/295 (90%)

    55 Query: 208
      NAERMESILQALEDIQLDLEAVNIKAGKAFLRLKRKFIQMRRPFLERRDLIIQHIPGFQV 267

```

NAERMESILQALEDIQLDLEAVNIKAGKAFLRLKRFIQMRRPFLERRDLIIQHIPGFUV  
 Sbjct: 1  
 NAERMESILQALEDIQLDLEAVNIKAGKAFLRLKRFIQMRRPFLERRDLIIQHIPGFUV 60

5 Query: 268  
 KAFLNHPRISILINRRDEDIFRYLTNLQVQDLRHISMGYKMKLYFQTNPYFTNMVIVKEF 327

10 KAFLNHPRISILINRRDEDIFRYLTNLQVQDLRHISMGYKMKLYFQTNPYFTNMVIVKEF  
 Sbjct: 61  
 KAFLNHPRISILINRRDEDIFRYLTNLQVQDLRHISMGYKMKLYFQTNPYFTNMVIVKEF 120

15 Query: 328  
 QRNRSGRLVSHSTPIRWHRGQEPQARRHGNQDAXXXXXXXXXXXXXLPEADRIAETIKNDL 387  
 QRNRSGRLVSHSTPIRWHRGQEPQARRHGNQDA  
 LPEADRIAETIKNDL  
 Sbjct: 121  
 QRNRSGRLVSHSTPIRWHRGQEPQARRHGNQDASHSFFSWFSNHSLEADRIAETIKNDL 180

20 Query: 388  
 WVNPLRYYLREGRSXXXXXXXXXXXXXXXXXGRCEVVIMEDAPDYYAVEDIFSEISDIETI 447  
 WVNPLRYYLREGRS  
 GRCEVVIMEDAPDYYAVEDIFSEISDIETI  
 Sbjct: 181

25 WVNPLRYYLREGRSRIKRRKQEMKKRKTGRCEVVIMEDAPDYYAVEDIFSEISDIETI 240

Query: 448  
 HDIKISDFMETTDYFETTDNEITDINENICDSENPDHNEVPNNETTDNNESADDH 502

30 HDIKISDFMETTDYFETTDNEITDINENICDSENPDHNEVPNNETTDNNESADDH  
 Sbjct: 241  
 HDIKISDFMETTDYFETTDNEITDINENICDSENPDHNEVPNNETTDNNESADDH 295

Score = 117 (17.6 bits), Expect = 9.0e-19, Sum P(4) = 9.0e-19  
 Identities = 32/77 (41%), Positives = 44/77 (57%)

35 Query: 426  
 DAPDYYAVEDIFSEISDIETIHDIKISDFMETTDYFETTDNEITDINENICDSENPDHN 485  
 + DY+ D +EI+DI+E I D E D+ E +NE TD NE+

40 D E D+N  
 Sbjct: 250 ETTDYFETTD--NEITDINENICD-----  
 SENPDHNEVPNNETTDNNESADDHETTDNN 301

45 Query: 486 EVP--NNETT-DNNESADDH 502  
 E NNE DNN++ DD+  
 Sbjct: 302 ESADDNNENPEDNNKNTDDN 321

Score = 94 (14.1 bits), Expect = 2.1e-165, Sum P(4) = 2.1e-165  
 Identities = 16/16 (100%), Positives = 16/16 (100%)

50 Query: 678 QVPNGWANPGKRGKTG 693  
 QVPNGWANPGKRGKTG  
 Sbjct: 471 QVPNGWANPGKRGKTG 486

55 Score = 90 (13.5 bits), Expect = 9.9e-16, Sum P(4) = 9.9e-16  
 Identities = 34/85 (40%), Positives = 45/85 (52%)

Query: 426 DAPDYYAVEDIFSEISDIETIHDIKISDFME-----TTDYFETTDN-  
 EITDINENICDS 479  
 + DY+ D +EI+DI+E I D + D E TTD E+ D+ E TD  
 NE+ D+

5 Sbjct: 250 ETTDYFETTD--  
 NEITDINENICDSENPDHNEVPNNETTDNNESESADDHETTDNNESESADDN 307

Query: 480 -ENPDHN-----EVPNN-ETTDNN 496  
 ENP+ N E PNN E T N

10 Sbjct: 308 NENPEDNNKNTDDNEENPNNNENTYGN 334

Score = 87 (13.1 bits), Expect = 2.1e-165, Sum P(4) = 2.1e-165  
 Identities = 14/14 (100%), Positives = 14/14 (100%)

15 Query: 543 FFKGGFWGSHGNNQ 556  
 FFKGGFWGSHGNNQ  
 Sbjct: 336 FFKGGFWGSHGNNQ 349

20 Score = 85 (12.8 bits), Expect = 2.1e-165, Sum P(4) = 2.1e-165  
 Identities = 16/18 (88%), Positives = 17/18 (94%)

Query: 601 RDIEYYEKVIEDFDKDQA 618  
 RDIEYYEK IEDFD+DQA

25 Sbjct: 394 RDIEYYEKGIEDFDRDQA 411

Score = 60 (9.0 bits), Expect = 5.3e-03, Sum P(4) = 5.3e-03  
 Identities = 21/66 (31%), Positives = 33/66 (50%)

30 Query: 426 DAPDYYAVEDIFSEISDIETIHD-IKIS-  
 DFMETTDYFETTDNEITDINENICDSENPD 483

D DY V +I S+ S +E I + I+ D E +Y E ++ + E+

DS+ D

Sbjct: 409 DQADYEDVIEIISDESVEEEGIEEGIQQDEDIYEEGNYYYYEGSEDVWEEGEDSDSDSDLED 468

35

Query: 484 HNEVPN 489  
 +VPN

Sbjct: 469 VLQVPN 474

40 Score = 49 (7.4 bits), Expect = 1.4e-06, Sum P(4) = 1.4e-06  
 Identities = 12/35 (34%), Positives = 21/35 (60%)

Query: 463 ETTDNEITDINENICDSENPDHNEVPNNETTDNNE 497  
 E +D+E D NE + + D NE +NE +D+++

45 Sbjct: 360 EASDDEDNDGNEGDNEGSDDDGNE-GDNEGSDDDD 393

Score = 42 (6.3 bits), Expect = 7.2e-06, Sum P(4) = 7.2e-06  
 Identities = 11/37 (29%), Positives = 18/37 (48%)

50 Query: 465 TDNEITDINENICDSENPDHNEVPNNETTDNNESESADD 501  
 +DNE + + D E+ D NE N + D+ D+

Sbjct: 354 SDNEADEAS----DDEDNDGNEGDNEGSDDDGNEGDN 386

55

Pedant information for DKFZphamy2\_7j5, frame 2

-208-

SEQ SHSFFSWFSNHSLPEADRIAIEIKNDLWVNPLRYYLRERGSRIKRRKKQEMKKRKTRGRCE  
SEG xxx  
PRD cccceeeccccccccccchhhhhhhhhhhhhcccccchhhhhhhhhhhhhhhhhcceecccccccc

5 SEQ VVIMEDAPDYYAVEDIFSEISDIDETIHDIKISDFMETTDYFETTDNEITDINENICDSE  
SEG .....  
PRD eeccccccccceehhhhhhhhhhhccccccccccccccccccccchhhhhhhhhcccccc

10 SEQ NPDHNEVPNNETTDDNESADDHETTDDNESADDNNENPEDNNKNTDDNEENPNNNENTYG  
SEG .....xx  
PRD cccccceeeccccccccccccccccccccchhhhhcccccccccccccccccccccccccc

15 SEQ NNFFKGGFWGSHGNNQDSSDSDNEADEASDDEDNDGNEGDNEGSDDDGNEGDNEGSDDDD  
SEG xx.....xx  
PRD ccc

20 SEQ RDIEYYEKVIEDFDKQADYEDVIEIISDESVEEEGIEEGIQQDEDIYEEGNYEEEGSED  
SEG .....xx  
PRD cchhhhhhhhhhhccccchhhhhheeeccccccccccccccccccccceccccccccccce

SEQ VWEEGEDSDSDLEDVLQVPNGWANPGKRGKTG  
SEG xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
PRD eeccccccccccccceeecccccccccccccccccc

25 (No Prosite data available for DKFZphamy2\_7j5.2)

(No Pfam data available for DKFZphamy2\_7j5.2)

30 Pedant information for DKFZphamy2\_7j5, frame 3  
-----

Report for DKFZphamy2\_7j5.3

35  
[LENGTH] 150  
[MW] 16810.69  
[pI] 12.88  
40 [BLOCKS] PRO0308A  
[KW] All\_Alpha  
[KW] LOW\_COMPLEXITY 61.33 %

45 SEQ MRTSATARILTTMRSPTTRPLITTRVLMTTKPLTTMRVQMTTTRILKTITRTLMTTKRTL  
SEG .....xxxxxxxxxxxxxxxxxxxxxxxxxxxx  
PRD ccchhhhhhhhhhhccccccccccccceeeccccccccchhhhhhhhhhhhhhhhhhhhhcccccc

50 SEQ TTTRTLTTATTSSKVASGAAMATTRTAATVTMKQMRPVMMKIMMATKVTMRAVMMAMKVT  
SEG xxx  
PRD cccccceccccccccchhhhhhhhhhhhhhhhhhhhhchhhhhhhhhhhhhhhhhhhhhhhhhhh

55 SEQ MKAAMMTTETLSTMRKLLKTLTRIRLTTRT  
SEG xxxxxxxx.xxxxxxxxxxxxxxxxxxxxx  
PRD hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccc

(No Prosite data available for DKFZphamy2\_7j5.3)

(No Pfam data available for DKFZphamy2\_7j5.3)

DKFZphfbr2\_78c12

5 -----

group: nucleic acid management

- 10 DKFZphfbr2\_78c12 encodes a novel 528 amino acid protein with high  
csimilarity to glutamyl-tRNA (Gln) amidotransferase subunit A of  
the hyperthermophilic bacterium Aquifex aeolicus.

- 15 The novel protein contains one ATP/GTP-binding site motif A (P-  
loop). This loop interacts with one of the phosphate groups of a  
A or G nucleotide. It is found in numerous ATP- or GTP-binding  
proteins, such as ATP synthase alpha and beta subunits, Myosin  
heavy chains, Kinesin heavy chains and kinesin-like proteins,  
Dynamins and dynamin-like proteins, several kinases, DNA and RNA  
20 helicases, GTP-binding elongation factors and the Ras family of  
GTP-binding proteins. The protein seems to be expressed  
ubiquitously.

- 25 The new protein can find application in the modulation of  
translational pathways.

- 30 similarity to glutamyl-tRNA (Gln) amidotransferase subunit A  
(Aquifex  
aeolicus)

Sequenced by MediGenomix

- 35 Locus: /map="b8b.3 cR from top of Chr6 linkage group"

Insert length: 3244 bp

Poly A stretch at pos. 3222, polyadenylation signal at pos. 3204

- 40 1 AGTGACAATT AAAGATGGCT GCGCCCATGT AACATCACTA GCGACCGGTG  
51 ACCTCTTTTT CCCCCTTGCC TGGCTCCTGT GGTGGCAGGC TGGGCACGAG  
101 GACCATGCTG GGCCGGAGCC TCCGAGAAGT TTCTGCGGCA CTGAAACAAG  
151 GCCAAATTAC ACCAACAGAG CTCTGTCAAA AATGTCTCTC TCTTATCAAG  
201 AAGGCCAAGT TTCTAAATGC CTACATTACT GTGTCAGAAG AGGTGGCCTT  
45 251 AAAACAAGCT GAAGAATCAG AAAAGAGATA TAAGAATGGA CAGTCACTTG  
301 GGGATTTAGA TGGAATTCCT ATTGCAGTAA AAGACAATTT CAGCACTTCT  
351 GGCATTGAGA CAACATGTGC ATCAAATATG CTGAAAGGTT ATATACCACC  
401 TTATAATGCT ACAGTAGTTC AGAAGTTGTT GGATCAGGGA GCTCTACTAA  
451 TGGGAAAAAC AAATTTAGAT GAGTTTGCTA TGGGATCTGG GAGCACAGAT  
50 501 GGTGTATTTG GACCAGTTAA AAACCCCTGG AGTTATTCAA AACGATATAG  
551 AGAAAAGAGG AAGCAGAATC CCCACAGCGA GAATGAAGAT TCAGACTGGC  
601 TGATAACTGG AGGAAGCCCA GGTGGGAGTG CAGCTGCTGT ATCGGCGTTC  
651 ACATGCTACG CGGCTTTAGG ATCAGATACA GGAGGATCGA CCAGAAATCC  
701 TGCTGCCCCAC TGTGGGCTTG TTGGTTTCAA ACCAAGCTAT GGCTTAGTTT  
55 751 CCCGTCATGG TCTCATTCCT CTGGTGAATT CGATGGATGT GCCAGGAATC  
801 TTAACCAGAT GTGTGGATGA TGCAGCAATT GTGTTGGGTG CACTGGCCGG  
851 ACCTGACCCC AGGGACTCTA CCACAGTACA TGAACCTATT AATAAACCAT  
901 TCATGCTTCC CAGTTTGGCA GATGTGAGCA AACTATGTAT AGGAATTCCA

5 951 AAGGAATATC TTGTACCGGA ATTATCAAGT GAAGTACAGT CTCTTTGGTC  
1001 CAAAGCTGCT GACCTCTTTG AGTCTGAGGG GGCCAAAGTA ATTGAAGTAT  
1051 CCCTTCCTCA CACCAGTTAT TCAATTGTCT GCTACCATGT ATTGTGCACA  
1101 TCAGAAAGTGG CATCGAATAT GGCAAGATTT GATGGGCTAC AATATGGTCA  
1151 CAGATGTGAC ATTGATGTGT CCACTGAAGC CATGTATGCT GCAACCAGAC  
1201 GAGAAGGATT TAATGATGTG GTGAGAGGAA GAATTCTCTC AGGAAACTTT  
1251 TTCTTATTAA AAGAAAACTA TGAAAATTAT TTTGTCAAAG CACAGAAAGT  
1301 GAGACGCCTC ATTGCTAATG ACTTTGTAAA TGCTTTTAAC TCTGGAGTAG  
1351 ATGTCTTGCT AACTCCCACC ACCTTGAGTG AGGCAGTACC ATACTTGGAG  
10 1401 TTCATCAAAG AGGACAACAG AACC CGAAGT GCCCAGGATG ATATTTTAC  
1451 ACAAGCTGTA AATATGGCAG GATTGCCAGC AGTGAGTATC CCTGTTGCAC  
1501 TCTCAAACCA AGGGTTGCCA ATAGGACTGC AGTTTATTGG ACGTGCGTTT  
1551 TGTGACCAGC AGCTTCTTAC AGTAGCCAAA TGGTTTGAAA AACAAGTACA  
1601 GTTTCCTGTT ATTCAACTTC AAGAACTCAT GGATGATTGT TCAGCAGTCC  
15 1651 TTGAAAATGA AAAGTTAGCC TCTGTCTCTC TAAAACAGTA AACATATCTT  
1701 ACAAATTAATA ATGACTTTTA GGCTGGGTGC AGTGGCTCAC ACCTGTAATC  
1751 CCAGCACTTT GGGAGGCCAA GGCAGCGGA TCATGAGGTC AGAAGATCTA  
1801 GAACAGCCTG GTCAACATGG TGAAACCCCG TCTCTACTAA AAATACAAAA  
1851 ATTAGCCAGG CTTAGTGGCG GGCATCTGTA GTCCCAGCTA CTCAGGAGGC  
20 1901 TGAGGCAGGA GAATCACTTG AACCCTGGAG GTGGAGGTTG CAGTGAGCCG  
1951 AGATCATGCC ACTGCACTGC ACTCCAGCCT GGGTGACAAA GCAAGACTGT  
2001 GTCTCAAAAT AAATAAATAA AATAAAATAA AATGACGTAC AGAGATTCTA  
2051 TATTCTAGAG AGTCAAATGG TCTTGCTCAA TTCTTGTAAT TAGGTTCTTG  
2101 TTAATACAGT CATTCCATGG AATTACTTTT TAAAATTCTT GTGACAATTA  
25 2151 ATAATAAATA ACGTGTCAAGC ATTTAGTAAG CATCCACTAA GTGTACAATA  
2201 CTTCTACAAT AACACAAGAT ACCTGTTCTT CAAAGACAAT GCATTCTGCC  
2251 ATAATGTTCA TTAAAGAGTT TACAGTAAAA ATAAGATTAG GGATAAACTT  
2301 CTCAAAAATT GTACATCTGT GTAACATAAG CACTAACAAA AACATGAATA  
2351 GTCCTTCTAG AGGTAACCTG GATAGCCTAG GCAGGCAACT TATCATGTGG  
30 2401 TGAAGGCCGC CTCAGGGGTT GTTAAAAATG CACAGAAACA ATTGAGTGCG  
2451 ATTATTGGCT TCTGAGCGCT GAGCAGAGCA GGTGGAAGAG GAACTTTGAG  
2501 CACAGGAGGA AATGCAACCA GTCAGGGCCC AGAATCATGC AAATCTCAGG  
2551 GGTATGCCTC TCTGGGGAGG AGCTCCACTT GCAGGGACTC CTTTTATTTC  
2601 CCTAAGAAAG AGCTGAAATG ACTGAGAACT TTCTTTCTT CCTTAGAGTT  
35 2651 ACAATTTTAC TTCTGCTATT CCGGAGCCCA TGCCTAGAAG CCAGAACAAC  
2701 TCCATGTTAC ACTGAGTTCA TGCTCCTATT TACTGATCAC AAATGAGCTC  
2751 ATTAATGTCA TCGAAACATT TATTGTAACC TAACAGACCA TCACAGATTG  
2801 GAAACTTGGT AGATAGCAGA GCATGGTATT AGTGAAAAAG GTTCAAAATA  
2851 CACAAGTAAC ATACACTCTG AAAAACATGC AGATAATTTG CTGATGAAGC  
40 2901 AGAAGAGGGG ATGCGCATGG CAAGAACTTG CCTTACCCA GATTCTCTAT  
2951 ATCTCATGGT TTCCTTTTCC TCTTGACTGT CTTTACGAGT GTTTTTTATT  
3001 TGGGACCCTC GAGCCCAGAG ATATTAATGG ATATCTGTAT TCAATATTTG  
3051 ACAAATCTA ATGGAAACCA TCCATTTACT CATGATAAGG CTTCATCACT  
3101 GGATTTCTGT GTCTTCACTA GAACACCATT GTCATCTCAT ATTGATCAGG  
45 3151 TATTTTAATC TAGCACTTAC ATATTGTTGA TAAATGAAAG CTGAATTGTT  
3201 ACTTAATAAA TTCACCTTGT TTAGCAAAAA AAAAAAAAAA AAAA

## BLAST Results

-----

50

No BLAST result

55

## Medline entries

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No Medline entry



## Peptide information for frame 3

5

ORF from 105 bp to 1688 bp; peptide length: 528

Category: similarity to known protein

Classification: Protein management

10 Prosite motifs: ATP\_GTP\_A (112-119)

1 MLGRSLREVS AALKQGGITP TELCQKCLSL IKKAKFLNAY ITVSEEVALK  
 51 QAESEKRYK NGQSLGDLDG IPIAVKDNFS TSGIETTCAS NMLKGYIPPY  
 15 101 NATVVQKLLD QGALLMGKTN LDEFAMGSGS TDGVFGPVKN PWSYSKRYRE  
 151 KRKQNPHESEN EDSDWLITGG SPGGSAAAVS AFTCYAALGS DTGGSTRNPA  
 201 AHCGLVGFKP SYGLVSRHGL IPLVNSMDVP GILTRCVDDA AIVLGALAGP  
 251 DPRDSTTVHE PINKPFMLPS LADVSKLCIG IPKEYLVPEL SSEVQSLWSK  
 301 AADLFESEGA KVIEVSLPHT SYSIVCYHVL CTSEVASNMA RFDGLQYGHR  
 20 351 CDIDVSTEAM YAATRREGFN DVVRGRILSG NFFLLKENYE NYFVKAQKVR  
 401 RLIANDFVNA FNSGVDVLLT PTTLSEAVPY LEFIKEDNRT RSAQDDIFTQ  
 451 AVNMAGLPAV SIPVALSNQG LPIGLQFIGR AFCDQQLLTV AKWFEKQVQF  
 501 PVIQLQELMD DCSAVLENEK LASVSLKQ

25

## BLASTP hits

No BLASTP hits available

30

Alert BLASTP hits for DKFZphfbr2\_78c12, frame 3

PIR:F70322 glutamyl-tRNA (Gln) amidotransferase subunit A -  
 Aquifex

35 aeolicus, N = 2, Score = 620, P = 4.3e-89

>PIR:F70322 glutamyl-tRNA (Gln) amidotransferase subunit A -  
 Aquifex

40 aeolicus

Length = 478

## HSPs:

45 Score = 620 (93.0 bits), Expect = 4.3e-89, Sum P(2) = 4.3e-89  
 Identities = 135/319 (42%), Positives = 195/319 (61%)

Query: 187

ALGSDTGGSTRNPAAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGILTRCVDDAAIVLGA 246

50 +LGSDTGGG R PA+ CG++G KP+YG VSR+GL+ +S+D G+ R

+D A+VL

Sbjct: 163

SLGSDTGGGIRQPAFCGVIGIKPTYGRVSRVGLVAFASSLDQIGVFGRRTEDVALVLEV 222

55 Query: 247

LAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLVPELSSEVQSLWSKAADLFE 306

++G D +DST+ P+ + + +V L IG+PKE+ EL +V+ +

E

Sbjct: 223 ISGWDEKDSSTSAKVPVPE-  
WSEEVKKEVKGLKIGLPKEFFEYELQPVKEAFENFIKELE 281

Query: 307

5 SEGAKVIEVSLPHTSYSIVCYHVLCTSEVASNMARFDGLQYGHRCDDIDVSTEAMYAATTR 366  
EG ++ EVSLPH YSI Y+++ SE +SN+AR+DG++YG+R

MYA TR

Sbjct: 282

10 KEGFEIKEVSLPHVKYSIPTYYIIAPSEASSNLARYDGVRYGYRAKEYKDIFEMYARTRD 341

Query: 367

EGFNDVVRGRILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLLTPTTLSE 426  
EGF V+ RI+ G F L Y+ Y++KAQKVRRLI NDF+ AF VDV+  
+PTT

15 Sbjct: 342 EFGGPEVKRRIMLGTFALSAGYYDAYYLKAQKVRRLITNDFLKAFEE-  
VDVIASPTT--P 398

Query: 427

20 AVPYLEFIKEDNRTRSAQDDIFTQAVNMAGLPAVSIPVALSNQGLPIGLQFIGRAFCDDQ 486  
+P+ + +N DI T N+AGLPA+SIP+A + GLP+G Q

IG+ + +

Sbjct: 399 TLPFKFGERLENPIEMYLSIDILTVPANLAGLPAISIPIAWKD-  
GLPVGGQLIGKHWDETT 457

25 Query: 487 LLTVAK-WFEKQVQFPVIQL 505

LL ++ W +K + I L

Sbjct: 458 LLQISYLWEQKFKHYEKIPL 477

30 Score = 289 (43.4 bits), Expect = 4.3e-89, Sum P(2) = 4.3e-89  
Identities = 64/143 (44%), Positives = 90/143 (62%)

Query: 4 RSLREVSAALKQGGITPTELCQKCLSLIKKAKF-  
LNAYITVSEEVALKQAESEKRYKNG 62

35 +SL E+ LK+G+++P E+ + + + AYIT ALKQAE

++R

Sbjct: 5

KSLSELRELLKRGEVSPKEVVESFYDRYNQTEEVKAYITPLYGKALKQAESLKER---- 60

Query: 63

40 QSLGDLGDIPIAVKDNFSTSGIETTCASNMLKGYIPPYNATVVQKLLDQGALLMGKTNLD 122  
L L GIPIAVKDN G +TTCAS +L+ ++ PY+ATV+++L

GAL++GKTNLD

Sbjct: 61 -EL-

45 PLFGIPIAVKDNILVEGEKTTASKILENFVAPYDATVIERLKKAGALIVGKTNLD 118

Query: 123 EFAMGSGSTDGVFGPVKNPWSYSK 146

EFAMGS + F P KNPW +

Sbjct: 119 EFAMGSSTEYSAFFPTKNPWDLER 142

50

Pedant information for DKFZphfbr2\_78c12, frame 3

Report for DKFZphfbr2\_78c12.3

55

[[LENGTH]] 528

[[MW]] 57468.78

-214-

SEQ YAATRREGFNDVVRGRILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLLT  
 SEG .....  
 PRD hhhhhhccccchhhhhhhhhhhheeeccccchhhhhhhhhhhhhhhhhhhhhhhhhhhheeeee

5 SEQ PTTLSEAVPYLEFIKEDNRTRSAQDDIFTQAVNMAGLPAVSIPVALSNQGLPIGLQFIGR  
 SEG .....  
 PRD cccccccccccccccccccccccccceeeccccccccccccccccccccccccceeeec

10 SEQ AFCDQQLLTVAKWFEKQVQFPVIQLQELMDDCSAVLENEKLASVSLKQ  
 SEG .....  
 PRD cccchhhhhhhhhhhhhhhhhhhheeehhhhhhheeeccccceeeccccc

15 Prosite for DKFZphfbr2\_78cl2.3

PS00017 112->120 ATP\_GTP\_A PD0C00017

20 (No Pfam data available for DKFZphfbr2\_78cl2.3)

DKFZphfbr2\_78d18

-----

25 group: brain derived

DKFZphfbr2\_78d18 encodes a novel 535 amino acid protein with weak  
 similarity to a human putative mitogen-activated protein kinase  
 30 kinase kinase.

No informative BLAST results; No predictive prosite, pfam or SCOP  
 motife.

35 The new protein can find application in studying the expression  
 profile of brain-specific genes.

similarity to putative mitogen-activated protein kinase kinase  
 40 (Homo sapiens)

Sequenced by MediGenomix

Locus: unknown

45

Insert length: 2158 bp

Poly A stretch at pos. 2138, polyadenylation signal at pos. 2117

50 1 ATCCGGGGCC CCGGAACCCG AGCTGGAGCT GAAGCGCAGG CTGCGGGGCG  
 51 CGGAGTCGGG AGTGCAGGCC TGAGTGTTCC TTCCAGCATG TCGGAGGGGG  
 101 AGTCCCAGAC AGTACTTAGC AGTGGCTCAG ACCCAAAGGT AGAATCCTCA  
 151 TCTTCAGCCC CTGGCCTGAC ATCAGTGTCA CCTCCTGTGA CCTCCACAAC  
 201 CTCAGCTGCT TCCCCAGAGG AAGAAGAAGA AAGTGAAGAT GAGTCTGAGA  
 55 251 TTTTGGAAGA GTCGCCCTGT GGGCGCTGGC AGAAGAGGCG AGAAGAGGTG  
 301 AATCAACGGA ATGTACCAGG TATTGACAGT GCATACCTGG CCATGGATAC  
 351 AGAGGAAGGT GTAGAGGTTG TGTGGAATGA GGTACAGTTC TCTGAACGCA  
 401 AGAACTACAA GCTGCAGGAG GAAAAGGTTT GTGCTGTGTT TGATAATCTG

```

451 ATTCAATTGG AGCATCTTAA CATTGTTAAG TTTCACAAAT ATTGGGCTGA
501 CATTAAAGAG AACAAGGCCA GGGTCATTTT TATCACAGAA TACATGTCAT
551 CTGGGAGTCT GAAGCAATTT CTGAAGAAGA CCAAAAAGAA CCACAAGACG
601 ATGAATGAAA AGGCATGGAA GCGTTGGTGC ACACAAATCC TCTCTGCCCT
5 651 AAGCTACCTG CACTCCTGTG ACCCCCCCAT CATCCATGGG AACCTGACCT
701 GTGACACCAT CTTCATCCAG CACAACGGAC TCATCAAGAT TGGCTCTGTG
751 GCTCCTGACA CTATCAACAA TCATGTGAAG ACTTGTGAG AAGAGCAGAA
801 GAATCTACAC TTCTTTGCAC CAGAGTATGG AGAAGTCACT AATGTGACAA
851 CAGCAGTGGG CATCTACTCC TTTGGCATGT GTGCACTGGA GATGTCAGTG
10 901 CTGGAGATTG AGGGCAATGG AGAGTCCTCA TATGTGCCAC AGGAAGCCAT
951 CAGCAGTGCC ATCCAGCTTC TAGAAGACCC ATTACAGAGG GAGTTCATTC
1001 AAAAGTGCCT GCAGTCTGAG CCTGCTCGCA GACCAACAGC CAGAGAACTC
1051 CTGTTCCACC CAGCATTGTT TGAAGTGCCC TCGCTCAAAC TCCTTGCGGC
1101 CCACTGCATT GTGGGACACC AACACATGAT CCCAGAGAAC GCTCTAGAGG
15 1151 AGATCACCAA AAACATGGAT ACTAGTGCCG TACTGGCTGA AATCCCTGCA
1201 GGACCAGGAA GAGAACCAGT TCAGACTTTG TACTCTCAGT CACCAGCTCT
1251 GGAATTAGAT AAATTCCTTG AAGATGTCAG GAATGGGATC TATCCTCTGA
1301 CAGCCTTTGG GCTGCCTCGG CCCCAGCAGC CACAGCAGGA GGAGGTGACA
1351 TCACCTGTCTG TGCCCCCCTC TGTCAAGACT CCGACACCTG AACCAGCTGA
20 1401 GGTGGAGACT CGCAAGGTGG TGCTGATGCA GTGCAACATT GAGTCGGTGG
1451 AGGAGGGAGT CAAACACCAC CTGACACTTC TGCTGAAGTT GGAGGACAAA
1501 CTGAACCGGC ACCTGAGCTG TGACCTGATG CCAAATGAGA ATATCCCCGA
1551 GTTGGCGGCT GAGCTGGTGC AGCTGGGCTT CATTAGTGAG GCTGACCAGA
1601 GCCGGTTGAC TTCTCTGCTA GAAGAGACCT TGAACAAGTT CAATTTTGCC
25 1651 AGGAACAGTA CCCTCAACTC AGCCGCTGTC ACCGTCTCCT CTTAGAGCTC
1701 ACTCGGGCCA GGCCCTGATC TGCGCTGTGG CTGTCCCTGG ACGTGCTGCA
1751 GCCCTCCTGT CCCTTCCCCC CAGTCAGTAT TACCCTGTGA AGCCCTTCC
1801 CTCCTTTATT ATTCAGGAGG GCTGGGGGGG CTCCCTGGTT CTGAGCATCA
1851 TCCTTTCCCC TCCCCTCTCT TCCTCCCCCTC TGCACTTTGT TTAATTGTTT
30 1901 TGACACAGACG TGGGCCTGGG CTTTCTCAGC AGCCGCCTTC TAGTTGGGGG
1951 CTAGTCGCTG ATCTGCCGGC TCCCGCCAG CCTGTGTGGA AAGGAGGCCC
2001 ACGGGCACTA GGGGAGCCGA ATTCTACAAT CCCGCTGGGG CGGCCGGGGC
2051 GGGAGAGAAA GGTGGTGCTG CAGTGGTGGC CCTGGGGGGC CATTGATTTC
2101 GCCTCAGTTG CTGCTGTAAT AAAAGTCTAC TTTTGGCCAA AAAAAAAAAA
35 2151 AAAAAAAA

```

## BLAST Results

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40

No BLAST result

## Medline entries

-----

45

No Medline entry

50

## Peptide information for frame 1

-----

55

ORF from 88 bp to 1692 bp; peptide length: 535

Category: similarity to unknown protein

Classification: Protein management

1 MSEGESQTVL SSGSDPKVES SSSAPGLTSV SPPVTSTTSA ASPEEEEESE

```

5  51 DESEILEESP CGRWQKRREE VNQRNVPGID SAYLAMDTTEE GVEVVWNEVQ
101 FSERKNYKLQ EEKVRVAFDN LIQLEHLNIV KFHKYWADIK ENKARVIFIT
151 EYMSSGSLKQ FLKKTCKNHK TMNEKAWKRW CTQILSALSY LHSCDPPIIH
201 GNLTCDTIFI QHNGLIKIGS VAPDTINNHV KTCREEQKNL HFFAPEYGEV
5  251 TNVTTAVDIY SFGMCALEMA VLEIQNGES SYVPQEAISS AIQLLEDPLQ
301 REFIQKCLQS EPARRPTARE LLFHPALFEV PSLKLLAAHC IVGHQHMIPE
351 NALEEITKNM DTSAVLAEIP AGPGREPVT LYSQSPAEL DKFLEDVRNG
401 IYPLTAFGLP RPQQPQQEEV TSPVVPPSVK TPTPEPAEVE TRKVVLMOCN
451 IESVEEGVKH HLTLLKLED KLNRLHSCDL MPNENIPELA AELVQLGFIS
10 501 EADQSRILTSL LEETLNKFNF ARNSTLNSAA VTVSS

```

## BLASTP hits

15

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2\_78d18, frame 1

```

20 TREMBL:AC009465_14 gene: "T9J14.14"; product: "putative mitogen
activated protein kinase kinase"; Arabidopsis thaliana
chromosome III
BAC T9J14 genomic sequence, complete sequence., N = 1, Score =
372, P =
25 1.9e-33

```

```

TREMBL:AF145690_1 gene: "BcDNA.LD28657"; product:
"BcDNA.LD28657";
Drosophila melanogaster clone LD28657 BcDNA.LD28657
30 (BcDNA.LD28657)
mRNA, complete cds., N = 1, Score = 1140, P = 1.3e-115
PIR:T02951 probable mitogen activated protein kinase - rice, N =
1,
35 Score = 391, P = 1.4e-35

```

```

>TREMBL:AF145690_1 gene: "BcDNA.LD28657"; product:
"BcDNA.LD28657";
40 Drosophila melanogaster clone LD28657 BcDNA.LD28657
(BcDNA.LD28657) mRNA,
complete cds.
Length = 637

```

45 HSPs:

Score = 1140 (171.0 bits), Expect = 1.3e-115, P = 1.3e-115  
Identities = 230/465 (49%), Positives = 304/465 (65%)

```

50 Query:      61
CGRWQKRREEVNQRNVPGIDSAYLAMDTTEEGVEVVWNEVQFSERKNYKLQEEKVRVAFDN 120
          CGRW KRREEV+QR+VPGID +LAMDTTEEGVEVVWNEVQ++ + K
QEEK+R VFDN
Sbjct:      102
55 CGRWLKRREEVDQRDVPGLDCVHLAMDTTEEGVEVVWNEVQYASLQELKSQEEKMRQVFDN 161

```

Query: 121 LIQLEHLNIVKFHXYWADIKE-  
NKARVIFITEYMSSGSLKQFLKKTCKNHKTMNEKAWKR 179

L+QL+H NIVKFH+YW D ++ + RV+FITEYMSSGSLKQFLK+TK+N K  
 + ++W+R  
 Sbjct: 162  
 LLQLDHQNIIVKFHRYWTD TQQAERPRVVFITEYMSSGSLKQFLKRTKRNAKRLPLESWRR 221  
 5 Query: 180  
 WCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSVAPDTINNHVKTCEEQKN 239  
 WCTQILSALSYLHSC PPIIHGNLTCD+IFIQHNGL+KIGSV PD ++ V+  
 RE ++  
 10 Sbjct: 222  
 WCTQILSALSYLHSCSPPIIHGNLTCD SIFIQHNGLVKIGSVVPDAVHYSVRRGRERERE 281  
 Query: 240 ----LHFF-APEYGEVTNVTTAVDIYSFGMCALEMAVLEIQ-  
 GNGESSYVPQEAISSAIQ 293  
 15 H+F APEYG +T A+DIY+FGMCALEMA LEIQ N ES+ +  
 +E I I  
 Sbjct: 282  
 RERGAHYFQAPEYGAADQLTAALDIYAFGMCALEMAALEIQPSNSESTAINETIQRITF 341  
 20 Query: 294 LLEDPLQREFIQKCLQSEPARRPTARELLFHPALFEVPSLKLLAAHCIV---  
 GHQHMIPE 350  
 LE+ LQR+ I+KCL +P RP+A +LLFHP LFEV SLKLL AHC+V  
 ++ M E  
 Sbjct: 342  
 25 SLENDLQRDLIRKCLNPQRPQDRPSANDLLFHPLLFEVHSLKLLTAHCLVFSPANRTMFSE 401  
 Query: 351 NALEEITKNM-  
 DTSVLAELIPAGPGREPVTLYSQSPALEDKFLEDVRNGIYPLTAFGL 409  
 A + + + V+A++ G+E L S A +L+KF+EDV+  
 30 G+YPL +  
 Sbjct: 402  
 TAFDGLMQRYYQPDVVMAQLRLAGGQERQYRLADVSGADKLEKFVEDVKYGVYPLITYS- 460  
 Query: 410  
 35 PRXXXXXXXXXXXXXXXXXXXXXXXXXAEVETRKVVLMQCNIESVEEGVXXXXXXXXXXXX 469  
 + + E+R++V M C+++ E+  
 Sbjct: 461  
 GKKPPNFRSRAASPERADSVKSATPEPVDTESRRIVNMMCSVKIKEDSNDITMTILLRMD 520  
 40 Query: 470 XXXXXXXXSCDLMPNENIPELAAELVQLGFISEADQSRLTSLLEETL 515  
 +C + N+ +L +ELV+LGF+ DQ ++ LLEETL  
 Sbjct: 521 DKMNRQLTCQVNENDTAADLTSELVRLGFVHLDDQDKIQVLLEETL 566

45 Pedant information for DKFZphfbr2\_78d18, frame 1  
 -----

Report for DKFZphfbr2\_78d18.1

50 [LENGTH] 564  
 [MW] 62464.87  
 [pI] 5.10  
 [HOMOL] TREMBL:AF145690\_1 gene: "BcDNA-LD28657"; product:  
 55 "BcDNA-LD28657"; Drosophila melanogaster clone LD28657  
 BcDNA-LD28657 (BcDNA-LD28657) mRNA, complete cds. 1e-123  
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae,  
 YJL095w] 6e-15

- 1 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YJL095w] 6e-15  
 [FUNCAT] 11.01 stress response [S. cerevisiae, YJL095w] 6e-15  
 5 [FUNCAT] 03.01 cell growth [S. cerevisiae, YJL095w] 6e-15  
 [FUNCAT] 10.02.11 key kinases [S. cerevisiae, YJL095w] 6e-15  
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YJL095w] 6e-15  
 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YLR096w] 2e-09  
 10 [FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YLR096w] 2e-09  
 [FUNCAT] 10.03.11 key kinases [S. cerevisiae, YNR031c] 3e-09  
 [FUNCAT] 09.01 biogenesis of cell wall [S. cerevisiae, YNR031c] 3e-09  
 15 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YLR362w] 4e-08  
 [FUNCAT] 10.05.11 key kinases [S. cerevisiae, YLR362w] 4e-08  
 [FUNCAT] 10.04.11 key kinases [S. cerevisiae, YLR362w] 4e-08  
 20 [FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision repair) [S. cerevisiae, YPL153c] 1e-07  
 [FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YPL153c] 1e-07  
 [FUNCAT] 03.22.01 cell cycle check point proteins [S. cerevisiae, YPL153c] 1e-07  
 25 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YPL153c] 1e-07  
 [FUNCAT] 03.25 cytokinesis [S. cerevisiae, YDR507c] 1e-07  
 [FUNCAT] 10.99 other signal-transduction activities [S. cerevisiae, YPL153c] 1e-07  
 30 [FUNCAT] 03.13 meiosis [S. cerevisiae, YDR523c] 3e-07  
 [FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YDR523c] 3e-07  
 [FUNCAT] 03.16 dna synthesis and replication [S. cerevisiae, YMR001c] 2e-06  
 35 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YDR490c] 3e-05  
 [FUNCAT] 05.07 translational control [S. cerevisiae, YDR283c] 1e-04  
 [FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YDR477w] 1e-04  
 40 [BLOCKS] PF00637A  
 [BLOCKS] BP03191J  
 [BLOCKS] PF01317B  
 [SCOP] d1ir3a\_ 5.1.1.2.6 insulin receptor Complex  
 45 (transferase/substrate) 2e-53  
 [SCOP] d1phk\_ 5.1.1.1.6 gamma-subunit of glycogen phosphorylase kinase 3e-68  
 [SCOP] d1fgkb\_ 5.1.1.2.5 Fibroblast growth factor receptor 1 [Human (Homo)] 1e-55  
 50 [SCOP] d1abo\_ 5.1.1.1.14 Protein kinase CK2, alpha subunit [Maize (Zea)] 2e-55  
 [SCOP] d3lck\_ 5.1.1.2.2 Lymphocyte kinase (lck) [Human (Homo sapiens)] 7e-54  
 [SCOP] d2erk\_ 5.1.1.1.11 MAP kinase Erk2 [Rat (Rattus norvegicus)] 9e-71  
 55 [SCOP] d1cdkb\_ 5.1.1.1.2 cAMP-dependent PK, catalytic subunit Complex 1e-55



```

[SCOP]          dlhcl_ 5.1.1.1.1 Cyclin-dependent PK [Human
(Homo sapiens) 4e-67
[EC]            2.7.1.12 Protein-tyrosine kinase 4e-06
[EC]            2.7.1.37 Protein kinase 3e-09
5  [PIRKW]       phosphotransferase 2e-28
   [PIRKW]       nucleus 3e-06
   [PIRKW]       RNA binding 3e-10
   [PIRKW]       tandem repeat 4e-07
   [PIRKW]       cell cycle control 3e-06
10 [PIRKW]       serine/threonine-specific protein kinase 2e-13
   [PIRKW]       transmembrane protein 4e-07
   [PIRKW]       autophosphorylation 3e-10
   [PIRKW]       tyrosine-specific protein kinase 4e-06
   [PIRKW]       magnesium 4e-07
15 [PIRKW]       ATP 2e-13
   [PIRKW]       receptor 4e-07
   [PIRKW]       phosphoprotein 2e-13
   [PIRKW]       apoptosis 3e-06
   [PIRKW]       glycoprotein 4e-07
20 [PIRKW]       protein kinase 2e-28
   [PIRKW]       signal transduction 2e-08
   [PIRKW]       cell division 1e-11
   [PIRKW]       calmodulin binding 3e-06
   [SUPFAM]      protein kinase byr2 1e-06
25 [SUPFAM]      unassigned Ser/Thr or Tyr-specific protein kinases 2e-
   13
   [SUPFAM]      leucine-rich alpha-2-glycoprotein repeat homology 4e-07

   [SUPFAM]      double-stranded RNA-binding repeat homology 3e-10
30 [SUPFAM]      SAM homology 1e-06
   [SUPFAM]      death-associated protein kinase 3e-06
   [SUPFAM]      ankyrin repeat homology 3e-06
   [SUPFAM]      protein kinase homology 2e-28
   [SUPFAM]      kinase-related transforming protein 2e-06
35 [SUPFAM]      protein kinase SPK1 3e-06
   [SUPFAM]      protein kinase Xa21 4e-07
   [SUPFAM]      protein kinase TIK 3e-10
   [SUPFAM]      kinase interaction domain homology 3e-06
   [PFAM]        Eukaryotic protein kinase domain
40 [KW]          All_Alpha
   [KW]          3D
   [KW]          LOW_COMPLEXITY      16.49 %

45 SEQ  IRGPGTRAGAEAQAAGRGVGSAGLSVPSSMSEGESQTVLSSGSDPKVESSSSAPGLTSVS
SEG    .....xxxxxxx.....xxxxx
lkobA
.....

50 SEQ  PPVTSTTSAASPEEEEESEDESEILEESPCGRWQKRREEVNQRNVPGIDSAYLAMDTTEG
SEG    xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.....
lkobA
.....

55 SEQ  VEVVWNEVQFSEKKNYKLQEEKVRAVFDNLIQLEHLNIVKFHKEYWADIKENKARVIFITE
SEG    .....
lkobA    .....CHHHHHHHHHHHHHHTTTBTTCCEE---
EEEETTTEEEEEEC

```

```

SEQ  YMSSGSLKQFLKKTKKNHKT MNEKA WKRWCTQILSALS YLHSCDPPIIHGNLTCDTIFIQ
SEG  .....
1koba  CCCCEEH--HHHHCTTTTC-CCHHHHHHHHHHHHHHHHHHHHH--
5  HHCEETTTTTTTTEETT

SEQ  HNGLIKIGSVAPDTINN HVKTCREEQKNLHFFAPEYGEVTVTTAVDIYSFGMCALEMAV
SEG  .....
1koba
10  TTCCEEECCTTTTTEECTTTTTEEEETTTGGGCCCHHHHHCCCBCHHHHHHHHHHHHHHHHC

SEQ  LEIQNGESSYVPQEAISSAIQLLEDPLQREFIQKCLQSEPARRPTARELLFHPALFEVP
SEG  .....
1koba
15  CCTTTTCCCHHHHHHHHHHCCCCTTTHHHHHHHHHTTTTTGGGCCCHHHHHHTTTT....

SEQ  SLKLLAAHCIVGHQHMIPENALEEITKNM DTS AVLAEIPAGPGREP VQTLYSQSPALED
SEG  .....
1koba
20  .....

SEQ  KFLEDVRNGIYPLTAFGLPRPQQPQQEEVTS PVVPPSVKTPTPEPAEVETR KVVLMO CNI
SEG  .....
1koba
25  .....

SEQ  ESVEEGVKHHLTLLLKLEDKLN RHLSCDLMPNENIPELAAELVQLGFISEADQSRLTSLL
SEG  .....
1koba
30  .....

SEQ  EETLNKFN FARNSTLNSAAVTVSS
SEG  .....
1koba
35  .....

```

(No Prosite data available for DKFZphfbr2\_78d18.1)

40 Pfam for DKFZphfbr2\_78d18.1

HMM\_NAME Eukaryotic protein kinase domain

```

45  HMM
    *rLnHPNIIRFYDwFed...ddDHIYMIMEYMeGGDLFDYIrrng...p
      +L H NI++F ++ D + ++ +I+EYM G+L +++++ +
    Query 152
    QLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLKKTKKNHKT 200
50  HMM
    MsEweIrfIMyQILrGMeYLHSMg..IIHRDLKPENILIDeNgqIKIcDF
      M+E+ +++ +QIL++++YLHS IIH L + I+I +NG
    IKI+
55  Query 201
    MNEKA WKRWCTQILSALS YLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSV 250

```

HMM

GLARqMnnYerMttfCGTPWYMMAPEVIImgnyYttkVDMWSFGCILWEM

++ N+ + + + APE + ++ TT+VD++SFG+

EM

5 Query 251 APDTINNHVKTCTREEQKNLHFF-APEY-  
 GEVTNVTTAVDIYSFGMCALEM 298

HMM

MTGepPFyddnMemImrIiqrfrrrpfWpnCSeElyDFMrwCwnyDPekRP

10 + ++ + N E + ++ + ++ + + ++F+ +C++

P++RP

Query 299 A--VLEIQ-  
 GNGESSYVPQEAISSAIQLLEDPLQREFIQKCLQSEPARRP 345

15 HMM TFrQILnHPWF\*

T+R++L HP +

Query 346 TARELLFHPAL 356

DKFZphfbr2\_78d4

-----

group: transmembrane protein

5

DKFZphfbr2\_78d4 encodes a novel 188 amino acid protein without similarity to known proteins.

10

The novel protein contains 1 transmembrane region and a Cytochrome c family heme-binding site.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

15

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for amygdala cells.

20

weak similarity to hypothetical protein of *Arabidopsis thaliana*

perhaps complete cds.

Pedant: TRANSMEMBRANE 1

25

Sequenced by MediGenomix

Locus: unknown

Insert length: 1547 bp

30

Poly A stretch at pos. 1527, polyadenylation signal at pos. 1508

```

      1 TTGCCGCCGC CGCCACCCCC GCCCAGGATG GCGGAAGTGG AGGCGCCGAC
    51 GGCGCCCGAG ACGGACATGA AGCAATATCA AGGCTCCGGC GGCCTCGCCA
   101 TGGATGTGGA ACGGAGTCGC TTCCCCTACT GCGTGGTGTG GACGCCCATC
   35 151 CCGGTGCTCA CGTGGTTTTT CCCCATCATC GGCCACATGG GCATCTGCAC
      201 ATCCACAGGA GTCATTGCGG ACTTCGCGGG CCCCTACTTT GTCTCAGAGG
      251 ACAACATGGC CTTTGGAAAG CCTGCCAAGT ACTGGAAGTT GGACCTGCT
      301 CAGGTCTATG CTAGCGGGCC CAACGCATGG GACACGGCTG TGCACGACGC
      351 CTCTGAGGAG TACAAGCACC GCATGCACAA TCTCTGCTGT GACAAC TGCC
   40 401 ACTCGCACGT GGCATTGGCC CTGAATCTGA TGCCTACAA CAACAGCACC
      451 AACTGGAATA TGGTGACGCT CTGCTTCTTC TGCCTGCTCT ACGGGAAGTA
      501 CGTCAGCGTT GGGGCCTTCG TGAAGACCTG GCTGCCCTTC ATCCTTCTCC
      551 TGGGCATCAT CCTCACCGTC AGCCTGGTCT TTAACCTCCG GTGATGGCTG
      601 CTCGGTGGCC CCACACCCAC CAGGGTCCCG AGGAAACAGC CGCCATCCCT
   45 651 TTTGGTTCCA GATTTTTTTC TCCTCACCCC AAAAGGCAGG GTTGGGCCTG
      701 CTGTTGTGGA CCGGGGGTCC GGGCTGGCAG GATGGAAGGA CTGAGGACCA
      751 GCATGAAGTG GGGGTTTGTT GTCTCCCTGC CTCTCAGAAG CACCCTGTCC
      801 CCTCCTCCCC AGGCCTGTGA CTCCGGCCCT GGAAGCCCTT TTGTTCTTCT
      851 GTTGAAAGGC TTTGGCTTCC CTCTGTAGAG CTGCTCCCGC CACCACCTGC
   50 901 TGGGGTCTCT CCTCAGCCCA GTGCCAGTA TGGGGAGAGG AGGACATTTG
      951 GGCTCACCTG TCAAGGTGGC CCTGGGACCA GAGCTGGTCC CAGCATGGGG
   1001 TGCACCGGGT ACACTTAACG TGCTCTCTATA AGCCAAGTTG CTTCAGGACC
   1051 TTCACCACTG GCCTCTAGAA TGGTCCAGAG GGGCTGGCTG GGTCCCTTTG
   1101 TCAGACTCCT GCCGGCAGCT GCCCTGGGGG ACATGTGTGC CCATCTGGCA
   55 1151 TCCTCCAGCC CGTGCAGTCC GCTCTTCACT GTTCCACGGC CTCCAGTGC
   1201 CTCCAGCAT TGGACCCATC TCCCCTGCA GTTTGAGGCC AGAGAGGTGA
   1251 GTGGACCTGA CAAGTGCCAG AGTAACCGTG TAGACAGAGC AGTGTAGACA
   1301 GCGCTCAGCC CCAGCCCCAG GTGTGGACCT CATGCTGGTG ATGGCTCCCC

```

1351 TGGGTGGCCT GCCAGCACAG CCAGTGCCAT CAGGGAGCTG AAGGGGCTGT  
1401 CCCCCACCTA ACTCCAGCTC CCCCTTCACG TTGTCACCAA GGCCCTGTGC  
1451 CGCCCGCCTC GCCCCCCTGC TCTGTGGATT CCTTTGGGAA GGGCTCCCTG  
1501 GGCAGGACAA TAAAGAGTTT TGACTCCAAA AAAAAAAAAA AAAAAAA

5

## BLAST Results

-----

10 Entry T02616 from database PIR:  
hypothetical protein T19L18.12 - Arabidopsis thaliana  
Score = 229, P = 1.3e-17, identities = 57/161, positives =  
78/161,  
frame +1

15

## Medline entries

-----

20

No Medline entry

25

## Peptide information for frame 1

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ORF from 28 bp to 591 bp; peptide length: 188  
Category: similarity to unknown protein  
30 Classification: no clue  
Prosites motifs: CYTOCHROME\_C (121-119)

35

1 MAEVEAPTAA ETDKQYQGS GGVAMDVERS RFPYCVVWTP IPVLTWFFPI  
51 IGHMGICTST GVIRDFAGPY FVSEDNMAFG KPAKYWKLDP AQVYASGPNA  
101 WDTAVHDASE EYKHRMHNLC CDNCHSHVAL ALNLMRYNNS TNWNMVTLCF  
151 FCLLYGKYVS VGAFVKTWLP FILLGIIILT VSLVFNLR

40

## BLASTP hits

No BLASTP hits available

45

Alert BLASTP hits for DKFZphfbr2\_78d4, frame 1

PIR:T02616 hypothetical protein T19L18.12 - Arabidopsis thaliana,  
N =  
2, Score = 226, P = 4.5e-21

50

>PIR:T02616 hypothetical protein T19L18.12 - Arabidopsis thaliana  
Length = 267

55

HSPs:

Score = 226 (33.9 bits), Expect = 4.5e-21, Sum P(2) = 4.5e-21  
Identities = 52/132 (39%), Positives = 71/132 (53%)

Query: 25  
MDVERSRFPYCVVWTPVIPVLTWFFPIIGHMGICTSTGVIRDFAGPYFVSEDNMAFGKPAK 84  
+D ++S+FP C+VWTP+PV++W P IGH+G+C GVI DFAG F++ D+

5 AFG PA+  
Sbjct: 61  
IDTKKSKFPCCIWWTPLPVVSWLAPFIGHIGLCREDGVILDFAGSNFINVDDFAFGPPAR 120

Query: 85 YWKLDPAQVYASGPNAWDTAVHDAEEYKHRMHNL--  
10 CDNCHSHVALALNLMRYNNST- 141  
Y +LD + PN H +KH DN S +

YN T  
Sbjct: 121 YLQLDRTKCCLP-PNMGG---  
HTCKYGFKHTDFGTARTWDNALSSSTRSFEHKTYNIFTC 176

15 Query: 142 NWN-MVTLCFFCLLYG 156  
N + V C L YG  
Sbjct: 177 NCHSFVANCLNRLCYG 192

20 Score = 157 (23.6 bits), Expect = 1.8e-13, Sum P(2) = 1.8e-13  
Identities = 27/81 (33%), Positives = 50/81 (61%)

Query: 101  
25 WDTAVHDAEEYKHRMHNLCCDNCHSHVALALNLMRYNNSTNWNMVTLCFFCLLYGKYVS 160  
WD A+ ++ ++H+ +N+ NCHS VA LN + Y S WNMV +

++ GK+++  
Sbjct: 155  
WDNALSSSTRSFEHKTYNIFTCNCHSFVANCLNRLCYGGSMEWNMVNVAILLMIKGKWIN 214

30 Query: 161 VGAFVKTWLPFILL--LGIIL 179  
+ V+++LP ++ LG++L  
Sbjct: 215 GSSVVRSLPCAVVTSLGVVL 235

Score = 36 (5.4 bits), Expect = 4.5e-21, Sum P(2) = 4.5e-21  
35 Identities = 7/21 (33%), Positives = 14/21 (66%)

Query: 10 AETDMKQYQGS GG VAMDVERS 30  
++ ++K +G G MD++RS  
40 Sbjct: 12 SDRNLKMSRGRGVPMMDLKRS 32

Pedant information for DKFZphfbr2\_78d4, frame 1

45 Report for DKFZphfbr2\_78d4.1

50 [LENGTH] 188  
[MW] 21178.66  
[pI] 6.27  
[HOMOL] PIR:T02616 hypothetical protein T19L18.12 -  
Arabidopsis thaliana 7e-32  
[PROSITE] CYTOCHROME\_C 1  
[KW] TRANSMEMBRANE 1

55 SEQ MAEVEAPTAAETDMKQYQGS GG VAMDVERSRFPYCVVWTPVIPVLTWFFPIIGHMGICTST  
PRD cccccchhhhhhhhhhhcc

```
SEQ      GVIRDFAGPYFVSEDNMAFGKPAKYWKLDPAQVYASGPNAWDTAVHDASEEYKHRMHNLC
PRD      eeeeeccccccccccccccccccccceeecccccceecccccccccccccccccchhhhhhhee
MEM      .....

```

```
SEQ  CDNCHSHVALALNLMRYNNSTNWNMVTLCFFCLLYGKYVSVGAFVKTWLPFILLGIIIT
PRD  eccccchhhhhhhhhhhccccccchhhhhhhhhhhccceeeeeeeeeeeccceeeceeeec
MEM  .....MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM
```

```
SEQ  VSLVFNLR
PRD  ceeeeccc
MEM  MMMMM...
```

Prosites for DKFZphfbr2\_78d4.1

PS00190 121->127 CYTOCHROME\_C PD0C00169

(No Pfam data available for DKFZphfbr2\_78d4.1)

DKFZphfbr2\_78e18

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5 group: brain derived

DKFZphfbr2\_78e18 encodes a novel 307 amino acid protein without similarity to known proteins.

10 The mRNA is differentially polyadenylated.  
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

15 The new protein can find application in studying the expression profile of brain-specific genes.

similarity to hypothetical protein of Arabidopsis thaliana

20 differential polyadenylation  
> 7 exons  
complete on human genomic clone 451B21ap.  
perhaps complete cds.

25 Sequenced by MediGenomix

Locus: /map="144.50 cR from top of Chr6 linkage group"

Insert length: 3096 bp

30 Poly A stretch at pos. 3075, polyadenylation signal at pos. 3047

```

      1 TGGTGAGTTC GGAGTAGAGA TGGCCGCGCT TGCACCGCTG CCCCCGCTCC
      51 CCGCACAGCT CAAGAGCATA CAGCATCATC TGAGGACGGC TCAGGAGCAT
35 101 GACAAGCGAG ACCCTGTGGT GGCTTATTAC TGTCGTTTAT ACGCAATGCA
    151 GACTGGAATG AAGATCGATA GTAAAACTCC TGAATGTCGC AAATTTTTAT
    201 CAAAGTTAAT GGATCAGTTA GAAGCTCTAA AGAAGCAGTT GGGTGATAAT
    251 GAAGCTATTA CTCAAGAAAT AGTGGGCTGT GCCCATTGTG AGAATTATGC
    301 TTTGAAAATG TTTTGTATG CAGACAATGA AGATCGTGCT GGACGATTTC
40 351 ACAAAAACAT GATCAAGTCC TTCTATACTG CAAGTCTTTT GATAGATGTC
    401 ATAACAGTAT TTGGAGAACT CACTGATGAA AATGTGAAAC ACAGGAAGTA
    451 TGCCAGATGG AAGGCAACAT ACATCCATAA TTGTTTAAAG AATGGGGAGA
    501 CTCCTCAAGC AGGCCCTGTT GGAATTGAAG AAGATAATGA TATTGAAGAA
    551 AATGAAGATG CTGGAGCAGC CTCTCTGCCC ACTCAGCCAA CTCAGCCATC
45 601 ATCATCTTCA ACTTATGACC CAAGCAACAT GCCATCAGGC AACTATACTG
    651 GAATACAGAT TCCTCCGGGT GCACACGCTC CAGCTAATAC ACCAGCAGAA
    701 GTGCCTCACA GCACAGGTGT AGCAAGTAAT ACTATCCAAC CTACTCCACA
    751 GACTATACCT GCCATTGATC CCGCACTTTT CAATACAATT TCCCAGGGGG
    801 ATGTTTCGTCT AACCCAGAA GACTTTGCTA GAGCTCAGAA GTACTGCAAA
50 851 TATGCTGGCA GTGCTTTGCA GTATGAAGAT GTAAGCACTG CTGTCCAGAA
    901 TCTACAAAAG GCTCTCAAGT TACTGACGAC AGGCAGAGAA TGAAGCCTTT
    951 GTATGACAGA CCCATGTATT TTTGGCATGA GGAACATAACA GTCCATTACT
1001 CTATCTTCAG CCTATCAGGA TCACAGTTTT AAGGAAGACT TGGTTTTGTT
1051 GAATATGACA ATGAAATCTG TGTGTATCAG ATTTTTATTG AAGCATTTCAT
55 1101 CAGCAGCCTC AACCAGTTTT CATTGTCCAT TTAGTAGATT CAATCGTCTC
    1151 TGAGTATATA GGGCTGATGT TAGCAAGACC CTAAAAATGT CCATTGAACC
    1201 CTGCTTCAAA AAATGAAAC ACACCTCTAT AAAATGTGTA CTGGGAATAA
    1251 GCTTTGTATT TACATACATT AGGGGAATTT TTTAAATCT GTAATGTTTG

```



1301 GACAAACAGA TGATATTACT TTGCTATAAA ATTATAAATG TAACTTTTAA  
1351 TAAAGATAGC CAGAATATTC TAAATTAGAA ATTACGTTTT TGTTCCTCCTC  
1401 AAGACATAAA ACAAAATATA ACATTCTAAA CTGCTGGATG AATCTGAAAA  
1451 GACATTAAAGT TCAAATTTTA ATTTATTCTC ATATTAAATA TAACTCCATT  
5 1501 AAAAGTTTTAA AATTTTCATGG GAGAAAAATAT AATAAGGTAA AGAGGTAGAA  
1551 TCACTTTTCAG ACTTAAGAAT AATGTTGATT TCCCAAGTGC TTTACCTTAT  
1601 CTGTTAAAGC GTAAGATGAA TTGGTATTTG CTTCATAGGC AGTTTGACTG  
1651 CATGTATTAG AGAATGAAAA GAAGATATTT GTAGTAATGC CTGGAAACTT  
1701 GGTGCTTTAA ATTAAGGTAC TCCTCTGCTG CTGTAGAATG GATTCCACAC  
10 1751 AGTGGATAGC TATGGGTGAT TCAGAATATT ATGTTTAGAT TCCCATTGTGT  
1801 TAAGTTTATA AGTTTTGTGG GGAATTATGA ACTTACTGTG TACTACCTGC  
1851 ATTTGTGCTG TGTGAAAAAT AAATACAAGG ATTCGTTTAG CTAATTCAAC  
1901 TTAATAACAA GACAAATGTC TGTTTTTATT TGCCTGCTAG GATTGTCTTT  
1951 TTTAAAAGTC ATTTTTATTT ATAGGAATAT GGGTGTCTTCT ATAGGAAGAA  
15 2001 ACAGGTTTTT TGTTTTTTGT TTTTAAAGAT AAATTTGACA AAGTTAACTG  
2051 AAATTTATCT GGTCCATTTT ATTCATGCTA CTAAGATGGG AATCTTTAAA  
2101 CACAAGGGTC AGCAAGCTTT GGCCCATGGA TTGGCCACCT GTTACGTAAA  
2151 TAAAGTTTCT TTGAAACAAG CCTACACTCA TTCATTTATG TTTTGTCTGT  
2201 GGTGCTTTTC CACAAGTACA GAGTTGTATG GCTTGCAAGT CTAATAACAT  
20 2251 TTAATAATTT GGCCTCTAAG AAAAAGTTAA GACACCTAGT CTAATGGCCT  
2301 TTTGGGAAAA AACAAATCAC TAACCTATAA TCATTTATAT CCATTATTTT  
2351 CTGCATAAAT GTAATGCTAT TGTACAGGGT TTGGTAGAAT AAATATTTCAG  
2401 ACTGACTAAA CTGTTCTAAA TTCTCACAAA AAAGTCCCCA AACAACATGC  
2451 CTCCTAAAAA ACATTTTCCT ATCTTTTACA AGAGGTATGA ACATTTGTAG  
25 2501 GGTTCACAT TTGCATCTAG AAATCCAATG CTCTTTAGAA TGTTATTACG  
2551 AATAGAAAGA TGGCCAGGAT GACCTTTAGT GTTACATGAT GTTCAGCAAA  
2601 TTTTAATTCA AACCTTGATA TGCCTGGACA CTGAAAAGTA AACGCATCAC  
2651 CTCCTATTTT ATACCCTACC TTCTGGTTCC CAATTGGGAG AGCACATAGA  
2701 GGGAAAGGAGA CAATATAGAA ACTACGGAGT CCGCTGGTAG TGGGCTGCAT  
30 2751 GGTGTGACAG AGCCCTTCTC TGTAATAATG AAATGACACC ACTAGCCATC  
2801 TCAATAGTTA CAAGAATTAA AAGAGATACA GTACCTGAAG TGCTTAGCGC  
2851 ATGGTAGCAT TTCATAAATG TTTAGTGTCA ATACTAATGC TCTAATAATG  
2901 TAAATTGTTA ATAATTTATT TCCCTAATAT CAGGAAATCC CAGTTGTCTA  
2951 TGTGGCCAG TGCTTAAAAA CGCCTTCTTG CATGAGGGGA TTGAACTATA  
35 3001 CAATGTTTGT TAACTTTGTA TTTGTATTTT TTCCTATAAA ATCTTAAAT  
3051 AAAATTAGGA GATGTGTTCT GATGTAAAAA AAAAAAAAAA AAAAAA

## BLAST Results

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Entry HS451B21 from database EMBL:

Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
451B21

45 Score = 11219, P = 0.0e+00, identities = 2287/2343

## Medline entries

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No Medline entry

## Peptide information for frame 2

-----

ORF from 20 bp to 940 bp; peptide length: 307

Category: similarity to unknown protein

Classification: no clue

```

5      1 MAALAPLPPL PAQLKSIQHH LRTAQEHDKR DPVVAYYCRL YAMQTGMKID
      51 SKTPECRKFL SKLMDQLEAL KKQLGDNEAI TQEI VGCAHL ENYALKMFLY
     101 ADNEDRAGRF HKNMIKSFYT ASLLIDVITV FGELTDENVK HRKYARWKAT
     151 YIHNCLKNGE TPQAGPVGIE EDNDIEENED AGAASLPTQP TQPSSSSTYD
     201 PSNMPSGNYT GIQIPPGAHA PANTPAEVPH STGVASNTIQ PTPQTIPAI
10    251 PALFNTISQG DVRLTPEDFA RAQKYCKYAG SALQYEDVST AVQNLQKALK
     301 LLTTGRE

```

## 15 BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2\_78e18, frame 2

20

No Alert BLASTP hits found

Pedant information for DKFZphfbr2\_78e18, frame 2

25

Report for DKFZphfbr2\_78e18.2

```

30  [LENGTH] 313
    [MW] 34463.95
    [pI] 5.64
    [HOMOL] PIR:T04798 hypothetical protein F10M23.90 -
    Arabidopsis thaliana 3e-22
    [KW] All_Alpha
35  [KW] LOW_COMPLEXITY 16.61 %

```

```

SEQ GEFQVEMAALAPLPPLPAQLKSIQHHLRTAQEHDKRDPVVAYYCRLYAMQTGMKIDSKTP
SEG .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
40 PRD ccchhhhhheeeccccchhhhhhhhhhhhhhhhhhhhhccceehhhhhhhhhhhcccccccc

SEQ ECRKFLSKLMDQLEALKKQLGDNEAITQEI VGCAHLENYALKMFLYADNEDRAGRFHKNM
SEG .....
45 PRD chhhhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhhhhhhhhhhhhhhccccccccchh

SEQ IKSFYTASLLIDVITVFGELTDENVKHRKYARWKATYIHNCLKNGETPQAGPVGIEEDND
SEG .....xxxxxxxx.
PRD hhhhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhhhhhhhhhhhhhhcccccccccccccc

50 SEQ IEENEDAGAASLPTQPTQPSSSSTYDPSNMPSGNYTGIQIPPGAHA PANTPAEVPHSTGV
SEG xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.
PRD ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

55 SEQ ASNTIQPTPQTIPAI DPALFNTISQGDVRLTPEDFARAQKYCKYAGSALQYEDVSTAVQN
SEG .....
PRD cccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhhhhccceecchhhhhh

SEQ LQKALKLLTTGRE

```

SEG .....  
PRD hhhhhhhhcccc

5 (No Prosite data available for DKFZphfbr2\_78e18.2)

(No Pfam data available for DKFZphfbr2\_78e18.2)

DKFZphfbr2\_78i21

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5 group: metabolism

DKFZphfbr2\_78i21 encodes a novel 477 amino acid protein with similarity to beta-aspartate methyltransferases.

10 The L-isoaspartyl methyltransferase (Pimt), as an example, is a highly conserved enzyme utilising S-adenosylmethionine (AdoMet) to methylate aspartate residues of proteins damaged by age-related isomerisation and deamidation.

15 The new protein can find application in diagnosis/modulation of protein damage and age-related degenerative processes.

unknown protein

20

weak similarity to beta-aspartate methyltransferase pimT of *Mycobacterium leprae*  
perhaps complete cds.

25 Sequenced by MediGenomix

Locus: unknown

Insert length: 1842 bp

30 Poly A stretch at pos. 1819, polyadenylation signal at pos. 1802

```

      1 CCTTCGCGAA ACACATATGCT AATGGCATGG TGCCGCGGTC CTGTCTTGCT
      51 GTGCCTGCGG CAGGGGCTCG GAACCAATTC ATTCCTGCAC GGCCTGGGGC
35 101 AGGAGCCCTT CGAGGGAGCT CGGTCACTGT GTTGCAGGTC CTCGCCTAGA
      151 GACCTGCGAG ATGGAGAAAG AGAGCACGAG GCGGCACAAA GGAAAGCCCC
      201 AGGAGCAGAG TCTTGCCCAT CTCTCCCTCT GAGCATCTCG GACATTGGGA
      251 CTGGATGTCT TTCGTCACTG GAAAACCTCA GACTGCCGAC GCTGCGGGAA
      301 GAGTCATCCC CTCGAGAGCT CGAGGACTCG AGCGGAGACC AGGGCCGGTG
40 351 CGGTCCCACA CACCAGGGAT CCGAGGATCC TTCGATGCTC TCGCAGGCCC
      401 AGTCCGCTAC CGAGGTCGAA GAGCGTCACG TCTCCCCTTC TTGTTCAACT
      451 TCCAGAGAGA GACCCTTTCA GGCTGGGGAA CTGATTTTAG CTGAGACTGG
      501 GGAGGGAGAA ACAAATTATA AGAAATTATT TAGGTTGAAC AACTTCGGAC
      551 TCTTAAATAG TAACTGGGGG GCAGTCCCGT TCGGCAAGAT CGTGGGGAAG
45 601 TTCCCCGGCC AGATACTGAG GAGTTCCTTC GGTAAGCAGT ACATGCTGAG
      651 GAGGCCAGCC TTGGAAGACT ATGTAGTATT GATGAAAAGA GGGACTGCCA
      701 TAACATTCCC AAAGGATATT AATATGATTC TCTCAATGAT GGATATCAAC
      751 CCAGGTGATA CTGTTTTTGA AGCTGGCTCA GGCTCTGGTG GAATGAGCTT
      801 ATTTTATATC AAAGCAGTTG GATCACAAGG ACGAGTCATA AGTTTTGAGG
50 851 TACGAAAAGA CCACCATGAT CTGGCTAAGA AGAATTACAA AACTGGCGT
      901 GATTCATGGA AATTAAGTCA TGTAGAAGAG TGGCCAGACA ATGTGGATTT
      951 TATTCATAAG GACATTTTCA GAGCAACCGA AGACATAAAA TCTTTAACAT
1001 TTGACGCAGT AGCTTTGGAT ATGTTAAATC CTCATGTTAC TTTGCCTGTT
1051 TTTTACCCAC ATCTTAAGCA TGGTGGTGTA TGTGCTGTAT ATGTAGTAAA
55 1101 CATCACACAG GTTATTGAAC TTTTAGATGG AATTCGCACC TGTGAACCTG
      1151 CTCTTTCATG TGAAAAGATA AGCGAGGTCA TTGTCAGAGA TTGGTTGGTT
      1201 TGCCTTGCAA AACAGAAAAA TGGAATTTTA GCTCAAAAAG TAGAATCTAA
      1251 AATCAACACA GATGTACAAC TAGATTCTCA AGAGAAAATT GGAGTTAAAG

```

1301 GTGAGCTGTT TCAAGAGGAT GACCATGAAG AATCGCATTC TGATTTTCCA  
 1351 TATGGATCAT TTCCCTATGT TGCTAGACCA GTACACTGGC AACCTGGTCA  
 1401 TACAGCTTTT CTTGTCAAGT TGAGGAAGGT CAAACCACAA CTTAACTGAG  
 1451 TACTCCAGAT GACAGTAACT GACTTGAAGA TGGAAAAATA TCAAAATAGA  
 5 1501 ACTTTATATT GAAAATCACT GCTTCCATAG ATTGGCATT TTAGCTATTA  
 1551 CTATGACTTA TATAACTTAT ACATATAATT TTGAAAATAA CAACTAAAAG  
 1601 ATGTATAACA TAGCAAACT GCTTAAACAT CCCATTTTGA CACTTGTCTT  
 1651 GCAGTTAGTT TGACATTTTG TAGTTAATGA TTCCAAATTG GTTTAGTTGG  
 1701 GCCATCTCAT TCTTCACTTC CTGTAAACCA CTCCATAGAT TTGTCTTTCT  
 10 1751 TCAAGAAATT AGTTTTCTTT CCTTTATTG ATTGATGGTC ATTGACTACT  
 1801 GAAATAAAAT ATGCATTTTA AGAAAAA AAAA AAAA AA

## BLAST Results

15

No BLAST result

20

## Medline entries

No Medline entry

25

## Peptide information for frame 1

30 ORF from 16 bp to 1446 bp; peptide length: 477  
 Category: putative protein  
 Classification: no clue

35 1 MLMAWCRGPV LLCLRQGLGT NSFLHGLGQE PFEGARSLCC RSSPRDLRDLG  
 51 EREHEAAQRK APGAESCPSL PLSISDIGTG CLSSLENLRL PTLREESSPR  
 101 ELEDSSGDQG RCGPTHQGE DPSMLSQAQS ATEVEERHVS PSCSTSRERP  
 151 FQAGELILAE TGEGETKFKK LFRNNFGLL NSNWGAVPFG KIVGKFPQGI  
 201 LRSSFQKQYM LRRPALEDYV VLMKRGTAIT FPKDINMILS MMDINPGDTV  
 251 LEAGSGSGGM SLFLSKAVGS QGRVISFEVR KDHHDLAKKN YKHWRDSWKL  
 40 301 SHVEEWPQNV DFIHKDISGA TEDIKSLTFD AVALDMLNPH VTLPVFYPHL  
 351 KHGGVCAVYV VNITQVIELL DGIRTCELAL SCEKISEVIV RDWLVCLAKQ  
 401 KNGILAQKVE SKINTDVQLD SQEKIGVKGE LFQEDDHEES HSDFPYGSFP  
 451 YVARPVHWQP GHATAFLVKLR KVKPQLN

45

## BLASTP hits

No BLASTP hits available

50

Alert BLASTP hits for DKFZphfbr2\_78i21, frame 1

No Alert BLASTP hits found

55

Pedant information for DKFZphfbr2\_78i21, frame 1

Report for DKFZphfbr2\_78i21.1

5    [LENGTH]   482  
       [MW]       53521.20  
       [pI]       6.28  
       [HMOL]       TREMBL:AF088800\_2 product: "unknown"; Rhodococcus  
       erythropolis ARC (arc) gene, complete cds; and unknown genes. 2e-  
       23  
 10    [FUNCAT]   r general function prediction       [M. jannaschii,  
       MJ0134]   6e-10  
       [FUNCAT]   05.07 translational control       [S. cerevisiae, YJL125c]  
       6e-04  
       [BLOCKS]   BL00801E  
       [BLOCKS]   BL01279A  
 15    [KW]       Alpha\_Beta  
       [KW]       LOW\_COMPLEXITY       2.49 %

20    SEQ   PSRNTMLMAWCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSLCCRSSPRDLRDGEREHE  
       SEG   .....  
       PRD   ccccccccccccccccchhhhhccccccccccccccccccccccccccccccccchhhhh  
  
       SEQ   AAQRKAPGAESCPSLPLSISDIGTGCLSSLENLRLPTLREESSPRELEDSSGDQGRCGPT  
       SEG   .....  
 25    PRD   hhhhhcc  
  
       SEQ   HQGSEDPMSLSQAQSAATEVEERHVSPSCSTSRERPFQAGELILAETGEGETKFKKLFRLN  
       SEG   .....  
 30    PRD   ccccccccchhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccccccccc  
  
       SEQ   NFGLLNSNWGAVPFGKIVGKFPQGILRSSFGKQYMLRRPALEDYVVL MKRGTAITFPKDI  
       SEG   .....  
       PRD   cc  
  
 35    SEQ   NMILSMMDINPGDTVLEAGSGSGGMSLFLSKAVGSQGRVISFEVRKDHHDLAKKNYKHWR  
       SEG   .....xxxxxxxxxxxx.....  
       PRD   cc  
  
       SEQ   DSWKLSHVEEWPDNVDFIHKDISGATEDIKSLTFDAVALDMLNPHVTLPVFYPHLKHGGV  
       SEG   .....  
 40    PRD   cc  
  
       SEQ   CAVYVVNITQVIELLDGIRTCELALSCEKISEVIVRDWLVLAKQKNGILAQKVESKINT  
       SEG   .....  
 45    PRD   eeeeeechhhhhhhhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccccc  
  
       SEQ   DVQLDSQEKIGVKGELFQEDDHEESHSDFPYGSFPYVARPVHWQPGHTAFLVKLRKVKPQ  
       SEG   .....  
       PRD   cc  
  
 50    SEQ   LN  
       SEG   ..  
       PRD   cc

55    (No Prosite data available for DKFZphfbr2\_78i21.1)  
       (No Pfam data available for DKFZphfbr2\_78i21.1)

DKFZphmel2\_12j1

-----

5

group: melanoma derived

DKFZphmel2\_12j1 encodes a novel 905 amino acid protein, which has similarity to integrin I of *Saccharomyces cerevisiae*.

10

The novel protein contains a leucine zipper.

No informative BLAST results; No predictive prosite, pfam or SCOP motif.

15

The new protein can find application in studying the expression profile of melanoma-specific genes.

weak similarity to integrin I (*Saccharomyces cerevisiae*)

20

Sequenced by EMBL

Locus: unknown

25

Insert length: 2942 bp

Poly A stretch at pos. 2926, no polyadenylation signal found

```

30      1 CGAAAGCTAA AGGCCGGCGC ACGCTGGGCG GTGGTGGTCC CTAAGCCGGG
      51 CCGCGGCCCGG TGCAATGGAC TCCACTGCCT GCTTGAAGTC CTTGCTCCTG
     101 ACTGTCAGTC AGTACAAAGC CGTGAAGTCA GAGGCGAACG CCACTCAGCT
     151 TTTGCGGCAC TTGGAGGTAA TTTCTGGACA GAAACTCACA CGACTATTTA
     201 CATCAAATCA GATATTAACA AGTGAATGCT TGAGTTGCCT TGTAGAGCTA
     251 CTTGAAGACC CCAACATAAG TGCTTCACTG ATCTTAAGTA TTATCGGTTT
35     301 GCTGTCTCAA CTAGCAGTAG ACATTGAAAC CAGAGATTGT CTTCAGAATA
     351 CATATAATCT GAATAGTGTG CTGGCGGGAG TGGTTTGTCT GAGCAGCCAC
     401 ACTGATTTCGG TGTTTTGTCA GTGCATTCAA CTTCTACAGA AGTTAACATA
     451 TAATGTCAAA ATTTTCTATT CTGGTGCCAA TATAGATGAA TTAATTACGT
     501 TCCTGATAGA TCACATTCAA TCTTCTGAAG ATGAGTTAAA ATGCCTTTGT
40     551 CTAGGATTAT TGGCAAATCT TTGTCGGCAC AATCTTTCTG TTCAAACGCA
     601 CATAAAGACA TTGAGTAATG TGAAATCTTT TTATCGAACT CTTATCACCT
     651 TGTGTTGCCA TAGTAGTTTA ACTGTGGTTG TGTGTTGCACT TTCAATATTA
     701 TCCAGTTTGA CATTAAATGA AGAGGTGGGG GAAAAGCTAT TCCATGCTCG
     751 AAACATTCAT CAGACTTTTC AACTAATATT TAATATTCTC ATAAACGGTG
45     801 ATGGCACTCT AACTAGAAAG TATTCAGTTG ACCTACTGAT GGATCTCCTT
     851 AAGAATCCTA AAATTGCTGA TTATCTCACC AGATATGAGC ACTTTTCTTC
     901 ATGTCTTCAC CAAGTATTAG GTCTTCTTAA TGGAAAGGAT CCTGATTCTT
     951 CTTCAAAGGT TTTAGAATTA CTTCTTGCCT TCTGTTTCACT GACTCAGCTG
50    1001 CGCCATATGC TCACTCAGAT GATGTTTGA CAGTCTCCAC CTGGCAGCGC
     1051 CACTCTGGGA AGCCATACTA AATGTTTGA ACCTACTGTG GCTCTACTGC
     1101 GCTGGTTAAG CCAACCTTTG GACGGATCAG AAAACTGTTT TGTGTTAGCA
     1151 TTGGAGTTGT TCAAGGAAAT ATTTGAGGAT GTCATAGATG CTGCTAACTG
     1201 TTCCTCGGCT GATCGTTTTG TGACCCTTCT GCTGCCTACA ATCCTTGATC
     1251 AACTTCAGTT CACAGAACAA AATCTAGATG AGGCTTTAAC AAGAAAAAAT
55    1301 GTGAAAGGGA TTGCCAAGGC CATTGAAGTT TTGTAACTC TCTGTGGAGA
     1351 TGATACACTA AAAATGCATA TTGCAAAAAT CTTGACAACT GTCAAGTGTA
     1401 CCACTCTTAT AGAACAACAA TTTACATATG GCAAGATTGA CCTGGGATTT
     1451 GGAACAAAGG TTGCAGATTC TGAATTATGC AAACCTTGCTG CTGATGTAAT
```

1501 TTTGAAAAC TTTGATTTGA TTAACAAACT TAAACCATTG GTTCCTGGTA  
 1551 TGGGAAGTAAG CTTCTACAAA ATACTTCAGG ACCCACGTTT GATTACTCCT  
 1601 TTGGCTTTTG CTTTAACGTC AGATAATAGA GAACAAGTAC AGTCTGGACT  
 1651 GAGAATATTA TTGGAGGGCTG CTCCACTGCC AGATTTTCCT GCTTTAGTAC  
 5 1701 TTGGAGAAAG TATAGCAGCA AACAATGCCT ATAGACAACA GGAAACAGAA  
 1751 CATATACCCA GAAAAATGCC CTGGCAATCA TCAAATCACA GTTTTCCAAC  
 1801 ATCAATAAAG TGTTTAACTC CTCATTTGAA AGATGGTGT TCTGGATTGA  
 1851 ATATTGAAGA ATTAATAGAG AAACCTTCAGT CTGGAATGGT GGTAAAGGAT  
 1901 CAGATTTGTG ATGTGAGAAT ATCTGACATA ATGGATGTAT ATGAAATGAA  
 10 1951 ACTATCCACA TTAGCTTCCA AAGAAAGCAG GCTACAAGAT CTTTTGGAAA  
 2001 CAAAAGCTCT AGCCCTTGCA CAGGCTGATA GACTGATTGC TCAGCATCGC  
 2051 TGTCAAAGAA CTCAAGCTGA AACAGAGGCA CGGACACTTG CTAGTATGTT  
 2101 GAGAGAAGTT GAGAGAAAAA ATGAAGAGCT TAGTGTGTTG CTGAAGGCGC  
 2151 AGCAAGTTGA ATCAGAAAGA GCGCAGAGTG ATATTGAGCA TCTCTTTCAA  
 15 2201 CATAATAGGA AGTTAGAGTC TGTGGCTGAA GAACATGAAA TACTGACAAA  
 2251 ATCCTACATG GAACCTTCTC AGAGAAATGA AAGTACTGAA AAGAAGAATA  
 2301 AAGATTTACA GATCACATGT GATTCTCTGA ATAAACAAAT TGAGACAGTG  
 2351 AAAAAGTTGA ATGAGTCACT CAAGGAACAA AATGAAAAAA GTATTGCCCA  
 2401 ATTAATAGAG AAAGAAGAAC AGAGAAAAGA AGTACAGAAT CAGCTAGTAG  
 20 2451 ACAGAGAACA TAAGCTAGCA AATTTGCATC AAAAAACAAA AGTACAAGAA  
 2501 GAAAAGATTA AAACCTTACA AAAGGAAAGG GAAGATAAGG AAGAAACCAT  
 2551 TGATATCCTT AGAAAAGAAT TAAGCAGAAC AGAACAGATA AGAAAAGAGT  
 2601 TGAGCATTAA GGCTTCCTCC CTAGAGGTTC AAAAGGCACA ATTAGAAGGT  
 2651 CGTTTGGAAG AGAAAGAGTC CTTGGTGAAA CTTCAGCAAG AGGAATTGAA  
 25 2701 CAAACACTCC CACATGATAG CAATGATCCA CAGTTTAAGT GGTGGAAAAA  
 2751 TAAATCCAGA AACTGTGAAT CTCAGTATAT AGACATTATG GCATTTTGGA  
 2801 ATTTGTAATC TCATGATATT TTTGATGTAT TTATCTATTG GAGGGGGGGT  
 2851 GGGTAGGGGA GTTAATTTGT GACTTCGTAA CAATAAGAAG TTATTATCTA  
 2901 ATTTAGTAAA GACCCTGATC TGTGCAAAA AAAAAAAAAA AA

## BLAST Results

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35 No BLAST result

## Medline entries

-----

40 96039111:  
 Hostetter MK, Tao NJ, Gale C, Herman DJ, McClellan M, Sharp RL,  
 Kendrick KE.; Antigenic and functional conservation of an  
 integrin  
 45 I-domain in  
*Saccharomyces cerevisiae*. *Biochem Mol Med* 1995 Aug;55(2):122-30  
 99458454:  
 Berton G, Lowell CA.; Integrin signalling in neutrophils and  
 50 macrophages. *Cell Signal* 1999 Sep;11(9):621-35

55 Peptide information for frame 2

-----

ORF from 65 bp to 2779 bp; peptide length: 905



Category: putative protein

Classification: Cellular transport and traffic

Prosite motifs: LEUCINE\_ZIPPER (331-352)

```

5      1 MDSTACLKSL LLTVSØYKAV KSEANATØLL RHLEVISGØK LTRLFTSNØI
      51 LTSECLSCLV ELLEDPNISA SLILSIIGLL SØLAVDIETR DCLØNTYNLN
     101 SVLAGVVCRS SHTDSVFLØC IØLLØKLTYN VKIFYSGANI DELITFLIDH
     151 IØSSEDELKM PCLGLLANLC RHNLSVØTHI KTLSNVKSFY RTLITLLAHS
    10  201 SLTVVVFALS ILSSLTLNEE VGEKLFHARN IHØTFØLIFN ILINGØGTLT
      251 RKYSVDLLMD LLKNPKIADY LTRYEHFSSC LHØVLGLLNG KØPDSSSKVL
      301 ELLLAFCSVT ØLRHMLTØMM FEØSPPGSAT LGSHTKCLEP TVALLRØLSØ
      351 PLDØSENCVS LALØLFKEIF EDVIDAANCS SADRFVTLLL PTILDØLØFT
      401 EØNLDEALTR KNVKGIKAI EVLLTLCØDØ TLKMHIKIL TTVKCTTLIE
    15  451 ØØFTYØKIDL GFGTKVADSE LCKLAADVIL KTLDLINKLK PLVPGMEVSF
      501 YKILØDPRLI TPLAFALTSØ NREØVØSGLR ILLEAAPLØ FPALVLGESI
      551 AANNAYRØQE TEHIPRKMPW ØSSNHSFPTS IKCLTPHLKØ GVPGLNIEEL
      601 IEKLØSGMVV KØØICØVRIS DIMØVYEMKL STLASKEØRL ØDLLETØALA
      651 LAØADRLIAØ HRCØRTØAET EARTLASMLR EVERKNEELS VLLKAOØVES
    20  701 ERAØSDIEHL FØHNRKLESV AEEHEILTKS YMELLØRNES TEKKNKØLØI
      751 TØDSLØKØIE TVKKLØESLK EØNEKSIAØL IEKEEØRKEV ØNØLVØREHK
      801 LANLHØKTKV ØEEKIKTLØK EREDKEETID ILRKELSRTE ØIRKELSIKA
      851 SSLEVØKAØL EGRLEEKESL VKLØØEELNK HSHMIAMIHS LSGGKINPET
     901 VNLSI
25

```

## BLASTP hits

30 No BLASTP hits available

Alert BLASTP hits for DKFZphm12\_12j1, frame 2

```

35  TREMBL:SCINTANA_1 Saccharomyces cerevisiae integrin analogue
    gene,
    complete cds., N = 1, Score = 216, P = 1.3e-13

```

```

40  >TREMBL:SCINTANA_1 Saccharomyces cerevisiae integrin analogue
    gene, complete
        cds.

```

Length = 1,015

## HSPs:

```

45  Score = 216 (32.4 bits), Expect = 1.3e-13, P = 1.3e-13
    Identities = 80/302 (26%), Positives = 155/302 (51%)

```

```

50  Query:   597 IEELIEKLØSGMVVKØØICØVRISØIM---
    DVYEMKLSTLASKEØRLØDLLETØALALAO 653
          I L EKL++   Ø+  + +IS++   + E +L+   + ++ L+
    LET   AL +
    Sbjct:  275 ISLLKEKLETATTANDENVN-
    KISELTKTREELEAELAAYKNLKNELETØKLETSEKALKE 333

```

```

55  Query:   654 A---ØRLIAØHRCØRTØAETEAR----TLASMLREVERKNEELSVLLKA--
    ØØVESERAØ 704

```

+ + + + Q + TE + +L + L +E+++E+L+ LK  
 +Q+ ++ Q  
 Sbjct: 334  
 VKENEEHLKEEKIQLEKEATETKQQLNSLRANLESLEKEHEDLAAQLKKYEEQIANKERQ 393  
 5 Query: 705 SDIEHLFQHNRLKESVAEEHEILTKSYMEL---LQRNESTEKKNKDLQIT-  
 CDSL NKQIE 760  
 + E + Q N ++ S +E+E + K EL ++ +ST ++ +L+ +  
 D+LN QI+  
 10 Sbjct: 394 YN-  
 EEISQLNDEITSTQENESIKKKNDELEGEVKAMKSTSEEQSNLKKSEIDALNLQIK 452  
 Query: 761  
 TVKKLNESLKEQNEKSIAQLIEKEEQRKEVQNLVDREHKLANLHQKTKVQEEKIKT--- 817  
 15 +KK NE+ + +SI + + + KE+Q++ +E +++ L K K  
 E+K  
 Sbjct: 453  
 ELKKKNETNEASLLESIKSIESETVKIKELQDECNFKEKEVSELEDKCLKASEDKNSKYLE 512  
 20 Query: 818 LQKEREDKEETIDI----LRKELSRTEQIRKELSIKASSLE-  
 VQKAQLEGRLEEKESLVK 872  
 LQKE E +E +D L+ +L + + K S L ++K E R  
 +E L K  
 Sbjct: 513  
 25 LQKESEKIKEELDAKTTELKIQLEKVTNLSKAKEKSESELSRLKKTSSSEERKNAEEQLEK 572  
 Query: 873 LQQE 876  
 L+ E  
 Sbjct: 573 LKNE 576  
 30 Score = 186 (27.9 bits), Expect = 2.0e-10, P = 2.0e-10  
 Identities = 82/301 (27%), Positives = 155/301 (51%)  
 Query: 598 EELIEKLQSGMVVKDQICQVRISDIMDVYEMKLSTLASKESR---LQD-  
 35 LLETALALAQ 653  
 +ELI +LQ+ +K + D S++ V L K++ LQD +L  
 K  
 Sbjct: 611 DELI-  
 RLQENELKAKEIDNTRSELEKVSLSNDELLEEKQNTIKSLQDEILSYKDKITRN 669  
 40 Query: 654  
 ADRLIAQHRCQRTQAE TEARTLASMLREVERKNEELSVLLKAQQVESERAQSDIEHLFQH 713  
 ++L++ R + E+ L LR + ++ LK + ES +  
 ++++E +  
 45 Sbjct: 670 DEKLLSIEDSKRDLES----  
 LKEQLRAAQESKAKVEEGLKKLEEESSEKAELEKSKEM 725  
 Query: 714 NRKLESVAEEHEILTKSYMELLQRN-ESTEKKNKDLQITCDSL-  
 NKQIETVKKLNESLKE 771  
 50 +KLES E +E KS ME ++++ E E+ K + +L +++ + +  
 ++NES K+  
 Sbjct: 726  
 MKKLESTIESNETELKSSMETIRKSDEKLEQSKKSAEEDIKNLQHEKSDLISRINESEKD 785  
 55 Query: 772 QNE-KSIAQLIEKEEQRKE-VQNLVDREHKL-  
 ANLHQKTKVQEEKIKTLQKEREDKEET 828  
 E KS ++ K E V+ +L + + K+ N + T V + K++  
 +++E +DK+

Sbjct: 786 IEELKSKLRIEAKSSSELETVKQELNNAQEKIRVNAEENT-  
VLKSKLEDIERELKDKQAE 844

5 Query: 829 IDILR--KEL--SRTEQIRKEL-----SIKASSLEVQKAQLE-  
GRLEEKESLVKLQ 874  
I + KEL SR +++ +EL S + S EV+K Q+E  
+L+EK L++ +  
Sbjct: 845  
IKSNQEEKELLTSRLKELEQELDSTQKAQKSEESRAEVRKFQVEKSQLEKAMLLET 904  
10 Query: 875 QEEL-NK 880  
+L NK  
Sbjct: 905 YNDLVNK 911

15 Score = 173 (26.0 bits), Expect = 5.7e-09, P = 5.7e-09  
Identities = 77/287 (26%), Positives = 146/287 (50%)

20 Query: 601 IEKLQSGMVVKDQICDVRISDMDVYEMKLSTLASKES--  
RLQDLLETALALAQADRLI 658  
++K + + K++ + IS + D E+ ST ES + D LE +  
A+  
Sbjct: 380 LKKYEEQIANKERQYNEEISQLEND--EIT-  
STQQENESIKKKNDELEGEVKAMKST---- 432

25 Query: 659 AQHRCQRTQAE TEARTLASMLREVERKNE--  
ELSVLLKAQQVESERAQSDIEHLFQH-NR 715  
++ + ++E +A L ++E+++KNE E S+L + +ESE + I+  
L N  
Sbjct: 433 SEEQSNLKKSEIDALNL--QIKELKKKNETNEASLLESIKSIESETVK--  
30 IKELQDECNF 488

35 Query: 716 KLESVAEEHEILTKSY---  
MELLQARNESTEKKNKDLQITCDLNLKQIETVKKLNESSLKEQ 772  
K + V+E + L S + L+ + +EK ++L L Q+E V  
L+++ KE+  
Sbjct: 489  
KEKEVSELEDKLGASEDKNSKYLELQKESEKIKEELDAKTTELKIQLEKVTNLSKA-KEK 547

40 Query: 773 NEKSIAQLE-KEEQRKEVQNL--VDREHKLAN--  
LHQKTKVQEEKIKTLQKEREDEKEE 827  
+E +++L + E+RK + QL + E ++ N ++ K+ E T+  
+E +K  
Sbjct: 548  
SESELSRLKKTSSSEERKNAEEQLEKLNKNEIQIKNQAFEKERKLLNEGSSTITQYSEKIN 607

45 Query: 828 TI-  
DILRKELSRTEQIRKELSIKASSLEVQKAQLEGRLEEKESLVKLQEEELNKHSHMI 885  
T+ D L + + E KE+ S LE + LEEK++ +K Q+E+  
+ I  
50 Sbjct: 608  
TLEDELIRLQENELKAKEIDNTRSELEKVSLSNDELLEEKQNTIKSLQDEILSYKDKI 666

55 Score = 171 (25.7 bits), Expect = 9.3e-09, P = 9.3e-09  
Identities = 76/311 (24%), Positives = 152/311 (48%)

Query: 596 NIEELIEKLQSGMVVKDQ-----  
ICDVRISDMDVYEMKLSTLASKESRLQDLLET 648

N EE +EKL++ + +K+Q + + S I Y K++TL +  
 RLQ+ E KA  
 Sbjct: 565  
 NAEEQLEKLEKNEIQIKNQAFERKLLNEGSSTITQYSEKINTLEDELIRLQENELKA 624

5 Query: 649 LALAQADRLIAQHRCQRTQA-ETEARTLASMLREVERKNEELSVL-  
 LKAQQVESERAQSD 706  
 + + + E + T+ S+ E+ ++++ K  
 +E + ++ D

10 Sbjct: 625  
 KEIDNTRSELEKVSLSNDELLEEKQNTIKSLQDEILSYKDKITRNDEKLLSIED-SKRD 683  
 Query: 707 IEHLFQHNRL-ESVAEEHEILTKSYMELLQNESTTEKN---  
 KDLQITCDS---LNKQ 758

15 +E L + R ES A+ E L K E + EK K L+ T +S  
 L  
 Sbjct: 684  
 LESLKEQLRAAQESKAKVEEGLKKLEEESSEKAELEKSKEMMKLESTIESNETELKSS 743

20 Query: 759 IETVKKLNESSLKEQNEKSIAQLIEK-  
 EEQRKEVQNLVDREHKLNLHQKTKVQEE---K 814  
 +ET++K +E L EQ++KS + I+ + ++ ++ +++ + E + L K  
 +++ + +

25 Sbjct: 744 METIRKSDEKL-  
 EQSKSAEEDIKNLQHEKSDLISRINESEKDIEELKSKLRIEAKSSSE 802  
 Query: 815 IKTLQKEREDKEETIDILRKE----LSRTEQIRKELSIKASSL---  
 EVQKAQLEGRLEEK 867  
 ++T+++E + +E I + +E S+ E I +EL K + + + +K

30 L RL+E  
 Sbjct: 803  
 LETVKQELNNAQEKIRVNAEENTVLKSKLEDIERELKDKQAEIKSNQEEKELLTSRLKEL 862

35 Query: 868 ESLVKLQEEELNK 880  
 E + Q++ K  
 Sbjct: 863 EQELDSTQQAQK 875

Score = 165 (24.8 bits), Expect = 4.1e-08, P = 4.1e-08  
 Identities = 65/286 (22%), Positives = 149/286 (52%)

40 Query: 595 LNIEELIEKLQSGMVVKDQICDVR-ISDMDVYEMKLSTLASKESRL-  
 QDLLETALALA 652  
 +N ++ + L+ + K I +++ I++ ++ +++ + L+ ++ +  
 ++L+E K+

45 Sbjct: 114 VNHQKETKSLKEDIAAK--  
 ITEIKAINENLEKMKIQCNNLSKEKEHISKELVEYKS-RFQ 170  
 Query: 653 QADRLIAQHRCQRTQAETEARTLASMLREVERKNEELSVLLKAQQVESE---  
 -RAQSDIE 708

50 D L+A+ T+ + ++LA+ ++++ +NE L ++ + ES  
 Q+ I+  
 Sbjct: 171 SHDNLVAK----LTE---  
 KLKSLANNYKDMQAEENSLIKAVEESKNESSIQLSNLQNKID 223

55 Query: 709 HLFQH--NRKLE--  
 SVAEEHEILTKSYMELLQNESTTEKNKDLQITCDSLQNKQIETVKK 764  
 + Q N ++E S+ + E L K+ +L Q E K+ + D  
 QI +K+

Sbjct: 224 SMSQEKENFQIERGSIEKNIEQLKKTISDLEQTKEEIISKSDSSK---  
DEYESQISLLKE 280

Query: 765

5 LNESLKEQNEKSIAQLIEKEEQRKEVQNLVDREHKLHLHQTQVQEEKIKTLQKERED 824  
E+ N++++ ++ E + R+E++ +L ++ L K + E+ +K

+++ E

Sbjct: 281

10 KLETATTANDENVNKISELTKTREELEAELAAYKNLKNELETKLETSEKALKEVKENEH 340

Query: 825 -

KEETIDILRKELSRTEQIRKELSIKASSLEVQKAQLEGRLEEKESLVKLQEEELNK 880  
KEE I L KE + T+Q L SLE + L +L++ E + ++  
+ N+

15 Sbjct: 341 LKEEKIQ-  
LEKEATETKQQLNSLRANLESLEKEHEDLAAQLKKYEEQIANKERQYNE 396

Score = 158 (23.7 bits), Expect = 1.9e-07, P = 1.9e-07  
Identities = 74/268 (27%), Positives = 136/268 (50%)

20 Query: 598 EELIEKLQSGMVVKDQICDVRISDIMDVYEM--KL-  
STLASKESRLQDLLET--KALALA 652

+E K++ G+ ++ +++ EM KL ST+ S E+ L+ +ET

K+

25 Sbjct: 695  
QESKAKVEEGLKKLEEESKEKAELEKSKEMMKLESTIESNETELKSSMETIRKSDEKL 754

Query: 653

30 QADRLIAQHRCQRTQAE TEARTLASMLREVERKNEELSVLLKAQQVESERAQSDIEHLFQ 712  
+ + A+ + Q E L S + E E+ EEL L+ + S

++ + L

Sbjct: 755 EQSKKSAEEDIKNLQHEKS--  
DLISRINESEKDIEELKSKLRIEAKSSSELETQVQELNN 812

35 Query: 713 HNRKLESVAEEHEILTKSYMELLQRNESTTEKKNKDLQITCDSLNKQIET--  
VKKLNESLK 770

K+ AEE+ +L KS +E ++R E K+K +I + K++ T

+K+L + L

40 Sbjct: 813 AQEKIRVNAEENTVL-KSKLEDIER----  
ELKDKQAEIKSNQEEKELLTSRLKELEQELD 867

Query: 771 EQNEKSIAQLIEKEEQRKEVQNLVDREHKLHLHQTQVQEEKIKTLQKEREDKEE 827

+K AQ E EE R EV+ V++ + K L K K +

45 +++ + ++

Sbjct: 868 STQK--AQKSE-

EESRAEVRKFQVEKSQLEKAMLLETQYNDLVNKEQAWKRDEDTVKK 924

Query: 828 TIDILRKELSRTEQIRKEL-SIKASSLEVQKAQLEGRLE 865

50 T D R+E+ E++ KEL ++KA + ++++A E R E

Sbjct: 925 TTDSQRQEI--EKLAKELDNLKAENSKLKEAN-EDRSE 959

Score = 155 (23.3 bits), Expect = 3.9e-07, P = 3.9e-07  
Identities = 73/269 (27%), Positives = 133/269 (49%)

55 Query: 624 DVYEMKLSTLASKESRLQD-LLETQALALAQADRLIAQHRCQRTQAE---  
EARTLASML 679

++ E K +T+ S LQD +L K ++L++ R + E+ +  
 R  
 Sbjct: 643 ELLEEKQNTIKS----  
 LQDEILSYKDKITRNDKLLSIEDSKRDLESKEQLRAAQESK 698  
 5  
 Query: 680 REVE---  
 RKNEELSVLLKAQAVESERAQSDIEHLFQHNRKLESVAEEHEILTKSYMELLQ 736  
 +VE +K EE S KA+ +S+ +E + N + E +  
 KS +L Q  
 10 Sbjct: 699 AKVEEGLKKLEEESKEKAELEKSKEMMKLESTIESNET--  
 ELKSSMETIRKSDEKLEQ 756  
 Query: 737 RNESTEKKNKDLQITCDSLNKQIETVKKLNESLKEQ---  
 NEKSIAQLIEKEEQRKEVQNQ 793  
 15 +S E+ K+LQ L +I +K E LK + KS ++L  
 +++ Q +  
 Sbjct: 757  
 SKKSAEEDIKNLQHEKSDLISRINESEKDIEELKSKLRIEAKSSSELETVKQELNNAQEK 816  
 20 Query: 794 L-VDREH-----  
 KLANLHQKTKVQEEKIKTLQKEREKKEETIDILRKELSRTEQIRKEL 846  
 + V+ E KL ++ ++ K ++ +IK+ Q+E+E + L +EL  
 T+Q + +  
 Sbjct: 817  
 25 IRVNAEENTVLKSKLEDIERELKDKQAEIKSNQEEKELLTSRLKELEQELDSTQQ-KAQK 875  
 Query: 847 SIKASSLEVQKAQLE-GRLEEKESLVKLQAEEL-NK 880  
 S + S EV+K Q+E +L+EK L++ + +L NK  
 30 Sbjct: 876 SEESRAEVRKFQVEKSQLDKAMLLETKYNDLVNK 911  
 Score = 146 (21.9 bits), Expect = 3.5e-06, P = 3.5e-06  
 Identities = 73/311 (23%), Positives = 152/311 (48%)  
 Query: 520 DNREQVQSGLRIL-----LEAAPLPDFFPALV--  
 35 LGESIAANNAYRQQETEHIPRK-MPWQ 571  
 +++ +V+ GL+ L E A L ++ L +I +N + E I  
 + +  
 Sbjct: 696  
 ESKAKVEEGLKKLEEESKEKAELEKSKEMMKLESTIESNETELKSSMETIRKSDEKLE 755  
 40 Query: 572 SSNHSFPTSILCLTPHLKDGVPGLNIEEL-  
 IEKLQSGMVVKDQICDVRISDIMDVYEMKL 630  
 S S IK L D + +N E IE+L+S + + + + S  
 ++ + +L  
 45 Sbjct: 756 QSKKSAEEDIKNLQHEKSDLISRINESEKDIEELKSKLRI-----  
 EAKSSSELETVKQEL 810  
 Query: 631 STLASK---  
 ESRLQDLLETALALAQADRLIAQHRCQRTQAETEARTLASMLREVERKNE 687  
 50 + K + +L++K L +R + + + + E L S  
 L+E+E++ +  
 Sbjct: 811 NNAQEKIRVNAEENTVLKSK---  
 LEDIERELKDKQAEIKSNQEEKELLTSRLKELEQELD 867  
 55 Query: 688  
 ELSVLLKAQAVESERAQSDIEHLFQHNRKLESVAEEHEILTKSYMELLQRNESTEKKNKD 747  
 S KAQ+ E E +++++ FQ + + E+ +L Y +L+ +  
 ++ ++

Sbjct: 868 --STQQAQKSEEE-SRAEVRK-FQVEKS--  
QLDEKAMLLKETKYNDLVNKEQAWKRDEDT 921

5 Query: 748 LQITCDSL NKQIETVKKLNESLKEQNEKSIAQLIEKEEQRKEVQNQLV---  
DREHKLANL 804  
++ T DS ++IE + K ++LK +N K L E E R E+ + ++ D  
+ K N

Sbjct: 922 VKKTTDSQRQEI EKLAKELDNLKAENSK----  
LKEANEDRSEIDDLMLLVTDLDEK--NA 975

10 Query: 805 HQKTKVQEEKIKTLQKEREDKEETID 830  
++K+++ ++ E +D+EE D  
Sbjct: 976 KYRSKLKDLGVEISSDEEDDEEEEDD 1001

15 Score = 146 (21.9 bits), Expect = 4.6e-06, P = 4.6e-06  
Identities = 82/313 (26%), Positives = 145/313 (46%)

20 Query: 598  
EELIEKLQSGMVVKDQICDVRISDIMDVYEMKLSTLASKE SRLQDLLET KALALAQAADRL 657  
EEL +L + +K+++ + + E+K + KE ++Q LE +A  
Q  
Sbjct: 304 EELEAELAAYKNL KNELET KLETSEKALKEVKENEHLKEEKIQ--  
LEKEATETKQ--- 358

25 Query: 658 IAQHRCQRTQAETEARTLASMLREVERK-----NEELSVL---  
LKAQQVESERAQSD 706  
+ R E E LA+ L++ E + NEE+S L + + Q  
E+E +  
Sbjct: 359

30 LNSLRANLESLEKEHEDLAAQLKKYEEQIANKERQYNEEISQLNDEITSTQQENESIKKK 418

Query: 707 IEHLFQHNRLKESVAEEHEILTKSYMELLQRN-  
ESTEKKNKDLQITCDSL NKQIET-VKK 764  
+ L + ++S +EE L KS ++ L + +KKN+ + + K  
35 IE+ K

Sbjct: 419  
NDELEGEVKAMKSTSEEQSNLKKSEIDALNLQIKELKKKNETNEASLLESIKSIESETVK 478

40 Query: 765 LNESLKEQN--EKSIAQLIEK---EEQRKEVQNQLVDREHKLAN-LHQKT--  
-KVQEEKI 815  
+ E E N EK +++L +K E + +L K+ L KT  
K+Q EK+

Sbjct: 479  
IKELQDECNFKEKEVSELEDK LKASEDKNSKYLELQKESEKIKEELDAKTTELKIQLEKV 538

45 Query: 816  
KTLQKEREDKEETIDILRKELSRTEQIRKELSIKASSLEVQKAQLEGRLEEKESLVKLQ 875  
L K +E E ELSR ++K S + + E Q +L+ ++ K  
+ ++

50 Sbjct: 539 TNLSKAKEKSES-----ELSR---  
LKKTSSSEERKNAEEQLEK LKNEIQIKNQAFEKER 588

Query: 876 EELNKHSHMIAMIHSLSGGKINPETVNL 903  
+ LN+ S I +S + E + L

55 Sbjct: 589 KLLNEGSSTITQ EYSEKINTLEDELIRL 616

Score = 145 (21.8 bits), Expect = 5.9e-06, P = 5.9e-06  
Identities = 59/246 (23%), Positives = 115/246 (46%)

Query: 634 ASKESRLQ-  
DLLETKALALAQADRLIAQHRCQRTQAE TEARTLASMLREVERKNEELSVL 692  
+ ES +Q L+ K +++Q + +R E L + ++E+

5 EE ++  
Sbjct: 207 SKNESSIQLSNLQNKIDSMSQEK---  
NFQIERGSIKQIEQLKKTISDLEQTKEE--II 261

Query: 693 LKAQQVESERAQSDIEHLFQHNRKLESVAEEHEI-----  
10 LTKSYMELLQARNESTTEKKNKD 747  
K+ + E +S I L + + + A + + LTK+ EL  
+ + +  
Sbjct: 262 SKSDSSKDEY-ESQIS-  
LLKEKLETATTANDENVNKISELTKTREELEAELAAYKNLKN 319

15 Query: 748  
LQITCDSLNKQIETVKKL NESLKEQNEKSIAQLIEKEEQRKEVQNLVDREHKLNLHQK 807  
L+ ++ K ++ VK+ E LKE+ + + E ++Q ++ L E  
+ +L +  
20 Sbjct: 320  
LETKLETSEKALKEVKENEHLKEEKIQLEKEATETKQQLNSLRANLESLEKEHEDLAAQ 379

Query: 808  
TKVQEEKIKTLQKEREDKEETIDILRKELSRTEQIRKELSIKASSLEVQKAQLEGRLEEK 867  
25 K EE+I KER+ EE I L E++ T+Q + + K LE +  
++ EE+  
Sbjct: 380 LKKYEEQIAN--KERQYNEE-  
ISQLNDEITSTQQENESIKKKNDELEGEVKAMKSTSEEQ 436

30 Query: 868 ESLVKLQDEELN 879  
+L K + + LN  
Sbjct: 437 SNLKKSEIDALN 448

Score = 137 (20.6 bits), Expect = 4.2e-05, P = 4.2e-05  
35 Identities = 81/312 (25%), Positives = 140/312 (44%)

Query: 598 EELIEKLQSGMVVKDQICDVRISDIMDVYEMKLSTLASK-ESRLQDLLET-  
KALALAQAD 655  
+EL ++++ ++ +++ S+I D +++ L K E+ LLE+

40 K++  
Sbjct: 420 DELEGEVKAMKSTSEEQSNLKKSEI-  
DALNLQIKELKKKNETNEASLLESISIESETVK 478

Query: 656  
45 RLIAQHRCQRTQAE TEARTLASMLREVERKNEELSVLLKAQQVESERAQSDIEHLFQHNR 715  
Q C E E L L+ E KN + L K + E +  
L  
Sbjct: 479 IKELQDECNFK--  
EKEVSELEDKCLKASEDKNSKYLELQKESEKIKEELDAKTTELKIQLE 536

50 Query: 716  
KLESVAEEHEILTKSYMELLQARNESTTEKKNKD LQITCDSLNKQIETVKKL NESLKEQNEK 775  
K+ ++++ E ++S + L++ S E+KN + Q+ QI+ + +  
K NE  
55 Sbjct: 537 KVTNLSKAKE-KSESELSRLKKTSSSEERKNAAEQLEKLNKNEIQIKN-  
QAFEKERKLLNEG 594



Query: 776 SIAQLIEKEEQRKEVQNLV--DREHKL-ANLHQKTKVQEEKIKTLQKER-  
EDKEETIDI 831

S E E+ ++++L+ E++L A T+ + EK+ E  
E+K+ TI

5 Sbjct: 595  
SSTITQYSEKINTLEDELIRLQENELKAKEIDNTRSELEKVSLSNDELLEEKQNTIKS 654

Query: 832 LRKE-LSRTEQI----RKELSIKASS---LEVQKAQLEGRLEEK----  
ESLVKLQAE--- 876

10 L+ E LS ++I K LSI+ S LE K QL E K E L  
KL++E

Sbjct: 655  
LQDEILSYKDKITRNDKLLSIEDSKRDLESLKEQLRAAQESKAKVEEGLKKLEEESK 714

15 Query: 877 ---ELNKHSHMIAMIHS 890

EL K M+ + S

Sbjct: 715 EKAELEKSKEMMKLES 731

Score = 128 (19.2 bits), Expect = 3.9e-04, P = 3.9e-04  
20 Identities = 80/356 (22%), Positives = 148/356 (41%)

Query: 546 LGESIAANNAYRQQETEHIPRKMPWQSSNHSFPTSIKCLTPHL-----  
KDGVPGLN-I 597

25 L E + ++ E+ + ++S+ H SIK L L K  
G+N +

Sbjct: 25  
LDEMTQLRDVLETKDKENQATALLEYKSTIHKQEDSIKLEKELETILSQQKKAEDGINKM 84

30 Query: 598 EELIEKLQSGMVVKDQICD--  
VRISDIMDVYEMKLSTLASKESRLQDLLETALALAQAD 655

+ + L M ++ C + D +V K T + KE + E  
KA+ +

Sbjct: 85 GKDLFALSREMQAVEENCKNLQKEKDKSNVNHQK-  
ETKSLKEDIAAKITEIKAIN-ENLE 142

35 Query: 656  
RLIAQHRCQRTQAETEARTLASMLREVERKNEELSVLLKAQQVESERAQSDIEHLFQHNHNR 715

++ Q C E E ++ L E + + + L+ + + ++  
+ + N

40 Sbjct: 143 KMKIQ--CNNLSKEKEH--  
ISKELVEYKSRFQSHQNLVAKLTEKLKSLANNYKDMQAEENE 198

Query: 716 KLESVAEEHEILTKSYMELLQRN-  
ESTEKKNKDLQITCDLNLQIETVKKLNESLKEQNE 774

45 L EE + + + LQ +S ++ ++ QI S+ K IE +KK  
L++ E

Sbjct: 199  
SLIKAVEESKNESSIQLSNLQNKIDSMSQEKENFQIERGSIEKNIEQLKKTISDLEQTK 258

50 Query: 775  
KSIAQLIEKEEQRKEVQNLVDREHKLANLHQKTKVQEEKIKTLQKEREDEKEETI----- 829

+ I++ + + E ++Q+ + KL KI L K RE+ E  
+

Sbjct: 259 EIISK---  
55 SDSSKDEYESQISLLKEKLETATTANDENVNKISELTKTREELEAELAAYKN 315

Query: 830 --DILRKELSRTEQIRKELSIKASSLEVQKAQLEGRLEE-KESLVKLQAE--  
EELNK-HSH 883

+ L +L +E+ KE+ L+ +K QLE E K+ L L+ E  
 L K H  
 Sbjct: 316  
 LKNELETKETSEKALKEVKENEHLKEEKIQLEKEATETKQQLNSLRANLESLEKEHED 375  
 5 Query: 884 MIAMI 888  
 + A +  
 Sbjct: 376 LAAQL 380  
 10 Score = 117 (17.6 bits), Expect = 3.8e-03, P = 3.8e-03  
 Identities = 50/240 (20%), Positives = 111/240 (46%)  
 Query: 634  
 ASKESRLQDLLETAKALALAQADRLIAQHRCQRTQAETEARTLASMLREVERKNEELSVLL 693  
 15 A E L+ L E + A+ ++ + + E+ L S + + +  
 +E+L  
 Sbjct: 699  
 AKVEEGLKKLEEESKEKAELEKSKEMMKLESTIESNETELKSSMETIRKSDEKLEQSK 758  
 20 Query: 694 KAQQVESERAQ---SD-  
 IEHLFQHNRKLESVAEEHEILTKSYMELLQRNESTEEKNKDLQ 749  
 K+ + + + Q SD I + + + +E+ + + I KS EL +  
 + ++  
 Sbjct: 759  
 25 KSAEEDIKNLQHEKSDLISRINESEKDIEELKSKLRIEAKSSSELETVKQELNNAQEKIR 818  
 Query: 750  
 ITCDSLNKQIETVKKLNESLKEQNEKSIAQLIEKEEQRKEVQNLVDREHKLNLHQKTK 809  
 + + N +++ KL + +E +K A++ +E+++ + ++L + E +L  
 30 + QK +  
 Sbjct: 819 VNAEE-NTVLKS--KLEDIERELKDKQ-  
 AEIKSNQEEKELLTSRLKELEQELDSTQQAQ 874  
 Query: 810 VQEEK----  
 35 IKTLQKEREDKEETIDILRKELSRTEQIRKELSIKASSLEVQKAQLEGRLE 865  
 EE+ ++ Q E+ +E +L E + + KE + K V+K  
 + + +  
 Sbjct: 875 KSEESRAEVRKFQVEKSQLDKAMLL--  
 ETKYNDLVNKEQAWKRDEDTVKKTT-DSQRQ 931  
 40 Query: 866 EKESLVK 872  
 E E L K  
 Sbjct: 932 EIEKLAK 938  
 45 Score = 109 (16.4 bits), Expect = 2.6e-02, P = 2.5e-02  
 Identities = 64/284 (22%), Positives = 135/284 (47%)  
 Query: 598  
 EELIEKLQSGMVVKDQICDVRIQDIMDVYEMKLSTLASKESRLQDLLETAKALALA---QA 654  
 50 +E+++KL+S + + + I E + S E +++L K+  
 ++ ++  
 Sbjct: 723  
 KEMMKLESTIESNETELKSSMETIRKSDEKLEQSKKSAEEDIKNLQHEKSDLISRINES 782  
 55 Query: 655 DRLIAQHRCQ-  
 RTQAETEARTLASMLREVERKNEELSVLLKAQQVESERAQSDIEH-LFQ 712  
 ++ I + + + R +A++ + L ++ +E+ E++ V + V + +  
 DIE L

Sbjct: 783 EKDIIEELKSKLRIEAKSSSE-LETVKQELNNAQEKIRVNAEENTVLKSKLE-DIERELKD 840

5 Query: 713 HNRKLESVAEEHEILTKSYMELLQRNESTEKK-NKDLQITCDSLK-QIETVKKLNES-- 768

+++S EE E+LT EL Q +ST++K K + + + K Q+E  
+L+E

10 Sbjct: 841 KQAEIKSNQEEKELLTSRLKELEQELDSTQQAQKSEESRAEVRKFQVEK-SQLEKAM 899

Query: 769 LKEQNEKSIA---QLIEKEEQ--  
RKEVQNLVDREHKLNLHQTQVQEEKIKTLQKERE 823

L E + Q +++E +K +Q + E KLA K +  
K+K ++R

15 Sbjct: 900 LLETKYNDLVNKEQAWKRDEDTVKKTTDSQRQEI-  
KLAKELDNLKAENSKLKEANEDRS 958

Query: 824 DKEETI----DILRKELSRTEQIRKELSIKASSLEVQKAQLEGRLEEKE  
868

20 + ++ + D+ K ++ K+L ++ SS E + E E+ E  
Sbjct: 959 EIDDLMLLVTDLDEKNAKYRSKL-KDLGVEISSDEEDDEEEDDEEDDE  
1006

25 Score = 96 (14.4 bits), Expect = 1.1e+00, P = 6.6e-01  
Identities = 40/210 (19%), Positives = 101/210 (48%)

Query: 681 EVERKN--  
EELSVLLKAQQVESERAQSDIEHLFQHNKLESVAEEHEILTKSYMELLQRN 738

30 E E KN + L + + + V + + + L ++ + + + L K  
+L +  
Sbjct: 15  
ETELKNVRDSDLDEMTQLRDVLETKDKENQTALLEYKSTIHKQEDSIKTLEKELETILSQK 74

35 Query: 739 ESTE----  
KKNKDLQITCDSLKQIETVKKLNESLKEQNEKSIAQLIEKEEQRKEVQNL 794

+ E K KDL +L+++++ V++ ++L+++ +KS + +++  
K ++ +  
Sbjct: 75 KKAEDGINKMGKDLF----ALSREMQAVEENCKNLQKEKDKN---  
VNHQKETKSLKEDI 127

40 Query: 795 VDREHKLNLHQTQVQEEKIKTLQKERE-  
KEETIDILRKELSRTEQIRKELSIKASSL 853

+ ++ +++ + + + L KE+E +E ++ + S + K  
L+ K SL

45 Sbjct: 128 AAKITEIKAINENLEKMKIQCNLSKEKEHISKELVEYKSRFQSHDNLVAK-  
LTEKLSL 186

Query: 854 EVQKAQLEGRLEEKESLVKLQEEELNKHSHMIAMIHS 890  
++ E ESL+K +E N+ S ++ + +

50 Sbjct: 187 ANNYKDMQA--ENESLIKAVEESKNESSIQLSNLQN 220

Score = 52 (7.8 bits), Expect = 2.0e-10, P = 2.0e-10  
Identities = 39/167 (23%), Positives = 74/167 (44%)

55 Query: 99 LNSVLAVGVCRSSHTDSVFLQCIQLLQKLTYNVKIFYSGANIDEL-  
ITFLIDHIQSSSEDE 157

LN + + ++ ++ L+ I+ ++ T +K N E ++ L D  
+++SED+

Sbjct: 447  
LNLQIKELKKKNETNEASLLESIKSIESETVKIKELQDECNFKEKEVSELEDKCLKASEDK 506

Query: 158 -  
5 LKMPCLGLLANLCRHNLVQTHIKTLSNVKSFYRTLITLLAHSSLTVVVFALSILSSLT 216  
K L + + L +T T ++ T ++ S + +

S  
Sbjct: 507 NSKYLELQKESEKIKEELDAKT---  
10 TELKIQLEKVTNLSKAKEKSESELSRLKKTSSSEER 563

Query: 217 LN-EEVGKELFHARNI-HQTFQLIFNILINGDGTLTRKYS--VDLLMDLL  
262

N EE EKL + I +Q F+ +L G T+T++YS ++ L D L  
Sbjct: 564 KNAEEQLEKLEKNEIQIKNQAFEKERKLLNEGSSTITQEYSEKINTLEDEL  
15 613

Pedant information for DKFZphm12\_12j1, frame 2

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20

# Report for DKFZphm12\_12j1.2

25 [LENGTH] 905  
[MW] 102067.81  
[pI] 5.85  
[HOMOL] TREMBL:SCINTANA\_1 Saccharomyces cerevisiae  
integrin analogue gene, complete cds. 1e-14  
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S.  
30 cerevisiae, YDL058w] 5e-16  
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae,  
YDL058w] 5e-16  
[FUNCAT] 1 genome replication, transcription, recombination and  
repair [M. jannaschii, MJ1322] 1e-10  
35 [FUNCAT] 09.10 nuclear biogenesis [S. cerevisiae, YDR356w]  
2e-10  
[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae,  
YDR356w] 2e-10  
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae,  
40 YDR356w] 2e-10  
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKR095w]  
1e-09  
[FUNCAT] 11.04 dna repair (direct repair, base excision repair  
and nucleotide excision repair) [S. cerevisiae, YKR095w] 1e-09  
45 [FUNCAT] 08.22 cytoskeleton-dependent transport [S. cerevisiae,  
YHR023w MY01 - myosin-1 isoform] 4e-09  
[FUNCAT] 03.04 budding, cell polarity and filament formation  
[S. cerevisiae, YHR023w MY01 - myosin-1 isoform] 4e-09  
[FUNCAT] 03.25 cytokinesis [S. cerevisiae, YHR023w MY01 -  
50 myosin-1 isoform] 4e-09  
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YNL091w]  
3e-08  
[FUNCAT] 09.25 vacuolar and lysosomal biogenesis [S.  
cerevisiae, YOR326w] 6e-08  
55 [FUNCAT] 08.16 extracellular transport [S. cerevisiae,  
YOR326w] 6e-08  
[FUNCAT] 09.13 biogenesis of chromosome structure [S.  
cerevisiae, YLR086w] 8e-08

- [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YJR134c] 1e-07  
 [FUNCAT] 06.07 protein modification (glycosylation, acylation, myristylation, palmitylation, farnesylation and processing) [S. cerevisiae, YKL201c] 4e-07  
 5 [FUNCAT] 30.05 organization of centrosome [S. cerevisiae, YIL144w] 4e-06  
 [FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YNL079c] 5e-06  
 10 [FUNCAT] 03.01 cell growth [S. cerevisiae, YNL079c] 5e-06  
 [FUNCAT] 08.99 other intracellular-transport activities [S. cerevisiae, YNL079c] 5e-06  
 [FUNCAT] 09.04 biogenesis of cytoskeleton [S. cerevisiae, YKL179c] 6e-06  
 15 [FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YER008c] 8e-06  
 [FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YNL250w] 1e-05  
 [FUNCAT] 03.13 meiosis [S. cerevisiae, YDR285w] 1e-05  
 20 [FUNCAT] 30.13 organization of chromosome structure [S. cerevisiae, YDR285w] 1e-05  
 [FUNCAT] 11.01 stress response [S. cerevisiae, YPR141c] 2e-05  
 [FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YPR141c] 2e-05  
 25 [FUNCAT] 06.01 protein folding and stabilization [S. cerevisiae, YNL227c] 9e-05  
 [FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YAL035w] 1e-04  
 [FUNCAT] 10.05.99 other pheromone response activities [S. cerevisiae, YHR158c] 1e-04  
 30 [FUNCAT] 0 chaperones [M. genitalium, MG355] 2e-04  
 [FUNCAT] 03.22.01 cell cycle check point proteins [S. cerevisiae, YGL086w] 2e-04  
 [FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YNL225c] 3e-04  
 35 [FUNCAT] r general function prediction [M. jannaschii, MJ1254] 4e-04  
 [FUNCAT] 08.01 nuclear transport [S. cerevisiae, YPL174c] 4e-04  
 [FUNCAT] 04.05.01.01 general transcription activities [S. cerevisiae, YMR227c TAF67 - TFIID subunit] 6e-04  
 40 [BLOCKS] PRO1002E  
 [BLOCKS] BL011608 Kinesin light chain repeat proteins  
 [BLOCKS] BL00326 Tropomyosins proteins  
 [SCOP] d2tmab\_1.105.4.1.1 Tropomyosin [rabbit (Oryctolagus cuniculus) 3e-23  
 45 [EC] 3.6.1.32 Myosin ATPase 4e-10  
 [PIRKW] nucleus 5e-09  
 [PIRKW] phosphotransferase 2e-07  
 [PIRKW] blocked amino end 1e-06  
 50 [PIRKW] duplication 2e-07  
 [PIRKW] citrulline 3e-08  
 [PIRKW] tandem repeat 4e-10  
 [PIRKW] heterodimer 1e-07  
 [PIRKW] heart 4e-08  
 55 [PIRKW] endocytosis 7e-08  
 [PIRKW] transmembrane protein 1e-14  
 [PIRKW] serine/threonine-specific protein kinase 2e-07  
 [PIRKW] cell wall 2e-06

	[[PIRKW]]	zinc finger 7e-08
	[[PIRKW]]	DNA binding 3e-09
	[[PIRKW]]	metal binding 7e-08
	[[PIRKW]]	muscle contraction 4e-10
5	[[PIRKW]]	brain 2e-06
	[[PIRKW]]	acetylated amino end 2e-07
	[[PIRKW]]	heterotetramer 5e-07
	[[PIRKW]]	actin binding 4e-10
	[[PIRKW]]	mitosis 1e-08
10	[[PIRKW]]	microtubule binding 1e-08
	[[PIRKW]]	ATP 4e-10
	[[PIRKW]]	chromosomal protein 1e-07
	[[PIRKW]]	thick filament 9e-10
	[[PIRKW]]	phosphoprotein 1e-09
15	[[PIRKW]]	skeletal muscle 1e-08
	[[PIRKW]]	calcium binding 3e-08
	[[PIRKW]]	alternative splicing 9e-10
	[[PIRKW]]	DNA condensation 1e-07
	[[PIRKW]]	coiled coil 1e-14
20	[[PIRKW]]	P-loop 2e-10
	[[PIRKW]]	heptad repeat 5e-09
	[[PIRKW]]	methylated amino acid 4e-10
	[[PIRKW]]	immunoglobulin receptor 2e-07
	[[PIRKW]]	peripheral membrane protein 7e-08
25	[[PIRKW]]	cardiac muscle 4e-08
	[[PIRKW]]	hydrolase 4e-10
	[[PIRKW]]	microtubule 5e-09
	[[PIRKW]]	muscle 4e-08
	[[PIRKW]]	membrane protein 5e-09
30	[[PIRKW]]	EF hand 3e-08
	[[PIRKW]]	cell division 1e-06
	[[PIRKW]]	cytoskeleton 6e-09
	[[PIRKW]]	hair 3e-08
	[[PIRKW]]	calmodulin binding 7e-08
35	[[PIRKW]]	Golgi apparatus 2e-07
	[[SUPFAM]]	hypothetical protein YJL074c 5e-09
	[[SUPFAM]]	unassigned Ser/Thr or Tyr-specific protein kinases 2e-07
	[[SUPFAM]]	myosin motor domain homology 2e-10
40	[[SUPFAM]]	alpha-actinin actin-binding domain homology 6e-09
	[[SUPFAM]]	tropomyosin 2e-08
	[[SUPFAM]]	kinesin heavy chain 5e-07
	[[SUPFAM]]	plectin 6e-09
	[[SUPFAM]]	SAM homology 1e-06
45	[[SUPFAM]]	trichohyalin 3e-08
	[[SUPFAM]]	ribosomal protein S10 homology 6e-09
	[[SUPFAM]]	protein kinase C zinc-binding repeat homology 5e-09
	[[SUPFAM]]	giantin 7e-08
	[[SUPFAM]]	protein kinase homology 2e-07
50	[[SUPFAM]]	protein 4.1 membrane-binding domain homology 9e-08
	[[SUPFAM]]	human early endosome antigen 1 7e-08
	[[SUPFAM]]	myosin MY02 2e-06
	[[SUPFAM]]	M5 protein 3e-09
	[[SUPFAM]]	Mycoplasma genitalium hypothetical protein MG218 5e-09
55	[[SUPFAM]]	myosin heavy chain 2e-10
	[[SUPFAM]]	conserved hypothetical P115 protein 3e-09
	[[SUPFAM]]	centromere protein E 1e-08
	[[SUPFAM]]	calmodulin repeat homology 3e-08

```

5  [SUPFAM] ezrin *9e-08
    [PROSITE] LEUCINE_ZIPPER 1
    [KW] TRANSMEMBRANE 2
    [KW] LOW_COMPLEXITY 3.09 %
    [KW] COILED COIL 18.34 %

```

```

15 COILS .....
MEM .....

```

```

.....
COILS .....
.....
MEM .....MMMMMMMMMMMMMMMMMMMM.....
.....

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```

.....
COILS .....
30 .....
MEM .....
.....

```

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COILS .....
MEM .....MMMMMMMMMMMMMMMMMMMM.....

```

```

COILS .....
45 MEM .....

```

```

50 COILS .....
MEM .....

```

55 SEQ L ALELFKEIFEDVIDAANCSSADRFVTL LPTILDQLQFTEQNLDEALTRKNVKGIAKAI  
 SEQ .....

MEM .....  
5 SEQ EVLLTLCGDDTLKMHIAKILTTVKCTTLIEQQFTYGTKIDLGFGTKVADSELCKLAADVIL  
SEG .....  
PRD hhhhhhccccchhhhhhhhhhhheeeeeeeeeeeccccccccceehhhhhhhhhhhhh  
COILS .....  
MEM .....  
10 SEQ KTLDLINKLKPLVPGMEVSFYKILQDPRLITPLAFALTSDNREQVQSGLRILLEAAPLPD  
SEG .....  
PRD hhhhhhhhhccccccccccccceeeccccccchhhhhhccccchhhhhhhhhhhhhcccc  
COILS .....  
15 MEM .....  
20 SEQ FPALVLGESIAANNAYRQQETEHIPRKMPWQSSNHSFPTSIKCLTPHLKDGVPGLNIEEL  
SEG .....  
PRD cceeeehhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccchhhhhhhhhhhhhhhhhhhhh  
COILS .....  
MEM .....  
25 SEQ IEKLQSGMVVKDQICDVRISDIMDVYEMKLSTLASKESRLQDLLETKALALAQADRLIAQ  
SEG .....  
PRD hhh  
COILS .....  
30 MEM .....  
35 SEQ HRCQRTQAE TEARTLASMLREVERKNEELSVLLKAQQVESERAQSDIEHLFQHNKLESV  
SEG .....  
PRD hhh  
COILS .....CC.....  
MEM .....  
40 SEQ AEEHEILTKSYMELLQARNESTEKKNDLQITCDSLNKQIETVKKL NESLKEQNEKSIAQL  
SEG .....  
PRD hhh  
COILS .....CC  
MEM .....  
45 SEQ IEKEEQRKEVQNLVDREHKL ANLHQKTKVQEEKIKTLQKEREQKEETIDILRKELSRTE  
SEG .....  
PRD hhh  
COILS .....CC  
50 MEM .....  
55 SEQ QIRKELSIKASSLEVQKAQLEGRLEEKESLVKLQAEELNKHSHMIAMIHSLSGGKINPET  
SEG .....  
PRD hhhcc  
COILS .....CC.....  
MEM .....



SEQ VNLSI  
SEG .....  
PRD ccccc  
COILS .....  
5 MEM .....

10 Prosite for DKFZphm12\_12j1.2  
PS00029 331->353 LEUCINE\_ZIPPER PD0C00029

15 (No Pfam data available for DKFZphm12\_12j1.2)

DKFZphmel2\_7g14

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5 group: intracellular transport and trafficking

DKFZphmel2\_7g14 encodes a novel 973 amino acid protein with similarity to the dor (deep orange) protein of drosophila melanogaster.

10 The novel protein is also similar to the vakuolar membrane protein pep3 of *Saccharomyces cerevisiae*, which is involved in protein sorting mechanisms. The expression profile is ubiquitous and a role in protein transport/targeting is likely.

15 The new protein can find application in modulation of the sorting of proteins into different compartments.

20 similarity to DEEP ORANGE (*Drosophila melanogaster*)

perhaps complete cds. and full length

Sequenced by MediGenomix

25

Locus: unknown

Insert length: 3951 bp

Poly A stretch at pos. 3893, polyadenylation signal at pos. 3874

30

```

      1  GCCCCGCGTCA  CGGGGGCGGG  AGTCAGCTGA  GCTGCCGGGG  CGAGGTTGGG
    51  ATCACCTGGC  ACCGGCTGAA  GGGAGCCTGT  GATTTTTTTT  TAGCGGGGGC
   101  GGGGAGTAAG  GTGCAAGACT  GCGCCAGATT  CAAGGACGAG  GGCTGCCCCG
   35  151  TTATCTCGCT  GCATAAGGCA  AGAGCAAGAG  GATCCTCAGG  ATTTTAAAGA
      201  GGAGGCGACG  GCTGCAGGTT  CCCAGGATCT  GTCAGAGGCT  GGGGAGTTAC
      251  AGCTTCCATT  CTGGGGCGAC  GGGGACCCCG  GGGGGGTAGC  CCTTTGTAA
      301  TCCCCAGGCC  CCGGACAAAG  AGCCCAGAGG  CCGGGCACCA  TGGCGTCCAT
      351  CCTGGATGAG  TACGAGAACT  CGCTGTCCCG  CTCGGCCGTC  TTGCAGCCCG
   40  401  GCTGCCCTAG  CGTGGGCATC  CCCCCTCGG  GGTATGTGAA  TGCCAGCTG
      451  GAGAAGGAAG  TGCCCATCTT  CACAAAGCAG  CGCATTGACT  TCACCCCTTC
      501  CGAGCGCATT  ACCAGTCTTG  TCGTCTCCAG  CAATCAGCTG  TGCATGAGCC
      551  TGGGCAAGGA  TACACTGCTC  CGCATTGACT  TGGGCAAGGC  AAATGAGCCC
   45  601  AACCACGTGG  AGCTGGGACG  TAAGGATGAC  GCAAAAGTTC  ACAAGATGTT
      651  CCTTGACCAT  ACTGGCTCTC  ACCTGCTGAT  TGCCCTGAGC  AGCACGGAGG
      701  TCCTCTACGT  GAACCGAAAT  GGACAGAAGG  TACGGCCACT  AGCACGCTGG
      751  AAGGGGCAGC  TGGTGGAGAG  TGTGGGTTGG  AACAAGGCAC  TGGGCACGGA
      801  GAGCAGCACA  GGCCCCATCC  TGGTCGGGAC  TGCCCAAGGC  CACATCTTTG
      851  AAGCAGAGCT  CTCAGCCAGC  GAAGGTGGGC  TTTTCGGCCC  TGCTCCGGAT
   50  901  CTCTACTTCC  GCCCATTGTA  CGTGCTAAAT  GAAGAAGGGG  GTCCAGCACC
      951  TGTGTGCTCC  CTTGAGGCCG  AGCGGGGCCC  TGATGGGCGT  AGCTTTGTTA
   1001  TTGCCACCAC  TCGGCAGCGC  CTCTTCCAGT  TCATAGGCCG  AGCAGCAGAG
   1051  GGGGCTGAGG  CCCAGGGTTT  CTCAGGGCTC  TTTGCAGCTT  ACACGGACCA
   1101  CCCACCCCCA  TTCCGTGAGT  TTCCCAGCAA  CCTGGGCTAC  AGTGAGTTGG
   55  1151  CCTTCTACAC  CCCCAGCTG  CGCTCCGCAC  CCCGGGCCTT  CGCCTGGATG
      1201  ATGGGGGATG  GTGTGTTGTA  TGGGGCATTG  GACTGTGGGC  GCCCTGACTC
      1251  TCTGCTGAGC  GAGGAGCGAG  TCTGGGAGTA  CCCAGAGGGG  GTAGGGCCTG
      1301  GGGCCAGCCC  ACCCCTAGCC  ATCGTCTTGA  CCCAGTTCCA  CTTCTGCTG

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1351 CTACTGGCAG ACCGGGTGGA GGCAGTGTGC AACTGACCG GGCAGGTGGT  
1401 GCTGCGGGAT CACTTCCTGG AGAAATTTGG GCCGCTGAAG CACATGGTGA  
1451 AGGACTCCTC CACAGGCCAG CTGTGGGCCT AACTGAGCG GGCTGTCTTC  
5 1501 CGCTACCACG TGCAACGGGA GGCCCGAGAT GTCTGGCGCA CCTATCTGGA  
1551 CATGAACCGC TTCGATCTGG CCAAAGAGTA TTGTGAGAG CGGCCCGACT  
1601 GCCTGGACAC GGTCTTGCC CGGGAGGCCG ATTTCTGCTT TCGCCAGCGT  
1651 GCGTACCTGG AGAGCGCACG CTGCTATGCC CTGACCCAGA GCTACTTTGA  
1701 GGAGATTGCC CTCAAGTTCC TGGAGGCCCG ACAGGAGGAG GCTCTGGCTG  
1751 AGTTCCTGCA GCGAAAACTG GCCAGTTTGA AGCCAGCCGA ACGTACCCAG  
10 1801 GCCACACTGC TGACCACCTG GCTGACAGAG CTCTACCTGA GCCGGCTTGG  
1851 GGCTCTGCAG GCGGACCCAG AGGCCCTGAC TCTCTACCGA GAAACCAAGG  
1901 AATGCTTTTC AACCTTCCTC AGCAGCCCCC GCCACAAAGA TTGGCTCTTT  
1951 GCCAGCCGGG CCTCTATCCA TGAGCTGCTC GCCAGTCATG GGGACACAGA  
2001 ACACATGGTG TACTTTGCAG TGATCATGCA GGACTATGAG CGGGTGGTGG  
15 2051 CTTACCACTG TCAGCACGAG GCCTACGAGG AGGCCCTGGC CGTGCTCGCC  
2101 CGCCACCGTG ACCCCAGCT CTTCTACAAG TTCTCACCCA TCCTCATCCG  
2151 TCACATCCCC CGCCAGCTTG TAGATGCCTG GATTGAGATG GGCAGCCGGC  
2201 TGGATGCTCG TCAGCTCATT CCTGCCCTGG TGA ACTACAG CCAGGGTGGT  
2251 GAGGTCCAGC AGGTGAGCCA GGCCATCCGC TACATGGAGT TCTGCGTGAA  
20 2301 CGTGCTGGGG GAGACTGAGC AGGCCATCCA CAACTACCTG CTGTCACTGT  
2351 ATGCCCGTGG CCGGCCGGAC TCACTACTGG CCTATCTGGA GCAGGCTGGG  
2401 GCCAGCCCCC ACCGGGTGCA TTACGACCTC AAGTATGCGC TGC GGCTCTG  
2451 CGCCGAGCAT GGCCACCACC GCGCTTGTGT CCATGTCTAC AAGGTCCTAG  
2501 AGCTGTATGA GGAGGCCGTG GACCTGGCCC TGCAGGTGGA TGTGGACCTG  
25 2551 GCCAAGCAGT GTGCAGACCT GCCTGAGGAG GATGAGGAAT TGC GCAAGAA  
2601 GCTGTGGCTG AAGATCGCAC GGCACGTGGT GCAGGAAGAG GAAGATGTAC  
2651 AGACAGCCAT GGCTTGCCCTG GCTAGCTGCC CCTTGCTCAA GATTGAGGAT  
2701 GTGCTGCCCT TCTTTCCTGA TTTCGTCACC ATCGACCACT TCAAGGAGGC  
2751 GATCTGCAGC TCACTTAAGG CCTACAACCA CCACATCCAG GAGCTGCAGC  
30 2801 GGGAGATGGA AGAGGCTACA GCCAGTGCCC AGCGCATCCG GCGAGACCTG  
2851 CAGGAGCTGC GGGGCCGCTA CGGCACTGTG GAGCCCCAGG ACAAATGTGC  
2901 CACCTGCGAC TTCCCCCTGC TCAACCGCCC TTTTACCTC TTCCTCTGTG  
2951 GCCATATGTT CCATGCTGAC TGCCTGCTGC AGGCTGTGCG ACCTGGCCTG  
3001 CCAGCCTACA AGCAGGCCCG GCTGGAGGAG CTGCAGAGGA AGCTGGGGGC  
35 3051 TGCTCCACCC CCAGCCAAGG GCTCTGCCCC GGCCAAGGAG GCCGAGGGTG  
3101 GGGCTGCCAC GGCAGGGCCC AGCCGGGAAC AGCTCAAGGC TGACCTGGAT  
3151 GAGTTGGTGG CCGCTGAGTG TGTGTACTGT GGGGAGCTGA TGATCCGCTC  
3201 TATCGACCGG CCGTTCATCG ACCCCAGCG CTACGAGGAG GAGCAGCTCA  
3251 GTTGGCTGTA GGAGGGTGTG ACCTTTGATG GGGGTGGGCA ATGGGGAGCA  
40 3301 GTGGCTTGAA CCCACTTGAG AAGGCTGCCT CTAGGCTCT GCTCAGTCAT  
3351 CTTGCAATTG CCACACTGTG ACCACGTTGA CGGGAGTAGA GTAGCGCTGT  
3401 TGGCCAGGAG GTGTCAGGTG TGAGTGTATT CTGCCAGCTT TTCATGCTGT  
3451 TCTTCAGAGC TGCAGTTATG CCAGACCATC AGCCTGCCTC CCAGTAGAGG  
3501 CCCTTCACCT GGAGAAGTCA GAAATCTGAC CCAATTCCAC CCCCTGCCTC  
45 3551 TAGCACCTCT TCTGTCCCTG TCATTCCCCA CACACGTCCT GTTACCTCG  
3601 AGAGAGAGAG AGAGAGAGCA CCTTCTTCC GTCTGTTTAC TCTGCGGCCT  
3651 CTGGAATCCC AGCTCTTCTC TCTCAGAAGA AGCCTTCTCT TCCTCTGCC  
3701 TGTAGGTGTC CCAGAAGTGA GAAGGCAGCC TTCGAAGTCC TGGGCATTGG  
3751 GTGAGAAAGT GATGCTAGTT GGGGCATGCT TTTGTGCACA CTCTCTGGGG  
50 3801 CTCCAGTGTG AAGGGTGCCC TGGGGCTGAG GGCCTTGTGG AGGATGGTGG  
3851 GTGGTGGTGA TGGAGGTGGA GAGCATTAAG CTGTCTGCAC TGC AAAAAAA  
3901 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAGAAAAAA AAAAAAAAAA  
3951 A

55

BLAST Results

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No BLAST result

## Medline entries

5

97218037:

Shestopal SA, Makunin IV, Belyaeva ES, Ashburner M, Zhimulev IF.; Mol

10 Gen Genet 1997 Feb 20;253(5):642-8

92049306:

Robinson JS, Graham TR, Emr SD.; A putative zinc finger protein, *Saccharomyces cerevisiae*

15 Vps18p, affects late Golgi functions required for vacuolar protein sorting and efficient alpha-factor prohormone maturation. Mol Cell Biol 1991 Dec;11(12):5813-24

92049305:

20 Preston RA, Manolson MF, Becherer K, Weidenhammer E, Kirkpatrick D,

Wright R,

Jones EW.; Isolation and characterization of PEP3, a gene required

25 for vacuolar biogenesis in *Saccharomyces cerevisiae*. Mol Cell Biol 1991 Dec;11(12):5801-12

30

## Peptide information for frame 1

35 ORF from 340 bp to 3258 bp; peptide length: 973

Category: similarity to known protein

Classification: Cellular transport and traffic

1 MASILDEYEN SLRSRAVLQRP GCPSVGIPHS GYVNAQLEKE VPIFTKQRID  
 40 51 FTPSERITSL VVSSNQLCMS LGKDTLLRID LGKANEPNHV ELGRKDDAKV  
 101 HKMFLDHTGS HLLIALSSTE VLYVNRNGQK VRPLARWKGQ LVESVGWNKA  
 151 LGTESSTGPI LVGTAQGHIF EAELSASEGG LFGPAPDLYF RPLYVLNEEG  
 201 GPAPVCSLEA ERGPDGRSFV IATTRQRLFQ FIGRAAEGAE AQGFSGLFAA  
 251 YTDHPPPFRE FPSNLGYSEL AFYTPKL RSA PRAFAWMMGD GVLYGALDCG  
 45 301 RPD SLLSEER VWEYPEGVGP GASPLAIVL TQFHFLLLLA DRVEAVCTLT  
 351 GQVVL RDHFL EKFGPLKHMV KDSSTGQLWA YTERAVFRYH VQREARDVWR  
 401 TYLDMNRFDL AKEYCRERPD CLDTVLAREA DFCFRQRRYL ESARCYALTQ  
 451 SYFEEIALKF LEARQEEALA EFLQRKLASL KPAERTQATL LTTWLTELYL  
 501 SRLGALQGD EALTLYRETK ECFRTFLSSP RHKEWLFASR ASIHELLASH  
 50 551 GDTEHVMYFA VIMQDYERVV AYHCQHEAYE EALAVLARHR DPQLFYKFSP  
 601 ILIRHIPRQL VDAWIEMGSR LDARQLIPAL VNYSQGGEVQ QVSQAIRYME  
 651 FCVNVLGETE QAIHNYLLSL YARGRPDSLL AYLEQAGASP HRVHYDLKYA  
 701 LRLCAEHGHH RACVHVYKVL ELYEEAVDLA LQVDVDLAKQ CADLPEEDEE  
 751 LRKKLWLKIA RHVVQEEEDV QTAMACLASC PLLKIEDVLP FFPDFVTIDH  
 55 801 FKEAICSSLK AYNHHIQELQ REMEEATASA QRIRRDLEL RGRYGTVEPQ  
 851 DKCATCDFPL LNRPFYFLC GHMFHADCLL QAVRPGLPAY KQARLEELQR  
 901 KLGAAPPAK GSARAKEAEG GAATAGPSRE QLKADLDELV AAECVYCCEL  
 951 MIRSIDRPFI DPQRYEEEL SWL

## BLASTP hits

5

No BLASTP hits available

Alert BLASTP hits for DKFZphm12\_7g14, frame 1

10 SWISSPROT:DOR\_DROME DEEP ORANGE PROTEIN., N = 1, Score = 1279, P  
= 2.4e-130

15 PIR:A41943 vacuolar membrane protein PEP3 - yeast (Saccharomyces  
cerevisiae), N = 3, Score = 266, P = 5.1e-27

>SWISSPROT:DOR\_DROME DEEP ORANGE PROTEIN.  
Length = 1,002

20

HSPs:

Score = 1279 (191.9 bits), Expect = 2.4e-130, P = 2.4e-130  
Identities = 303/847 (35%), Positives = 463/847 (54%)

25

Query: 130  
KVRPLARWKGQLVESVGWUNKALGTESSTGPILVGTAQGHIFEAELSASEGGLFGPAPDLY 189  
KVR + ++K + +V +N G ESSTGPIL+GT++G IFE EL+ + G

30 Sbjct: 155 KVRRIEKFKDHEITAVAFNPYHGNESSSTGPILLGTSRGLIFETELNPAADG-  
-----HVQ 208

Query: 190 FRPLYVLNEEGGPA-PVCSLEAERGPDG-  
RSFVIATTRQRLRFQFIGRAAEGAEAQGFSG 247

35

+ LY L G P P+ L+ R P+ R ++ T+ + ++ F +  
AE + +

Sbjct: 209 RKQLYDLGL-GRPKYPITGLKLLRVPNSSRYIIVVTSPECIYTF--  
QETLKAERSLQAI 265

40

Query: 248 FAAYTD--  
HPPPFREFPSNLGYSELAFTPKLRSAPRAFAWMMGDGVLYGAL--DCGRPD 303  
FA Y P E ++L +S+L F+ P P+ +AW+ G+G+ G L

+

Sbjct: 266  
45 FAGYVSGVQEPHCEERKTDLTFSQLRFFAPPNSKYPQWAWLCGEGIRVGELSIEANSAA 325

Query: 304 SLLSEERV---WEYPEGVGPGA---  
SPPLAIVLTQFHFLLLADRVEAVCTLTGQVVLRD 357

50

+L+ + +E + G + P A VLT++H +LL AD V A+C L  
+ V ++

Sbjct: 326  
TLIGNTLINLDFEKTMLHSYGERRLNTPKAFVLTEYHAVLLYADHVRAICLLNQEQVYQE 385

55

Query: 358 HFLE-  
KFGPLKHMVKDSSTGQLWAYTERAVFRYHVQREARDVWRTYLDNMRFDLAKEYCR 416  
F E + G + +D TG ++ YT + VF V RE R+VWR YLD

+++LA +

Sbjct: 386  
AFDEARVGKPLSIERDELGTGSIYVYTVKTVFNLRV TREERNVWRIYLDKGQYELATAHAA 445

Query: 417  
5 ERPDCLDTVLAREADFCFRQRRYLESARCYALTQSYFEEIALKFLEARQEEALAEFLQRK 476  
E P+ L VL + AD F Y +A YA T FEE+ LKF+ +  
+ +++++

Sbjct: 446  
10 EDPEHLQLVLCQRADAAAFADGSYQVAADYYAETDKSFEEVCLKFMVLPDKRPIINYVKKR 505

Query: 477 LASL--KPAERXXXXXXXXXXXXXXXXXSRLGALQ----  
GDPEALTLYRETKEC-FRTFLSS 529  
L+ + KP E L L P+ +R + +  
+ F+

15 Sbjct: 506  
LSRVTTKPMETDELDEDKMNIKALVIWLIDLYLIQINMPDKDEEWRSSWQTEYDEFMME 565

Query: 530  
20 PRHKEWLFASRASIELLASHGDTHEMVYFAVIMQDYERVVAYHCQHEAYEEALAVLARH 589  
+R ++ +L+A H D +M FA+ + DY+ VVA + E Y

EAL L  
Sbjct: 566  
AHVLSCTRQNRQTRQLIAEHADPRNMAQFAIAIGDYDEVVAQQLKAECYAEALQTLINQ 625

25 Query: 590  
RDPQLFYKFSPIILIRHIPRQLVDAWIEMGSRLDARQLIPALVNYSQGGEVQVSQAIRYM 649  
R+P+LFYK++P LI +P+ VDA + GSRL+ +L+P L+ + E ++

+Q RY+  
30 Sbjct: 626 RNPELFYKYAPELITRLPKPTVDALMAQGSRLVEKLVPTLI-  
IMENREQREQTQ--RYL 682

Query: 650  
EFCVNVLGETEQAIIHNYLLSLYARGRPDSLLAYLEQAGASPHRVHYDLKYALRLCAEHGH 709  
EF + L T AIHN+LL LYA P L+ YLE G VHYD+ YA

35 ++C +  
Sbjct: 683  
EFAIYKLNTTNDAIHNFLLHLYAEHEPKLLMKYLEIQGRDES LVHYDIYYAHKVCTDL DV 742

Query: 710  
40 HRACVHVYKVLLEYEAVDLALQVDVDLAKQCADLPEEDEELRKKLWLKLIARHVVQEEED 769  
A V + +L + AVDLAL D+ LAK+ A P D ++R+KLWL+IA

H ++ D  
Sbjct: 743 KEARVFLECMLRKWISAVDLALT FDMKLAKETASRPS-  
45 DSKIRRKLLWLRIAYHDIKGTND 801

Query: 770  
VQTAMACLASCPLLKIEDVLPFFPDPFVTIDHFKEAICSSLKAYNHHIQELQREMEETAS 829  
V+ A+ L C LL+IED+LPFF DF ID+FKEAIC +L+ YN

IQELQREM E T  
50 Sbjct: 802  
VKKALNLLKECDLLRIEDLLPFFADFEKIDNFKEAICDALRDYNQRIQELQREMAETTEQ 861

Query: 830  
AQRIRRDQLQELRGYGTVEPQDKCATCDFPLLNRPFYFLCGHMFHADCLLQAVRPGPLPA 889  
55 R +LQ+LR TVE QD C C+ LL +PF++F+CGH FH+DCL +

V P L  
Sbjct: 862  
TDRATAELQQLRQHSALTVESQDTCEICEMMLLVKPFIFICGHKFHSDCLEKHVVPLLT K 921

Query: 890  
 YKQARLEELQRKLGAA PPPXXXXXXXXXXXXXXXXXXXXPSREQLKADLDELVA AECVYCGE 949  
 + RL L+++L A R LK

5 +++++AA+C++CG

Sbjct: 922  
 EQCRRRLGTLKQQLAEVQTQAQPQSGALSKQQAMELQRKRAALKTEIEDILAADCLFCG- 980

Query: 950 LMIRSIDRPFI DPQRYEEELSW 972

10 L+I +ID+PF+D +E+ + W

Sbjct: 981 LLISTIDQPFVDD--WEQVNV EW 1001

Score = 268 (40.2 bits), Expect = 3.6e-19, P = 3.6e-19  
 Identities = 91/281 (32%), Positives = 146/281 (51%)

15

Query: 36 QLEKEVPIFTKQRIDF-TPSE---RITSLVSSNQLCMSLG---  
 KDTLLRIDLGKANEPN 88

+ ++E IF++ ++ PS + L VS N L LG + TLLR

L +A P

20 Sbjct: 37

ETDEEDEIFSRHKMVL RVPSNCTGDLMLHAVSRNWLVCLLGTPERTTLLRFFLPRAIPPG 96

Query: 89 HVELGRK---DDAKVHKMFLDHTGSHLLIAL---SST-----EVLYVN--  
 RNGQ---KV 131

25 L + K+ +MFLD TG H++IAL S+T + LY++ +

Q KV

Sbjct: 97

EAVLEKYLSGSGYKITRMFLDPTGHHIIIALVPKSATAGVSPDFLYIHCLESPQAQQLKV 156

30 Query: 132

RPLARWKGQLVESVGWNKALGTESSTGPILVGTAQGHIFEAELSASEGGLFGPAPDLYFR 191  
 R + ++K + +V +N G ESSTGPIL+GT++G IFE EL+ + G

+ +

35 Sbjct: 157 RRIEKFKDHEITAVAFNPYHGNESTGPILLGTSRGLIFETELNPAADG---  
 ---HVQRK 210

Query: 192 PLYVLNEEGGPA-PVCSLEAERGPDG-  
 RSFVIATTRQRLFQFIGRAAEGAEAGGFSGLFA 249

LY L G P P+ L+ R P+ R ++ T+ + ++ F + AE

40 + +FA

Sbjct: 211 QLYDLGL-GRPKYPITGLKLLRVPNSSRYIIVVTSPECIYTF--  
 QETLKAEERSLQAIFA 267

Query: 250 AYTD--HPPPFREFPSNLGYSELA FYTPKLR SAPRAFAWMMGDGVLYGAL  
 297

45 Y P E ++L +S+L F+ P P+ +AW+ G+G+ G L

Sbjct: 268 GYVSGVQEPHCEERKTDLTFSQLRFFAPPNSKYPKQWAWLCGEGIRVGEL  
 317

50

Pedant information for DKFZphm12\_7g14, frame 1

Report for DKFZphm12\_7g14.1

55

[[LENGTH]] 973  
 [[MW]] 110186.09

[pI] 5.72  
 [MOL] SWISSPROT:DOR\_DROME DEEP ORANGE PROTEIN. 1e-145  
 [FUNCAT] 30.25 vacuolar and lysosomal organization [S.  
 cerevisiae, YLR148w] 5e-41  
 5 [FUNCAT] 06.04 protein targeting, sorting and translocation  
 [S. cerevisiae, YLR148w] 5e-41  
 [FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S.  
 cerevisiae, YLR148w] 5e-41  
 10 [BLOCKS] BLO0106F Galactokinase proteins  
 [BLOCKS] PRO1094B  
 [BLOCKS] BP03306B  
 [BLOCKS] PF00600B  
 [PIRKW] yeast vacuole 1e-39  
 [PIRKW] transmembrane protein 1e-39  
 15 [KW] Alpha\_Beta  
 [KW] LOW\_COMPLEXITY 3.39 %  
 [KW] COILED\_COIL 4.83 %

20 SEQ MASILDEYENSLSRSAVLQPGCPSVGIPHSGYVNAQLEKEVPIFTKQRIDFTPSEIRITSL  
 SEG .....  
 PRD ccc  
 COILS .....

25 SEQ VVSSNQLCMSLGKDTLLRIDLGKANEPNHVELGRKDDAKVHKMFLDHTGSHLLIALSSTE  
 SEG .....  
 PRD ecc  
 COILS .....

30 SEQ VLYVNRNGQKVRPLARWKGQLVESVGWUNKALGTESSTGPILVGTAQGHIFEAELSASEGG  
 SEG .....  
 PRD eeeeeccccccchhhhhcc  
 COILS .....

35 SEQ LFGPAPDLYFRPLYVLNEEGGPAPVCSLEAERGPDGRSFVIATTRQRLFQFIGRAAEGAE  
 SEG .....  
 PRD ccc  
 COILS .....

40 SEQ AAGFSGLFAAYTDHPPPFREFPSNLGYSELAFYTPKLSAPRAFAWMMGDGVLYGALDCG  
 SEG .....  
 PRD hhhchhhhhhhhhcc  
 COILS .....

45 SEQ RPD SLLSEERVWEYPEGVGPASPLAIVLTQFHFLLLLADRVEAVCTLTGQVVLRDHFL  
 SEG .....  
 PRD cccccchhhhhhhcc  
 COILS .....

50 SEQ EKFGPLKHMVKDSSSTGQLWAYTERAVFRYHVQREARDVWRTYLD MNRFDLAKEYCRERPD  
 SEG .....  
 PRD hcc  
 COILS .....



.....

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.....

.....

[illegible]

((((((.....

.....

-260-

SEG .....  
PRD chhhhhhhhhccc  
COILS .....

5

(No Prosite data available for DKFZphm12\_7g14.1)

(No Pfam data available for DKFZphm12\_7g14.1)

5 group: melanoma derived

DKFZphmel2\_7k19 encodes a novel 234 amino acid protein without similarity to known proteins.

10 Transcripts can be found in almost any tissue, but are most abundant in kidney and retina.  
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

15 The new protein can find application in studying the expression profile of melanoma-specific genes.

unknown protein

20 first ATG in frame 1

Sequenced by MediGenomix

25 Locus: /map="3"

Insert length: 2386 bp

Poly A stretch at pos. 2343, polyadenylation signal at pos. 2323

30  
1 GGCAAAAGTC CAGGAATTAT CTTTCATCCCT GGCTATCTTT CTTATATGAA  
51 TGGTACAAAA GCGTTGGCGA TTGAGGAGTT TTGCAAATCT CTAGGTCACG  
101 CCTGCATAAG GTTTGATTAC TCAGGAGTTG GAAGTTCAGA TGGTAACTCA  
151 GAGGAAAAGCA CACTGGGGAA ATGGAGAAAA GATGTTCTTT CTATAATTGA  
35 201 TGACTTAGCT GATGGGCCAC AGATTCTTGT TGGATCTAGC CTTGGAGGGT  
251 GGCTTATGCT TCATGCTGCA ATTGCACGAC CAGAGAAGGT TGTGGCTCTT  
301 ATTGGTGTAG CTACAGCTGC AGATACCTTA GTGACAAAGT TTAATCAGCT  
351 TCCTGTTGAG CTAAAAAAGG AAGTAGAGAT GAAAGGTGTG TGGAGCATGC  
40 401 CATCAAAATA CTCTGAAGAA GGAGTTTATA ACGTTCAGTA CAGTTTCATT  
451 AAAGAAGCTG AACATCACTG CTTGTTACAT AGCCCAATTC CTGTGAACTG  
501 CCCCATAGA TTGCTCCATG GCATGAAGGA TGACATTGTA CCTTGGCATA  
551 CATCAATGCA GGTGCGCGAT CGAGTACTCA GCACAGATGT GGATGTCATC  
601 CTCCGAAAAC ACAGTGATCA CCGAATGAGG GAAAAAGCAG ACATTCAACT  
651 TCTTGTTTAC ACTATTGATG ACTTAATTGA TAAGCTCTCA ACTATAGTTA  
45 701 ACTAGTATCA CATGTTTAGT TGGTATGTAA ACTAATGTAT CCAGAAGATT  
751 GGAAGAGGGA TAAGAAATGA AAGATCCTGA TACTTTAGGT TTTTCCCTTT  
801 CCTCTATTTT GTAAATATAA GATGAGTATT ATTTAATGAT GTATTTGCAT  
851 AAGTAATGCA AATTGTGAAG AAGGACCAGC TGCTGTTTAG AAAATTTTCT  
901 CCTTCCTTCT GTCCTTGATT TTTTTTCATT AAAGTATTTT CTTTTTTTAA  
50 951 TTCAAGAAAA GTTTACCTTT CTTATGCTTA TGTAGCTAT GCCAGCTCTT  
1001 AATTGCATCC TTTTCTAATT AGGATTATTA ATAAAGCGTG AATATTTTGT  
1051 TTTTTATTAT AGACAGAAAT TTGTAACATT ACTTCTGATT TGAAAATGCA  
1101 ATTCACAAAA TATAGGGAAA TTTTTATTGA AGTAAATTTG AAATGATGGA  
1151 GAAATTTTCA AAGCATAATA AAGTTCACAA TAAGGATAAT ACTTTATATA  
55 1201 ATGTATAAAG TATATATAAT ATAATATATA TGTTATATAA ACTGCACATT  
1251 ATATTCAAAC TTAATATTGA GCTTTTTTTT TAAAGGCCCA AAATTGTACA  
1301 GTGATACAAG GAGCTATTTT TAAAATTTGG CTTATGTATA ATATATTTAA  
1351 ATGGGGGAATT TCATCTAAAA CAATGATGTA GTATTTTAA TATTCTGATT

```

1401 GGTAAAATTA AAGAGGAAAT TAATCTTTAT ATATTATTTT TTGCAGAAAC
1451 ATTCAATTATT TTATTAATAT TGCCCTAAGT ACAACTAGGC AAGTGATTGC
1501 CACCTAAATC AGAAGACGTT CTAAAGTCAG TAAGAAAGTG TGAAATGCTA
1551 GTATAAAGGT TATTTTTTTT CTTTCCTAAA TAACTAAAGT GAGGTGTAGA
5 1601 TTGAGCCTTG ATATTATTTA GTTAATGTTT TTTATTAATT AATTTTGGCT
1651 GGACTTTATT TAGCTTGATT AGGTTATTAT CTGTCAAACC TTTTAAGTTG
1701 ACAACATGAC TCATATATAT ACATGTGTAT AAGATGAGCA TGTGTGGAAG
1751 ACTTATTCGA CTCATTAATG AGGAAACCAG CAGATAGTAA ACCTGGTTCA
1801 AAGTACAATT CAAGAAACTG AGTATTTATG GGCATTGAAG AAAAAATGTT
10 1851 GAGATAAAAT TGCTGTGCAG AAAAAAGTGT TAATGAAGCC GACCTGACTA
1901 CTTAACCTTA GAGACCTGCT TTACAAGGTT GGCCCTTGAT TGGCATCTGG
1951 GAACTTGGAG TTCAGGGGGC TTCCACCATT CCCAGAACTG ATCAAAGTAG
2001 CTTACTATAT CTAAACTGTA AAACAATATA GTTCTCCTG AACACCTGCT
2051 TTCCTTCTGG GAGTCTGGAA TTTTGGTATG TGCCAGGCAG AGACTACCTT
15 2101 TGTGACCAGC TCCCAGTAAA AACCCAGGC ACTCAGTCTC TAACAAGCTT
2151 TTCTGGTTGA CAGTGTTTCA CAAGTGCTGT TACAAGTGGT TGCTGGGAGA
2201 ATTAAGCTCA TCCTCTGTGA TTCCACTGGC GGAGGATTCT TGGGAAGCTTG
2251 CACTTAGTTT CCCCTGACTT CACCCCATGT GTCTTTTTTC CTTTGCTGAT
2301 TTTGTTTTGT ATCCTTTCAC TGTAATAAAT CATGGCCGTG AGCAGAAAAA
20 2351 AAAAAAAAAA AAAAAAAAT AAAAAAAAAA AAAAAA

```

## BLAST Results

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25

No BLAST result

## Medline entries

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30

No Medline entry

35

## Peptide information for frame 1

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```

ORF from 46 bp to 702 bp; peptide length: 219
40 Category: similarity to unknown protein
Classification: unclassified

```

```

1 MNGTKALAIE EFCKSLGHAC IRFDYSGVGS SDGNSEESTL GKWRKDVLSI
51 IDDLADGPQI LVGSSLGGWL MLHAAIARPE KVVALIGVAT AADTLVTKFN
45 101 QLPVELKKEV EMKGVWSMPS KYSEEGVYNV QYSFIKEAEH HCLLHSPIPV
151 NCPIRLLHGM KDDIVPWHTS MQVADRVLST DVDVILRKHS DHRMREKADI
201 QLLVYTIDDL IDKLSTIVN

```

50

## BLASTP hits

No BLASTP hits available

55

Alert BLASTP hits for DKFZphm12\_7k19, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphmel2\_7k19, frame 1

## Report for DKFZphmel2\_7k19.1

5

[LENGTH] 219  
 [MW] 24309.18  
 [pI] 5.69

10 [HOMOL] PIR:A71691 hypothetical protein RP343 - Rickettsia  
 prowazekii 3e-29  
 [BLOCKS] BP04352K  
 [BLOCKS] PR00828E  
 [KW] Alpha\_Beta

15

SEQ MNGTKALAIIEEFCKSLGHACIRFDYSGVGSSDGNSEESTLGKWRKDVLSIIDDLADGPQI  
 PRD ccchhhhhhhhhhhhhccceeeeeeeeeccccccccccccccccchhhhhhhhhhhhhccceee

20 SEQ LVGSSLGGWMLHAAIARPEKVVALIGVATAADTLVTKFNQLPVELKKEVEMKGVWSMPS  
 PRD eeecccchhhhhhhhhhhccceeeeeeeeeehhhhhccccchhhhhhhhhhhhhheeeccc

SEQ KYSEEGVYNVQYSFIKEAEHHCLLHSPVPNCPIRLLHGMKDDIVPWHTSMQVADRVLST  
 PRD cccccceeeehhhhhhhhhhhhhhhccccccccceccccccccccccchhhhhhhhhhhhh

25

SEQ DVDVILRKHSDHRMREKADIQLLVYTIDDLIDKLSTIVN  
 PRD hheeeeeccccchhhhhhhhhheeeehhhhhhhhhcccccc

30 (No Prosite data available for DKFZphmel2\_7k19.1)

(No Pfam data available for DKFZphmel2\_7k19.1)

35 DKFZphtes3\_10i1b

-----

group: nucleic acid management

40

DKFZphtes3\_10i1b encodes a novel 742 amino acid protein with similarity to human ZK1.

45

The ZK1 gene is one of early response genes by exposure to ionizing radiation, and plays a role in radiation-induced apoptotic cell death on hematopoietic cells. The novel protein contains 18 zinc finger domains, a RGD cell attachment and a ATP GTP A domain.

50

The new protein can find application in diagnosis/therapy in leukemia predisposition/disease in the modulation of DNA repair.

similarity to ZK1 (Homo sapiens), complete cds.

55

Sequenced by Qiagen

Locus: unknown

Insert length: 2884 bp

Poly A stretch at pos. 2861, polyadenylation signal at pos. 2835

```

5      1 CGGAAATGGA GGGGGTCGCT TTCCTCACCT TCCTCGCTGC GCGGGCGGGCG
      51 GTTGGTAACC GGTGAGACCA GCGGAGAGG GACCTGGTGC CTGTACCCAG
     101 GCTTCTGTCT CTCTGTCGCC TGCCTATGC CCTGCTGTAG TCACAGGAGC
     151 TGTAAGAGAG ACCCCGGTAC ATCTGAAAGC CGGGAATGG ACCCAGTGGC
    10 201 CTTTGAGGAT GTGGCTGTGA ACTTCACCCA GGAAGAGTGG ACATTGCTGG
     251 ATATTTCCCA GAAGAATCTC TTCAGGGAAG TGATGCTGGA AACTTTCAGG
     301 AACCTGACCT CTATAGGAAA AAAATGGAGT GACCAGAACA TTGAATATGA
     351 GTACCAAAAC CCCAGAAAGAA GCTTCAGGAG TCTCATAGAA GAGAAAAGTCA
     401 ATGAAATTAA AGAAGACAGT CATTGTGGAG AAACCTTTTAC CCAGGTTCCA
    15 451 GATGACAGAC TGAACCTCCA GGAGAAGAAA GCTTCTCCTG AAGTAAAATC
     501 ATGTGACAGC TTTGTGTGTG CAGAAGTTGG CATAGGTAAC TCATCTTTTA
     551 ATATGAGCAT CAGAGGTGAC ACTGGACACA AGGCATATGA GTATCAGGAA
     601 TATGGACCAA AGCCATATAA GTGTCAACAA CCTAAAAATA AGAAAGCCTT
     651 CAGGTATCGC CCATCCATTA GAACACAAGA AAGGGATCAC ACTGGAGAGA
    20 701 AACCTATGCT TTGTAAAGTC TGTGGAAAAA CCTTTATTTT CCATTCAAGC
     751 ATTCGAAGAC ACATGGTAAT GCACAGTGGG GATGGAACCT ATAAATGTAA
     801 ATTTTGTGGG AAAGCCTTCC ATTCTTTCAG TTTATATCTT ATCCATGAAA
     851 GAACTCACAC TGGAGAGAAA CCATATGAAT GTAAACAATG TGGTAAATCC
     901 TTTACTTATT CTGCTACCCT TCAAATACAT GAAAGAACTC AACTGGGGGA
    25 951 GAAGCCCTAT GAATGTAGCA AATGTGATAA AGCATTTCAT AGTCTAGTT
    1001 CCTATCATAG ACATGAAAGA AGTCACATGG GAGAGAAGCC TTATCAATGC
    1051 AAAGAATGTG GAAAAGCATT TGCATATACC AGTTCTCTTC GTAGACATGA
    1101 AAGGACCCAC TCTGGGAAAA AACCGTATGA ATGTAAGCAA TATGGGGAAG
    1151 GCTTATCCTA TCTTATAAGT TTTCAAACAC ACATAAGAAT GAACTCTGGA
    30 1201 GAAAGACCTT ATAAATGTAA GATATGTGGG AAAGGCTTTT ATTCTGCCAA
    1251 GTCATTTCAA ACACATGAAA AAACCTCACAC TGGAGAGAAA CGCTATAAAT
    1301 GCAAGCAATG TGGTAAAGCC TTCAATCTTT CCAGTTCCTT TCGATATCAT
    1351 GAAAGGATTC ACACTGGAGA GAAACCCTAT GAGTGTAAGC AGTGTGGGAA
    1401 AGCCTTCAGA TCTGCCTCAC AGCTTCGAGT GCACGGTGGG ACTCACACTG
    35 1451 GAGAGAAACC CTATGAATGT AAGGAATGTG GGAAAGCCTT CAGATCTACC
    1501 TCACACCTTC GAGTGCATGG TAGGACTCAT ACTGGAGAGA AACCTATGA
    1551 ATGTAAGGAA TGTGGGAAAG CCTTCAGATA TGTGAAGCAC CTTCAAATTC
    1601 ATGAAAGGAC AGAAAAACAC ATAAGAATGC CCTCTGGAGA AAGACCTTAT
    1651 AAATGTAGTA TATGTGAGAA AGGCTTTTAT TCTGCCAAGT CATTTCAAAC
    40 1701 ACATGAAAAA ACTCACACTG GAGAGAAACC CTATGAATGC AACCAATGTG
    1751 GTAAAGCCTT CAGATGTTGC AATTCCCTTC GATATCATGA AAGGACTCAC
    1801 ACTGGAGAGA AACCTATGA GTGTAAGCAA TGTGGGAAAG CCTTCAGATC
    1851 TGCCTCACAC CTTCGAATGC ATGAAAGGAC TCACACTGGA GAGAAACCCT
    1901 ATGAGTGTA GCAATGTGGG AAAGCCTTCA GTTGTGCCTC AAACCTTCGA
    45 1951 AAGCATGGTA GGACTCACAC TGGAGAGAAA CCCTATGAGT GTAAGCAATG
    2001 TGGGAAAGCC TTCAGATCTG CCTCAAACCT TCAGATGCAT GAAAGGACTC
    2051 ACACTGGAGA GAAACCCTAT GAATGTAAGG AATGCGAAAA AGCATTCTGT
    2101 AAATTCTCTT CTTTTCAAAT ACATGAAAGG AAGCACAGAG GAGAGAAGCC
    2151 CTATGAATGT AAGCATTGTG GGAATGGATT CACATCTGCC AAGATTCTTC
    50 2201 AAATACATGC AAGAACACAC ATTGGAGAGA AACACTATGA ATGTAAGGAA
    2251 TCGGGAAGAG CATTCAATTA TTTTCTTCC TTGCATATAC ACGCAAGGAC
    2301 TCATATGGGA GAGAAGCCAT ATGAATGTAA GGATTGTGGG AAAGCATTCA
    2351 GCTAGCCTGG TTCCTTTTAT GGACATGAAT AGACTCACAC TGGGAAGGAAG
    2401 CACTATGAAT GCAAGCAATG TGGCAAAACT TTCACATTTT CCAGTTCTTT
    55 2451 TCGATATCAT GAAAGGACTC ACACTGGGGA GAAACCCTAT CAATGTAAGC
    2501 AGTGTGGGAA AGCCTTCATT CCTTTTACTT CTTTTCAATG TCATGAAAGG
    2551 ACTCACACGG GAGAGAAACC CTATGAGTGT ATTCTAGTTC CGTTTGATAT
    2601 CATGAAAGGA CTTACACTGG AGTGAACCCC TATGAATGTA AGCAATGTGG

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2651 GAAAGCCTTC AGATGTGCCT CGCACCTTCA ACGGCATGGA AGGGTTCACA  
 2701 CTTGGGAGAA ACTCTATGAA TGTAAGCAGT ATGGGAAAGC CTTCAGATCT  
 2751 GCCAAGATTCT TTTGAATACA GATAATTAAT GTAAACAATT ATCATAAGTA  
 2801 TACTAACATG TTATTCTTTT TAAATAAGAA GGTATAATAA AATATCCCAT  
 5 2851 TGGTTTTATG TATTAAAAAA AAAAAAAAAA AAAA

## BLAST Results

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10

No BLAST result

## Medline entries

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15

98401134:

Katoh O, Oguri T, Takahashi T, Takai S, Fujiwara Y, Watanabe H.;  
 ZK1, a

20 novel Kruppel-type zinc finger gene, is induced following  
 exposure to ionizing radiation and enhances apoptotic cell death  
 on hematopoietic cells. Biochem Biophys Res Commun 1998 Aug  
 28;249(3):595-600

25 95137393:

Wick MJ, Ann DK, Lee NM, Loh HH.; Isolation of a cDNA encoding a  
 novel

zinc-finger protein from

neuroblastoma x glioma NG108-15 cells. Gene 1995 Jan

30 23;152(2):227-32

35

## Peptide information for frame 1

-----

ORF from 127 bp to 2352 bp; peptide length: 742

Category: similarity to known protein

40 Classification: Nucleic acid management

Prosites motifs: RGD (146-148)

ATP\_GTP\_A (195-202)

ZINC\_FINGER\_C2H2 (196-216)

ZINC\_FINGER\_C2H2 (224-244)

45 ZINC\_FINGER\_C2H2 (252-272)

ZINC\_FINGER\_C2H2 (280-300)

ZINC\_FINGER\_C2H2 (308-328)

ZINC\_FINGER\_C2H2 (364-384)

ZINC\_FINGER\_C2H2 (392-412)

50 ZINC\_FINGER\_C2H2 (420-440)

ZINC\_FINGER\_C2H2 (448-468)

ZINC\_FINGER\_C2H2 (510-530)

ZINC\_FINGER\_C2H2 (538-558)

ZINC\_FINGER\_C2H2 (566-586)

55 ZINC\_FINGER\_C2H2 (594-614)

ZINC\_FINGER\_C2H2 (622-642)

ZINC\_FINGER\_C2H2 (650-670)

ZINC\_FINGER\_C2H2 (678-698)

ZINC\_FINGER\_C2H2 (706-726)  
ZINC\_FINGER\_C2H2 (476-498)

```

5      1 MPCCSHRSCR EDPGTSESRE MDPVAFEDVA VNFTQEEWTL LDISQKNLFR
      51 EVMLETFRNL TSIGKKWSDQ NIEYEYQNP RSFRSLIEEK VNEIKEDSHC
     101 GETFTQVPDD RLNFQEKAS PEVKSCDSFV CAEVGIGNSS FNMSIRGDTG
     151 HKAYEQEYG PKPYKQQPK NKKAQRYRPS IRTQERDHTG EKPYACKVCG
     201 KTFIFHSSIR RHMVMHSGDG TYKCKFCGKA FHSFSLYLIH ERTHTGEKPY
10    251 ECKQCGKSFT YSATLQIHER THTGEKPYEC SKCDKAFHSS SSSYHRHERSH
     301 MGEKPYQCKE CGKAFAYTSS LRRHERTHSG KKPYECKQYG EGLSYLISFQ
     351 THIRMNSGER PYKCKICGKG FYSAKSFQTH EKTHTEKRY KCKQCGKAFN
     401 LSSSFYHER IHTGEKPYEC KQCGKAQFSA SQLRVHGGTH TGEKPYECKE
     451 CGKAQFSTSH LRVHGRTHTG EKPYECKECG KAFRYVKHLQ IHERTEKHIR
15    501 MPSGERPYKC SICEKGFYSA KSFQTHEKTH TGEKPYECNQ CGKAQFCCNS
     551 LRYHERTHTG EKPYECKQCG KAFRSASHLR MHERTHTEK PYECKQCGKA
     601 FSCASNLRKH GRTHTEKPY ECKQCGKAQF SASNLQMHHER THTGEKPYEC
     651 KECEKAFCKF SSFQIHERKH RGEKPYECKH CGNGFTSAKI LQIHARTHIG
     701 EKHYECKECG KAFNYFSSLH IHARTHMG EK PYECKQCGKA FS
20

```

## BLASTP hits

25 No BLASTP hits available

Alert BLASTP hits for DKFZphtes3\_10i1b, frame 1

No Alert BLASTP hits found

30

## Peptide information for frame 2

-----

35 ORF from 1703 bp to 2584 bp; peptide length: 294  
Category: questionable ORF  
Classification: no clue

```

40      1 MKKLTLEARNP MNATNVVKPS DVAIPFDIMK GLTLERNPMS VSNVKGKPSDL
      51 PHTFECMKGL TLERNPMSVS NVGKPSVVPQ TFESMVGLTL ERNPMVSNSV
     101 GKPSDLPTF RCMKGLTLER NPMNVRNAKK HSVNSLLFKY MKGSTEERSP
     151 MNVSIVGMDS HLPFFKYMQ EHTLERNTMN VRNAEKHSII FLPCIYTQGL
     201 IWERSHMNVR IVGKHSASLV PFMDMNRLTL EGSTMNASNV AKLSHFVPLF
     251 DIMKGLTLGR NPINVSSVGK PSFLLLLFNV MKGLTRERNP MSVF
45

```

## BLASTP hits

50 No BLASTP hits available

Alert BLASTP hits for DKFZphtes3\_10i1b, frame 2

55 TREMBL:AF153201\_1 product: "zinc finger protein dp"; Homo  
sapiens zinc  
finger protein dp mRNA, complete cds., N = 1, Score = 225, P =  
4.1e-18



>TREMBL:AF153201\_1 product: "zinc finger protein dp"; Homo sapiens zinc

finger protein dp mRNA, complete cds.

5 Length = 423

HSPs:

Score = 225 (33.8 bits), Expect = 4.1e-18, P = 4.1e-18

10 Identities = 84/246 (34%), Positives = 122/246 (49%)

Query: 16 VVKPSDVA-

IPFDIMKGLTLERNPMSVSNVGKPSDLPHTFECMKGLTLERNPMSVSNVGK 74

V KPS A I F I + + L RN + V +V K S T ++G

15 TLERNP++V +VGK

Sbjct: 3 VGKPSVRAQILFCIRESI-

LG RNHIHVISVAKVSVRIQTLLNIEGSTLERNPINVMSVGK 61

Query: 75

20 PSVVPQTFESMVGLTLERNPMSVSNVGKPSDLPQTFRCMKGLTLERNPMNVRNAKKHSVN 134

+ Q+ + G LERNP+ V NV KPS Q + TLER+ +V

+A K V

Sbjct: 62

LLIRAQSLFYIRGFILERNPIPVINVAKPSVGFQILLIINEFTLERSLTHVISAIAKCLVE 121

25

Query: 135 SLLFKYMKGSTEERSPMNVSIIVGMD-

HLPRFFKYMQEHTLERNTMNVRNAEKHSIIFLP 193

+ + + R+PMNV VG P F +++E TLERN M+V

K +

30 Sbjct: 122 DEILLNITEFIQVRNPMNMNVGKPLVRAPTLF-

FIRESTLERNLMMHVIVLKAIVAVQI 180

Query: 194

CIYTQGLIERSHMNRIVGKHSASLVPFMDMNRLTLEGSTMNASNVAKLSHFPVLFDIM 253

35 + + ER+HM+V V K +++ TL S + A V K S

+ +

Sbjct: 181

LLSIKEYTLERNHMHVISVIKVLVKAQTSNIREYTLVKSIIAIVVRKPSVRVLTFFFI 240

40 Query: 254 KGLTLGRN 261

+ TL +N

Sbjct: 241 REFTLEKN 248

Score = 215 (32.3 bits), Expect = 1.1e-16, P = 1.1e-16

45 Identities = 82/246 (33%), Positives = 124/246 (50%)

Query: 44

VGKPSDLPHTFECMKGLTLERNPMSVSNVGKPSVVPQTFESMVGLTLERNPMSVSNVGK 103

VGKPS C++ L RN + V +V K SV QT ++G

50 TLERNP++V +VGK

Sbjct: 3

VGKPSVRAQILFCIRESIILGRNHIHVISVAKVSVRIQTLLNIEGSTLERNPINVMSVGKL 62

Query: 104 SDLPQTFRCMKGLTLERNPMNVRNAKKHSVNSLLFKYMKGSTEERSPMNV-

55 SIVGM---D 159

Q+ ++G LERNP+ V N K SV + + T ERS +V S

+ D

Sbjct: 63  
LIRAQSLFYIRGFILERNPIPVINVAKPSVGFQILLIINEFTLERSLTHVISAIAKCLVED 122

5 Query: 160 SHLPRFFKYMQEHTLERNTMNVRNAEKHSIIFLPCIY-  
TQGLIERSHMNVIRIVGKHSAS 218  
L +++Q RN MNV N K ++ P ++ + ER+ M+V

IV K +

Sbjct: 123 EILLNITEFIQV----RNPMNVMNVGK-  
PLVRAPTLFFIRESTLERNLMHVIVLKA 177

10

Query: 219 LVPFMDMNRLTLEGSTMNASNAK-  
LSHFPVLFDIMKGLTLGRNPINVS SVGKPSFLLLL 277  
+ + + TLE + M+ +V K L +I + TL ++ I V  
KPS +L

15

Sbjct: 178 VQILLSIKEYTLERNHMHVISVIKVLVKAQTSNIRE-  
YTLVKSIIIAIVVRKPSVRVLT 236

Query: 278 FNVMKGLTRERN 289  
++ T E+N

20

Sbjct: 237 LFFIREFTLEKN 248

Score = 207 (31.1 bits), Expect = 5.2e-15, P = 5.2e-15  
Identities = 80/270 (29%), Positives = 129/270 (47%)

25

Query: 1 MKKLTLERNPMTATNVVKPSDVAIPFDI-  
MKGLTLERNPMSVSNVVGKPSDLPHTFECMKG 59  
+++ L RN ++ +V K S V I + ++G TLERNP++V +VGK  
+ ++G

30

Sbjct: 16 IRESILGRNHIHVISVAKVS-  
VRIQTLLNIEGSTLERNPINVMSVGKLLIRAQSLFYIRG 74

Query: 60  
LTLERNPMSVSNVVGKPSVVPQTFESMVGLTLERNPMSVSNVVGKPSDLPQTFRCMKGLTLE 119  
LERNP+ V NV KPSV Q + TLER+ V + K +

35

Sbjct: 75  
FILERNPIPVINVAKPSVGFQILLIINEFTLERSLTHVISAIAKCLVEDEILLNITEFIQV 134

Query: 120  
40 RNPMNVRNAKHSVNSLLFKYMGSTEERSPMNVSI VGMDSHLPRFFKYMQEHTLERNTM 179  
RNPMNV N K V + +++ ST ER+ M+V IV +

++E+TLERN M

Sbjct: 135  
RNPMNVMNVGKPLVRAPTLFFIRESTLERNLMHVIVLKA 194

45

Query: 180  
NVRNAEKHSIIFLPCIYTTQGLIERSHMNVIRIVGKHSASLVPFMDMNRLTLEGSTMNASN 239  
+V + K + + + +S + +V K S ++ + TLE  
+ +

50

Sbjct: 195  
HVISVIKVLVKAQTSNIREYTLVKSIIIAIVVRKPSVRVLTFFIREFTLEKNYYLCTQ 254

Query: 240 VAKLSHFPVLFDIMKGLTL--GRNPINVS SVGK 270  
+K F + D++K + G P S K

55

Sbjct: 255 CSK--SFSQISDLIKHQRHTGEKPYKCSECRK 285

Score = 181 (27.2 bits), Expect = 1.4e-11, P = 1.4e-11  
Identities = 74/269 (27%), Positives = 116/269 (43%)

Query: 5  
 TLERNPMNATNVVKPSDVAIPFDIMKGLTLERNPMSVSNVGKPSDLPHTFECMKGLTLER 64  
 TLERNP+N +V K A ++G LERNP+ V NV KPS  
 5 + TLER  
 Sbjct: 48  
 TLERNPINVMSVGKLLIRAQSLFYIRGFILERNPIPVINVAKPSVGFQILLIINEFTLER 107

Query: 65  
 10 NPMSVSNVGKPSVVPQTFESMVGLTLERNPMSVSNVGKPSDLPQTFRCMKGLTLERNPMN 124  
 + V + K V + ++ RNPM+V NVGKP T ++  
 TLERN M+  
 Sbjct: 108  
 SLTHVISAIAKCLVEDEILLNITEFIQVRNPMNMNVGKPLVRAPTLFFIRESTLERNLMH 167

Query: 125 VRNAKKHSVNSLLFKYMKGSTEERSPMNV-  
 SIVGMDSHLPRFFKYMQEHTLERNTMNVNRN 183  
 V K V + +K T ER+ M+V S++ + ++E+TL  
 ++ +  
 20 Sbjct: 168 VVIVLKALVAVQILLSIKEYTLERNHMHVISVIKVLVKAQTSLN-  
 IREYTLVKSLIIAIV 226

Query: 184  
 25 AEKHSIIFLPCIYTQGLIWERSHMNVRIVGKHSASLVPFMDMNRLTLEGSTMNASNVAKL 243  
 K S+ L + + E+++ K + + + R+  
 S K  
 Sbjct: 227  
 VRKPSVRVLTLLFFIREFTLEKNYYLCTQCSKSFSQISDLIKHQRIHTGEKPYKCSECRKA 286

Query: 244 SHFPVLFDIMKGLTLGRNPINVSSVGKPSF 273  
 L + + + G+ P GK SF  
 Sbjct: 287 FSQCSLLALHQRIHTGKKPNPCDECGK-SF 315

Score = 166 (24.9 bits), Expect = 8.4e-10, P = 8.4e-10  
 35 Identities = 63/194 (32%), Positives = 89/194 (45%)

Query: 100  
 VGKPSDLPQTFRCMKGLTLERNPMNVNRNAKKHSVNSLLFKYMKGSTEERSPMNVSIIVGMD 159  
 VGKPS Q C++ L RN ++V + K SV ++GST  
 40 ER+P+NV VG  
 Sbjct: 3  
 VGKPSVRAQILFCIRESILGRNHIHVISVAKVSVRIQTLLNIEGSTLERNPINVMSVGKL 62

Query: 160  
 45 SHLPRFFKYMQEHTLERNTMNVNRNAEKHSIIFLPCIYTQGLIWERSHMNVRIVGKHSASL 219  
 + Y++ LERN + V N K S+ F + ERS +V  
 K  
 Sbjct: 63  
 LIRAQSLFYIRGFILERNPIPVINVAKPSVGFQILLIINEFTLERSLTHVISAIAKCLVED 122

Query: 220 VPFMDMNRLTLEGSTMNASNVAK-  
 LSHFPVLFDIMKGLTLGRNPINVSSVGKPSFLLLLF 278  
 +++ + MN NV K L P LF I + TL RN ++V V K  
 + +  
 50 Sbjct: 123 EILLNITEFIQVRNPMNMNVGKPLVRAPTLFFIRES-  
 TLERNLMHVIVLKALVAVQIL 181

Query: 279 NVMKGLTRERNPMSV 293

+K TERN M V  
 Sbjct: 182 LSIKEYTLERNHMHV 196

5 Pedant information for DKFZphtes3\_10i1b, frame 1  
 -----

Report for DKFZphtes3\_10i1b.1

10 [LENGTH] 784  
 [MW] 90857.05  
 [pI] 9.24  
 [HOMOL] TREMBL:AB011414\_1 gene: "ZK1"; product: "Kruppel-  
 15 type zinc finger protein"; Homo sapiens ZK1 mRNA for Kruppel-type  
 zinc finger protein, complete cds. 0.0  
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YJL056c]  
 6e-33  
 [FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae,  
 20 YJL056c] 6e-33  
 [FUNCAT] 04.99 other transcription activities [S. cerevisiae,  
 YOR113w] 5e-24  
 [FUNCAT] 04.01.01 rna synthesis [S. cerevisiae, YPR186c PZF1 -  
 TFIIIA] 1e-20  
 25 [FUNCAT] 04.03.01 trna synthesis [S. cerevisiae, YPR186c PZF1 -  
 TFIIIA] 1e-20  
 [FUNCAT] 13.04 homeostasis of other ions [S. cerevisiae,  
 YNL027w] 1e-13  
 [FUNCAT] 11.07 detoxification [S. cerevisiae, YGL254w] 2e-12  
 30 [FUNCAT] 01.02.04 regulation of nitrogen and sulphur utilization  
 [S. cerevisiae, YGL254w] 2e-12  
 [FUNCAT] 01.05.04 regulation of carbohydrate utilization [S.  
 cerevisiae, YGL209w] 2e-11  
 [FUNCAT] 04.05.99 other mrna-transcription activities [S.  
 35 cerevisiae, YER028c] 3e-10  
 [FUNCAT] 11.01 stress response [S. cerevisiae, YKL062w] 1e-09  
 [FUNCAT] 01.01.04 regulation of amino-acid metabolism [S.  
 cerevisiae, YDR253c] 5e-09  
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YBR066c]  
 40 3e-08  
 [FUNCAT] 03.07 pheromone response, mating-type determination,  
 sex-specific proteins [S. cerevisiae, YDR146c] 1e-07  
 [FUNCAT] 03.25 cytokinesis [S. cerevisiae, YLR131c] 2e-06  
 [BLOCKS] BL00466 TFIIS zinc ribbon domain proteins  
 45 [BLOCKS] BL00245A Phytochrome chromophore attachment site  
 proteins  
 [BLOCKS] DM01951B  
 [BLOCKS] PF01363B  
 [BLOCKS] BL01030  
 50 [BLOCKS] PF00096B  
 [BLOCKS] BL00028 Zinc finger, C2H2 type, domain proteins  
 [BLOCKS] BP04213E  
 [BLOCKS] BP04213C  
 [BLOCKS] BP04213B  
 55 [SCOP] d2adr\_ 7.31.1.1.4 ADR1 [synthetic based on yeast  
 (Saccharomyce 2e-05  
 [PIRKW] nucleus 1e-53  
 [PIRKW] RNA binding 2e-58

[PIRKW] duplication 1e-34  
 [PIRKW] tandem repeat 1e-171  
 [PIRKW] spermatogenesis 5e-62  
 [PIRKW] zinc 1e-169  
 5 [PIRKW] zinc finger 0.0  
 [PIRKW] DNA binding 0.0  
 [PIRKW] metal binding 1e-120  
 [PIRKW] phosphoprotein 2e-58  
 [PIRKW] leucine zipper 1e-53  
 10 [PIRKW] alternative splicing 2e-58  
 [PIRKW] eye lens 1e-111  
 [PIRKW] oocyte 1e-106  
 [PIRKW] transcription factor 1e-111  
 [PIRKW] embryo 1e-106  
 15 [PIRKW] segmentation 1e-34  
 [PIRKW] transcription regulation 1e-152  
 [SUPFAM] POZ domain homology 7e-83  
 [SUPFAM] transcription factor Krueppel 1e-34  
 [SUPFAM] zinc finger protein ZFP-36 1e-173  
 20 [SUPFAM] transcription factor IIIA 8e-31  
 [PROSITE] ATP\_GTP\_A 1  
 [PROSITE] RGD 1  
 [PROSITE] ZINC\_FINGER\_C2H2 18  
 [PFAM] Zinc finger, C2H2 type  
 25 [PFAM] TNFR/NGFR cysteine-rich region  
 [KW] Irregular  
 [KW] 3D  
 [KW] LOW\_COMPLEXITY 3.57 %

30  
 SEQ RKWRGSLSSPSSLRGRRLVTGQTSPRGTWCLYPGFCRSVACAMPCCSHRSCREDPGTSES  
 SEG .....  
 1meyF

35  
 SEQ REMDPVAFEDVAVNFTQEEWTLLDISQKNLFREVMLETFRNLTSIGKKWSDQNIYEYEQN  
 SEG .....  
 1meyF

40  
 SEQ PRRSFRSLIEEKVNEIKEDSHCGETFTQVPDDRNLNFQEKKASPEVKSCDSFVCAEVGIGN  
 SEG .....  
 1meyF

45  
 SEQ SSFNMSIRGDTGHKAYEYQEYGPYPYKCQPKNKKAFRYRPSIRTQERDHTGEKPYACKV  
 SEG .....  
 1meyF

50  
 SEQ CGKTFIFHSSIRRHMMHSGDGTYSKCKFCGKAFHSFSLYLIHERHTHTGEKPYECKQCGKS  
 SEG .....  
 1meyF

55  
 SEQ FTYSATLQIHERHTHTGEKPYECSKCDKAFHSSSSYHRHERSHMGEKPYQCKEKGAFAYT  
 SEG .....

.....

ImeyF

ImeyF

ImeyF

ImeyF

ImeyF

ImeyF

ImeyF

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lmevf      . . .
```

### Prosites for DKFZphtes3\_10i16.1

PS00028	266->287	ZINC_FINGER_C2H2	PD0C00028
PS00028	294->315	ZINC_FINGER_C2H2	PD0C00028
PS00028	322->343	ZINC_FINGER_C2H2	PD0C00028
PS00028	350->371	ZINC_FINGER_C2H2	PD0C00028
PS00028	406->427	ZINC_FINGER_C2H2	PD0C00028
PS00028	434->455	ZINC_FINGER_C2H2	PD0C00028
PS00028	462->483	ZINC_FINGER_C2H2	PD0C00028
PS00028	490->511	ZINC_FINGER_C2H2	PD0C00028
PS00028	552->573	ZINC_FINGER_C2H2	PD0C00028

	PS00028	580->601	ZINC_FINGER_C2H2	PD0C00028
	PS00028	608->629	ZINC_FINGER_C2H2	PD0C00028
	PS00028	636->657	ZINC_FINGER_C2H2	PD0C00028
	PS00028	664->685	ZINC_FINGER_C2H2	PD0C00028
5	PS00028	692->713	ZINC_FINGER_C2H2	PD0C00028
	PS00028	720->741	ZINC_FINGER_C2H2	PD0C00028
	PS00028	748->769	ZINC_FINGER_C2H2	PD0C00028
	PS00028	518->541	ZINC_FINGER_C2H2	PD0C00028

10

## Pfam for DKFZphtes3\_10116.1

15 HMM\_NAME TNFR/NGFR cysteine-rich region

HMM \*CpeGtYtD.WNHvpqClpC..trCePEMGQYMvqPCTwTQNTVC\*  
 C + +++ +++++C C ++C+++ G+++++ ++ V  
 Query 30 CLYPGFCRSVACAMPC--CSHRSCREDPGTSESREMDP----VA  
 20 67

HMM\_NAME Zinc finger, C2H2 type

25

HMM \*CpwPDGgKtFrrwsNLrRHMRT\*  
 C++ CGKTF S+ RRHM +H  
 Query 238 CKV--CGKTFIFHSSIRRHVMH 258

30 32.15 (bits) f: 266 t: 286 Target: dkfzphes3\_10116.1  
 similarity to ZK1 (Homo sapiens), complete cds.

Alignment to HMM consensus:

Query \*CpwPDGgKtFrrwsNLrRHMRT\*  
 C++ CGK+F + S + +H RTH  
 35 dkfzphes3 266 CKF--CGKAFHSFSLYLIHERTH 286

Query f: 294 t: 314 Target: dkfzphes3\_10116.1  
 similarity to ZK1 (Homo sapiens), complete cds.

Alignment to HMM consensus:

40 HMM \*CpwPDGgKtFrrwsNLrRHMRT\*  
 C+ CGK+F+++ +L++H RTH  
 Query 294 CKQ--CGKSFTYSATLQIHERTH 314

45 34.22 (bits) f: 322 t: 342 Target: dkfzphes3\_10116.1  
 similarity to ZK1 (Homo sapiens), complete cds.

Alignment to HMM consensus:

Query \*CpwPDGgKtFrrwsNLrRHMRT\*  
 C++ C+K+F ++S++ RH R+H  
 dkfzphes3 322 CSK--CDKAFHSSSSYHRHERSH 342

50

Query f: 350 t: 370 Target: dkfzphes3\_10116.1  
 similarity to ZK1 (Homo sapiens), complete cds.

Alignment to HMM consensus:

55 HMM \*CpwPDGgKtFrrwsNLrRHMRT\*  
 C++ CGK+F + S+LRRH RTH  
 Query 350 CKE--CGKAFAYTSSLRRHERTH 370

32.09 (bits) f: 406 t: 426 Target: dkfzphtes3\_10i1b.1  
 similarity to ZK1 (Homo sapiens), complete cds.  
 Alignment to HMM consensus:  
 Query \*CpwPDCgKtFrrwsNLrRHMRT\*  
 C++ CGK F ++ ++++H +TH  
 5 dkfzphtes3 406 CKI--CGKGFYSAKSFQTHEKTH 426

Query f: 434 t: 454 Target: dkfzphtes3\_10i1b.1  
 similarity to ZK1 (Homo sapiens), complete cds.  
 10 Alignment to HMM consensus:  
 HMM \*CpwPDCgKtFrrwsNLrRHMRT\*  
 C+ CGK+F+ +S++R H R+H  
 Query 434 CKQ--CGKAFNLSSSFYHERIH 454

32.94 (bits) f: 462 t: 482 Target: dkfzphtes3\_10i1b.1  
 similarity to ZK1 (Homo sapiens), complete cds.  
 Alignment to HMM consensus:  
 Query \*CpwPDCgKtFrrwsNLrRHMRT\*  
 C+ CGK+FR++S+LR H TH  
 20 dkfzphtes3 462 CKQ--CGKAFRSASQLRVHGGTH 482

Query f: 490 t: 510 Target: dkfzphtes3\_10i1b.1  
 similarity to ZK1 (Homo sapiens), complete cds.  
 Alignment to HMM consensus:  
 25 HMM \*CpwPDCgKtFrrwsNLrRHMRT\*  
 C++ CGK+FR+ S+LR H RTH  
 Query 490 CKE--CGKAFRSTSHLRVHGRTH 510

30.69 (bits) f: 518 t: 540 Target: dkfzphtes3\_10i1b.1  
 similarity to ZK1 (Homo sapiens), complete cds.  
 Alignment to HMM consensus:  
 Query \*CpwPDCgKtFrrwsNLrRHMRT..T.H\*  
 C++ CGK+FR+ +L++H R H  
 35 dkfzphtes3 518 CKE--CGKAFRYVKHLQIHERTE-KH 540

Query f: 552 t: 572 Target: dkfzphtes3\_10i1b.1  
 similarity to ZK1 (Homo sapiens), complete cds.  
 Alignment to HMM consensus:  
 HMM \*CpwPDCgKtFrrwsNLrRHMRT\*  
 C++ C+K F ++ ++++H +TH  
 40 Query 552 CSI--CEKGFYSAKSFQTHEKTH 572

31.33 (bits) f: 580 t: 600 Target: dkfzphtes3\_10i1b.1  
 similarity to ZK1 (Homo sapiens), complete cds.  
 Alignment to HMM consensus:  
 Query \*CpwPDCgKtFrrwsNLrRHMRT\*  
 C+ CGK+FR +LR H RTH  
 45 dkfzphtes3 580 CNQ--CGKAFRCCNSLRHERTH 600

Query f: 608 t: 628 Target: dkfzphtes3\_10i1b.1  
 similarity to ZK1 (Homo sapiens), complete cds.  
 Alignment to HMM consensus:  
 HMM \*CpwPDCgKtFrrwsNLrRHMRT\*  
 C+ CGK+FR++S+LR+H RTH  
 50 Query 608 CKQ--CGKAFRSASHLRMHERTH 628

35.30 (bits) f: 636 t: 656 Target: dkfzphtes3\_10i1b.1  
 similarity to ZK1 (Homo sapiens), complete cds.



Alignment to HMM consensus:

Query \*CpwPDGgKtFrrwsNLrRHMRT\*  
 C+ CGK+F+ +SNLR+H RTH  
 dkfzphtes3 636 CKQ--CGKAFSCASNLRKHGRTH 656

5

Query f: 664 t: 684 Target: dkfzphtes3\_10116.1  
 similarity to ZK1 (Homo sapiens), complete cds.

Alignment to HMM consensus:

HMM \*CpwPDGgKtFrrwsNLrRHMRT\*  
 C+ CGK+FR++SNL++H RTH  
 Query 664 CKQ--CGKAFRSASNLQMHERTH 684

10

31.74 (bits) f: 692 t: 712 Target: dkfzphtes3\_10116.1  
 similarity to ZK1 (Homo sapiens), complete cds.

Alignment to HMM consensus:

Query \*CpwPDGgKtFrrwsNLrRHMRT\*  
 C++ C+K+F+ S++++H R H  
 dkfzphtes3 692 CKE--CEKAFCKFSSFQIHERKH 712

15

Query f: 720 t: 740 Target: dkfzphtes3\_10116.1  
 similarity to ZK1 (Homo sapiens), complete cds.

Alignment to HMM consensus:

HMM \*CpwPDGgKtFrrwsNLrRHMRT\*  
 C++ CG F+++ L++H RTH  
 Query 720 CKH--CGNGFTSAKILQIHARTH 740

20

34.88 (bits) f: 748 t: 768 Target: dkfzphtes3\_10116.1  
 similarity to ZK1 (Homo sapiens), complete cds.

Alignment to HMM consensus:

Query \*CpwPDGgKtFrrwsNLrRHMRT\*  
 C++ CGK+F++ S+L +H RTH  
 dkfzphtes3 748 CKE--CGKAFNYFSSLHIHARTH 768

25

30

35

Pedant information for DKFZphtes3\_10116, frame 2

-----

Report for DKFZphtes3\_10116.2

40

[LENGTH] 294  
 [MW] 33083.98  
 [pI] 9.97

45

[HOMOL] TREMBL:AF153201\_1 product: "zinc finger protein  
 dp"; Homo sapiens zinc finger protein dp mRNA, complete cds. 7e-  
 17

[KW] All\_Alpha

50

SEQ MKKLTLEARNPMNATNVVKPSDVAIPFDIMKGLTLERNPMSVSNVGKPSDLPHTFECMKGL  
 PRD cccccccccccccccccccccchhhhhccccccccccccccccccccccccccccchhhhhhee

55

SEQ TLERNPMSVSNVGKPSVVPQTFESMVGLTLERNPMSVSNVGKPSDLPQTFRCMKGLTLER  
 PRD eccccccccccccccccccccchhhhhhhhhhhhhhhccccccccccccccccccccchhhhhhhhhhhcc

SEQ NPMNVRNAKKHSVNSLLFKYMKGSTEERSPMNVSVIGMDSHLPRFFKYMQEHTLERNTMN  
 PRD ccc

SEQ VRNAEKHSIIFLPCIYTQGLIWERSHMNVRIVGKHSASLVPFMDMNRLTLEGSTMNASNV  
PRD chhhhhhheeeccceeechhhhhccccceeecccccceeeccchhhhhhcccccccc

5 SEQ AKLSHFVLFDIMKGLTLGRNPINVSSVGKPSFLLLFNVMKGLTRERNPMSVF  
PRD cccccchhhhhhhccccccccccccccccchhhhhhhhcccccccccccc

(No Prosite data available for DKFZphtes3\_10i1b.2)

10

(No Pfam data available for DKFZphtes3\_10i1b.2)

DKFZphtes3\_10n10

-----

5 group: testis derived

DKFZphtes3\_10n10 encodes a novel 502 amino acid protein without similarity to known proteins.

10 The mRNA is differentially polyadenylated and the novel protein is ubiquitously expressed.  
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

15 The new protein can find application in studying the expression profile of testis-specific genes.

unknown protein

20 differentially polyadenylated

Sequenced by Qiagen

25 Locus: unknown

Insert length: 2551 bp

Poly A stretch at pos. 2531, polyadenylation signal at pos. 2513

30

```

      1 CTCAGCCTCC CAAGTGGCTG GGA CTGCAGG TTCTAAATGG CTTCTAAGAA
    51 GTTGGGTGCA GATTTTCATG GGA CTTTCAG TTACCTTGAT GATGTCCCAT
   101 TTAAGACAGG AGACAAATTC AAAACACCAG CTAAAGTTGG TCTACCTATT
   151 GGCTTCTCCT TGCCTGATTG TTTGCAGGTT GTCAGAGAAG TACAGTATGA
   35 201 CTTCTCTTTG GAAAAGAAAA CCATTGAGTG GGCTGAAGAG ATTAAGAAAA
   251 TCGAAGAAGC CGAGCGGGAA GCAGAGTGCA AAATTGCGGA AGCAGAAGCT
   301 AAAGTGAATT CTAAGAGTGG CCCAGAGGGC GATAGCAAAA TGAGCTTCTC
   351 CAAGACTCAC AGTACAGCCA CAATGCCACC TCCTATTAAC CCCATCCTCG
   401 CCAGCTTGCA GCACAACAGC ATCCTCACAC CAACTCGGGT CAGCAGTAGT
   40 451 GCCACGAAAC AGAAAGTTCT CAGCCACCT CACATAAAGG CGGATTTCAA
   501 TCTTGCTGAC TTTGAGTGTG AAGAAGACCC ATTTGATAAT CTGGAGTTAA
   551 AAAC TATTGA TGAGAAGGAA GAGCTGAGAA ATATTCTGGT AGGAACCACT
   601 GGACCCATTA TGGCTCAGTT ATTGGACAAT AACTTGCCCA GGGGAGGCTC
   651 TGGGTCTGTG TTACAGGATG AGGAGGTCCT GGCATCCTTG GAACGGGCAA
   45 701 CCCTAGATTT CAAGCCTCTT CATAAACCCA ATGGCTTTAT AACCTTACCA
   751 CAGTTGGGCA ACTGTGAAAA GATGTCACTG TCTTCCAAAG TGTCCCTCCC
   801 CCCTATACCT GCAGTAAGCA ATATCAAATC CCTGTCTTTC CCCAAACTTG
   851 ACTCTGATGA CAGCAATCAG AAGACAGCCA AGCTGGCGAG CACTTTCCAT
   901 AGCACATCCT GCCTCCGCAA TGGCACGTTT CAGAATTCCC TAAAGCCTTC
   50 951 CACCCAAAGC AGTGCCAGTG AGCTCAATGG GCATCACACT CTTGGGCTTT
  1001 CAGCTTTGAA CTTGGACAGT GGCACAGAGA TGCCAGCCCT GACATCCTCC
  1051 CAGATGCCTT CCCTCTCTGT TTTGTCTGTG TGCACAGAGG AATCATCACC
  1101 TCCAAATACT GGTCCCACGG TCACCCCTCC TAATTCTCA GTGTCACAAG
  1151 TGCCCAACAT GCCCAGCTGT CCCCAGGCCT ATTCTGAAC TGCAGATGCTG
   55 1201 TCCCCCAGCG AGCGGCAGTG TGTGGAGACG GTGGTCAACA TGGGCTACTC
  1251 GTACGAGTGT GTCCTCAGAG CCATGAAGAA GAAAGGAGAG AATATTGAGC
  1301 AGATTCTCGA CTATCTCTTT GCACATGGAC AGCTTTGTGA GAAGGGCTTC
  1351 GACCCTCTTT TAGTGGAAGA GGCTCTGGAA ATGCACCAGT GTTCAGAAGA

```

1401 AAAGATGATG GAGTTTCTTC AGTTAATGAG CAAATTTAAG GAGATGGGCT  
 1451 TTGAGCTGAA AGACATTAAG GAAGTTTTCG TATTACACAA CAATGACCAG  
 1501 GACAATGCTT TGGAAAGACCT CATGGCTCGG GCAGGAGCCA GCTGAGACCA  
 1551 GGGCCTGCCT AGGCCCTGCC GCAGAACCAC CATCCCTGGG AGGCCCTGCA  
 5 1601 GAGCCCACCT GTGGGGAAAG AGAAGGGGCA GCTTCCGGAT TTTCTTTTGG  
 1651 GGGTTAGAAG GTCAGGTGTG GAGACTGCTC GCCAGTCTCT GTGAGCCTAG  
 1701 GCCCTGAGCT GGGGAGGTGG GGAAGATTCT GGCATGTGAG TGCCCCCAGA  
 1751 ACTGTCCTGG CTCCTTCCGT ATTAACGCA TTTGCATTTT GAGAAGTGTC  
 1801 CTTCCCACTT CAGCCCTCCG GAGAGACTAC CCTAGTCTTT CTGGGGTGTT  
 10 1851 TATGTCCTCA GCTGAAGCCT GGCCTAGTTG CTGAGAGGGG CTGGGGAGAT  
 1901 GGGGCGGGAG GGCCAGACTC AGTGCTGCTG TGGAGCTAGG TGCTTCCCCC  
 1951 TTCCCTGAG ACTGGTTGAC TGAAGTCCAG TCAAGTTGAG TTCAAGTGAA  
 2001 AGATTCTTCC AGGGTTTTAT TTTTCCCCT CTAACAAAG TCTCATAGTG  
 2051 TTAACACTGG TTCTGCAATA TCTCTGAGGT GCAAAGAATG CACTTTTCCC  
 15 2101 TATGGGGCCC AGAGTTTGCC TTTTCTGCCA GGCAGTCACC ACGCTTCCCT  
 2151 ACCCCAGCCT GTTTCTTTTG GCTTGGTTTG GACCACAGTC CTCTGCTACC  
 2201 CAGGGTTTTA GAGCCCCTGC TCTAGGAAAC AGTTTAAGAA ATCATTGGCC  
 2251 CCTTCCCAGC ACATTGAATG GGTAAGCAGA CAGGCCATGA TTTAGTTGGC  
 2301 CAGCACTAAC TCCACCTCTG TTCTCCTTGA ACAGCTTCCC CTCCAGCCCA  
 20 2351 CTGCTTTAGG ATGACACAAT GAATAACACC TAGTCATAGA AATCAGTCTC  
 2401 TCTGGTTTGT TTTGTATTAT GTTGTACATC ATTAAGATC TAAATACAAA  
 2451 GGATATACAG TCTTGAATCT AAAATAATTT GCTAACTATT TTGATTCTTC  
 2501 AGAGAGAACT ACTAATAAAA ATCTAAAAGG TAAAAAATAA AAAAAAATAA  
 2551 A

## BLAST Results

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30 No BLAST result

## Medline entries

-----

35 No Medline entry

## Peptide information for frame 1

-----

ORF from 37 bp to 1542 bp; peptide length: 502

Category: putative protein

45 Classification: unclassified

1 MASKKLGADF HGTFSYLDV PFKTGDKFKT PAKVGLPIGF SLPDCLQVVR  
 51 EVQYDFSLEK KTIEWAEEIK KIEEAEREAE CKIAEAEAKV NSKSGPEGDS  
 101 KMSFSKTHST ATMPPIPIPI LASLQHNSIL TPTRVSSSAT KQKVLSPPHI  
 50 151 KADFNLADFE CEEDPFQDLE LKTIDEKEEL RNILVGTGTP IMAQLLDNNL  
 201 PRGGSGSVLQ DEEVLASLER ATLDFKPLHK PNGFITLPQL GNCEKMSLSS  
 251 KVSLLPIPAV SNIKSLSPFK LDSDDSNQKT AKLASTFHST SCLRNGTFQN  
 301 SLKPSTQSSA SELNGHHTLG LSALNLDSTG EMPALTSSQM PSLSVLSVCT  
 351 EESSPPNTGP TVTPPNFSVS QVPNMPSCPQ AYSELQMLSP SERQCVETVV  
 55 401 NMGYSECVL RAMKKKGENI EQILDYLFQAH GQLCEKGFDP LLVEEALEMH  
 451 QCSEKMMEF LQLMSKFKEG GFELKDIKEV LLLHNNDQDN ALEDLMARAG  
 501 AS

5 No BLASTP hits available

Alert BLASTP hits for DKFZphtes3 10n10, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphtes3 10n10, frame 1

Report for DKFZphtes3\_10n10.1

```

[LENGTH]    502
[MW]         55083.78
[pI]         5.02
[BLOCKS]     PRO1083D
[BLOCKS]     BL01306B
[KW]         All_Alpha
[KW]         LOW COMPLEXITY      8.57 %

```

```
SEQ    MASKKLGADFHGTFSYLDDVPFKTGDKFKTPAKVGLPIGFSLPDCLQVVREVQYDFSLEK
SEG    .....
PRD    cccccccccccccccccccccccccccccccccccccccchhhhhhhhcccch
```

```
SEQ      KTIIEWAAEEIKKIEEAEREAECKIAEAEAKVNSKSGPEGDSKMFSKTHSTATMPPPINPI
SEG      xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.....
PRD      hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccccccccccccccchhh
```

```
SEQ LASLQHNSILTPTRVSSSATKQKVLSPPHIKADFNLADFEEEDPFDNLELKTIDEKEEL
SEG .....
PRD hhhhhccccccccccccccccchhhhhccccccccchhhhhccccccccccccccccccccchhhhhhhh
```

```
SEQ  RNILVGTGPIMAQLLDNNLPRGGSGSVLQDEEVLASLERATLDFKPLHKPNGFITLPQL
SEG  .....
PRD  hhhhhccccchhhhhhhhhccccccccccccchhhhhhhhhhhhhhhcccccccccccccccccc
```

**SEQ** GNCEKMSLSSKVSLPPIPAVSNIKSLSFPKLDSDDSNQKTAKLASTFHSTSCLRNGTFQN  
**SEG** .....  
**PRD** cccccccccccccccccccccccccccccccchhhhhhhhccccccccccccccc

```
SEQ SLKPSTQSSASELNGHHTLGLSALNLD SGTEMPALTSSQMPSLSVLSVCTEESPNTGP
SEG .....xxxxxxx
PRD cccccccccccccccccccccccccc
```

```
SEQ TVTPPNFSVSQVPNMPSCPQAYSELQMLSPSERQCVETVVNMGYSYECVLRAMKKKGNI
SEG xxxxxxxx.....
PRD cccccccccccccccccccchhhhhhccccccchhhhhhccccccchhhhhhccccch
```

```
SEQ EQILDYLF AHGQLCEKGFDP LLVEEALEM HQCSE EKMM EFLQ LMSKF KEMGFEL KD I KEV
SEG .....
PRD hhhhhhhhhhhhccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
```

SEQ LLLHNNDDQDNALEDLMARAGAS

SEG .....  
 PRD hhccccchhhhhhhhhhhcc

5 (No Prosite data available for DKFZphtes3\_10n10.1)

(No Pfam data available for DKFZphtes3\_10n10.1)  
 DKFZphtes3\_11a17  
 -----

10

group: transmembrane protein

15 DKFZphtes3\_11a17 encodes a novel 428 amino acid protein without  
 similarity to known proteins.

The novel protein contains 2 transmembrane regions and one  
 leucine zipper. The protein is ubiquitously expressed with higher  
 abundance in stomach, brain and testis.

20 No informative BLAST results; No predictive prosite, pfam or SCOP  
 motife.

The new protein can find application in studying the expression  
 profile of testis-specific genes and as a new marker for  
 25 testicular cells.

unknown protein

30 Pedant: TRANSMEMBRANE 2  
 perhaps differential polyadenylation

Sequenced by Qiagen

35 Locus: unknown

Insert length: 2591 bp

Poly A stretch at pos. 2570, polyadenylation signal at pos. 2548

40

1 CTCTCCTGCG CCCTCTGGAG GAAGTGAGAA GAGTCAGTCC CACCCAGCTG  
 51 CCGCCTGGTA TCTGGGCTCC AGGCCACCGA GTATTTGGCC CCCAGCCACG  
 101 GAGCCCTTAG CACACACCTC CCCCACAGGT CCTGGAGATG TGGCTGAGCT  
 151 ACCTGCAGCC GTGGCGGTAC GCGCCTGACA AGCAGGCTCC GGGCAGCGAC  
 45 201 TCCCAGCCCC GGTGTGTGTC GGAGAAATGG GCACCCTTTG TCCAGGAGAA  
 251 CCTGCTGATG TACACCAAGT TGTTTGTGGG CTTTCTGAAC CGCGCGCTCC  
 301 GCACAGACCT GGTGAGCCCC AAGCACGCGC TCATGGTGTT CCGAGTGGCC  
 351 AAAGTCTTTG CCCAGCCCAA CCTGGCTGAG ATGATTGAGA AAGGTGAGCA  
 401 GCTATTCTTG GAGCCAGAGC TGGTCATCCC CCACCGCCAG CACCGACTCT  
 50 451 TCACGGCCCC CACATTCACT GGGAGCTTCC TGTCACCCTG GCCACCAGCG  
 501 GTCAGTGATG CCTCCTTCAA GGTGAAGAGC CACGTCTACA GCCTGGAGGG  
 551 CCAGGACTGC AAGTACACCC CGATGTTTGG GCCCGAGGCC CGCACCTTGG  
 601 TCCTGCGCCT CGCTCAGCTC ATCACACAGG CCAAACACAC AGCCAAGTCC  
 651 ATCTCCGACC AGTGTGCGGA GAGCCCGGCT GGCCACTCCT TCCTCTCATG  
 55 701 GCTGGGCTTT AGCTCCATGG ACACCAATGG CTCCTACACA GCCAACGACC  
 751 TGGACGAGAT GGGGCAAGAC AGTGTCCGGA AGACAGATGA ATACCTGGAG  
 801 AAGGCCCTGG AGTACCTGCG CCAGATATTC CGGCTCAGCG AAGCGCAGCT  
 851 CAGGCAGTTC AACTCGCCT TGGGCACCAC CCAGGATGAG AATGGAAAAA

```

901 AGCAACTCCC CGACTGCATC GTGGGTGAGG ACGGACTCAT CCTTACGCCC
951 CTGGGGCGGT ACCAGATCAT CAATGGGCTG CGAAGGTTTG AAATTGAGTA
1001 CCAGGGGGAC CCGGAGCTGC AGCCCATCCG GAGCTATGAG ATCGCCAGCT
1051 TGGTCCGCAC ACTCTTTAGG CTGTCGTCTG CCATCAACCA CAGATTTGCA
5 1101 GGACAGATGG CGGCTCTGTG TTCCCGGGAT GACTTCCTCG GCAGCTTCTG
1151 TCGCTACCAC CTCACAGAAC CTGGGCTGGC CAGCAGGCAC CTGCTGAGCC
1201 CTGTGGGGCG GAGGCAGGTG GCCGGCCACA CCCGCGGCC CAGGCTCAGC
1251 CTGCGCTTCC TGGGCAGTTA CCGGACGCTG GTCTCGCTGC TGCTGGCCTT
1301 CTTCGTGGCC TCTCTGTTCT GCGTCGGGCC CCTCCCATGC ACGTGCTGC
10 1351 TCACCTGCGG CTATGTCCTC TACGCTCTG CCATGACACT GCTGACCGAG
1401 CGGGGGGAAGC TGCACCAAGC CTGAAGGTGT CAGCTGCCTT CAGAGCAGGC
1451 TGGAGGGATT TGCCACACAG CCCCACCCTT GGGCTGAGAG GACCTGGGAA
1501 GCCCCCTCCAG GAGGGAACAC GGTCACTCTC GGGCTTCTGG AGCGGGGTTC
1551 CTGCAGCCGC AGAGGCATCT GGAGGAAACG CAACCAAGAA AGGAAGGCAG
15 1601 GTGGGCCCCA GCAAAGGAGT AGCTGCCAGG GCTCAACAGC TACGCTCTGT
1651 GACAGCGCAG AGCTCAGCGC CGGCCTTTCC CTCCCTCCGC CAAGGACTCA
1701 CGGCCAAGCC AGCTCTCGGG GCCTTTTTTC CAGTGCCCAT TTGGCTACTC
1751 TGCTGCACCA AGCTTGGGAG CCAGCCTGCC AACAGCCACC TGGGCTGGC
1801 CTCCCCACTG GCTGGCCTTG AGGTTGGCAG AGTGGGTTGT GGCCTTCCT
20 1851 CTCTCTGTGT GGGACCAGGA CAGTGGCTTA AGTCTCCACT CCAGGAAAGA
1901 ATCAAAGTTT CTAGAGTTGT GAGAAAACCA GAGAGTGGCT GTCCTGATTC
1951 TTCACTGTGA GGGGCGTTCT TCATGTTCTC CCAGCTGTTT CAAGACTGGG
2001 CCGTAGAATT CCATGTTTCA GGAGCCTAAG ACCCTCCCAG AGCCAGGGG
2051 CTTACCCGCA GACCCCAAGC CATTGAGCAC ATCACC AAA GCAGTGGCCA
25 2101 ACATCGCGGA CCCCTGTGCC TTGTACAGA TGGGTGCTGG TCCTCAGGCG
2151 TTGGGGACAC TGCTGGGTCG ATGGGGTCGG ATTCTGCCAG TTTCTGCTCT
2201 GCAGCCAAAG ATGGTCAGAA GCATTGTCAC TTCAGTAACA TCAAGTGCTC
2251 AAAGACATGG CAACCGTTCA GTGGTACTTA AGTATTCAA ATATACAACT
2301 ACAGATTCTC TGACAGAAAC CAGCACGGGG TCTTCACCTT CATTACCCCC
30 2351 ACAGGCGACA TCGGAGGGAG AACAGCATCT CAGTGGTGAT TTCCAAACCA
2401 AGCCTTTGTT TTCGGTGTGG GGTTTTGGGG GTTTGCTTTA ATGTTTTTGA
2451 AATTGTAAAT GTTGGGCTTT TTATTTTGAT GTAAACTGAG AATAATGGCA
2501 TTTTAGGGCC TGTGACCAAA AATGAAGCTT GTAACGACCA TGGATCTGAA
2551 TAAACATGTC CTTGCTTCTG AAAAAAAAAA AAAAAAAAAA A
35

```

## BLAST Results

-----

```

40 Entry AFD52134 from database EMBLNEW:
Homo sapiens clone 23585 mRNA sequence.
Score = 5765, P = 2.9e-254, identities = 1155/1156
3' UTR

```

45

## Medline entries

-----

50 No Medline entry

## Peptide information for frame 3

55

```

ORF from 138 bp to 1421 bp; peptide length: 428
Category: putative protein

```

Classification: Transmembrane proteins unclassified  
 Prosite motifs: LEUCINE\_ZIPPER (404-425)

```

5      1 MWSYLQPPWR YAPDKQAPGS DSQPRCVSEK WAPFVQENLL MYTKLFVGF
      51 NRALRTDLVS PKHALMVFRV AKVFAQPNLA EMIQKGEQLF LEPELVIPHR
     101 QHRLFTAPTf TGSFLSPWPP AVTDASFVKV SHVYSLEGQD CKYTPMFGPE
     151 ARTLVLRLAQ LITQAKHTAK SISDQCAESP AGHSFLSWLG FSSMDTNGSY
     201 TANDLDEMGA DSVRKTDEYL EKALEYLRQI FRLSEAQLRQ FTLALGTTQD
10     251 ENGKKQLPDC IVGEDGLILT PLGRYQIING LRRFEIEYQG DPELQPIRSY
     301 EIASLVRTLf RLSSAINHRF AGQMAALCSR DDFLGSFCRY HLTEPGLASR
     351 HLLSPVGRRQ VAGHTRGPRL SLRFLGSYRT LVSLLLAFFV ASLFCVGPLP
     401 CTTTTLGYV LYASAMTLLT ERGKLHP

```

## BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3\_11a17, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphtes3\_11a17, frame 3

# Report for DKFZphtes3\_11a17.3

```

30  [[LENGTH]] 428
    [[MW]] 48274.93
    [[pI]] 8.92
    [[PROSITE]] LEUCINE_ZIPPER 1
35  [[KW]] TRANSMEMBRANE 2
    [[KW]] LOW_COMPLEXITY 7.48 %

```

[illegible]

45	SEQ	PKHALMVFRVAKVFAQPNLAEMIQKGEQLFLEPELVIPHRQHRFLTAPTFTGSFLSPWPP
	SEG	.....
	PRD	cchhhhhhhhhhhhhccchhhhhhhccceeeccceeecccccccccccccccccccccccc
	MEM	.....

```

50 SEQ AVTDASFVKSHVYSLEGQDCKYTPMFGPEARTLVRLAQLITQAKHTAKSISDQCAESP
    SEG .....
    PRD ccccccccccccccccccchhhhhhhhhhhhhhhhhcccccccccccccc
    MEM .....

```

[illegible]



Prosite for DKFZphtes3\_11a17.3

(No Pfam data available for DKFZphtes3\_11a17.3)

DKFZphtes3\_11c22

-----

5 group: signal transduction

DKFZphtes3\_11c22 encodes a novel 482 amino acid protein with partial similarity to mouse PC32b.

10 The novel protein contains WD-repeats. WD-repeat proteins are known as regulatory elements in a large variety of pathways. The repeats form a propeller like structure, which serves as a platform for protein/protein interaction. The new protein is ubiquitously expressed, indicating that it takes an essential  
15 regulatory function in the cell.

The new protein can find application in modulating/blocking of regulatory pathways.

20 similarity to mouse PC32b

perhaps complete cds.

contains WD-Repeats: cf. BLASTX-S37694

25 perhaps differential polyadenylation

Sequenced by Qiagen

Locus: /map="1q23.2-24.3"

30

Insert length: 1952 bp

Poly A stretch at pos. 1932, polyadenylation signal at pos. 1912

35 1 GAAGCAAGTG AGGTTGCACA AAGCAATAGA GGACGAGGAA GATCTCGACC  
51 CAGAGGTGGA ACAAGTCAAT CAGATATTTT AACTCTTCCT ACGGTCCCAT  
101 CAAGTCCTGA TTTGGAAGTG AGTGAACTG CAATGGAAGT AGATACTCCA  
151 GCTGAACAA TTTCTCAGCC TTCTACATCC TCTACAATGT CAGCTCAGGC  
201 TCATTGACA TCATCTCCCA CAGAAAGCCC TCATTCTACT CCTTTGCTAT  
40 251 CTTCTCCAGA TAGTGAACAA AGGCAGTCTG TTGAGGCATC TGGACACCAC  
301 ACACATCATC AGTCTGATTC TCCTTCTTCT GTGGTTAACA AACAGCTCGG  
351 ATCCATGTCA CTTGACGAGC AACAGGATAA CAATAATGAA AAGCTGAGCC  
401 CCAAACCAGG GACAGGTGAA CCAGTTTAA GTTTGCACTA CAGCACAGAA  
45 451 GGAACAAC TAAGCACAAT AAACTGAAC TTTACAGATG AATGGAGCAG  
501 TATAGCATCA AGTTCTAGAG GAATTGGGAG CCATTGCAAA TCTGAGGGTC  
551 AGGAGGAATC TTTCGTCCCA CAGAGCTCAG TGCAACCACC AGAAGGAGAC  
601 AGTGAAACAA AAGCTCCTGA AGAATCATCA GAGGATGTGA CAAAATATCA  
651 GGAAGGAGTA TCTGCAGAAA ACCCAGTTGA GAACCATATC AATATAACAC  
701 AATCAGATAA GTTCACAGCC AAGCCATTGG ATTCCAAC TC AGGAGAAAGA  
50 751 AATGACCTCA ATCTTGATCG CTCTTGTTGG GTTCCAGAAG AATCTGCTTC  
801 ATCTGAAAAA GCCAAGGAAC CAGAACTTC AGATCAGACT AGCACTGAGA  
851 GTGCTACCAA TGAAAATAAC ACCAATCCTG AGCCTCAGTT CCAAACAGAA  
901 GCCACTGGGC CTTCAGCTCA TGAAGAAACA TCCACCAGGG ACTCTGCTCT  
951 TCAGGACACA GATGACAGTG ATGATGACCC AGTCCTGATC CCAGGTGCAA  
55 1001 GGTATCGAGC AGGACCTGGT GATAGACGCT CTGCTGTTGC CCGTATTTCAG  
1051 GAGTTCTTCA GACGGAGAAA AGAAAGGAAA GAAATGGAAG AATTGGATAC  
1101 TTTGAACATT AGAAGGCCGC TAGTAAAAAT GGTTTATAAA GGCCATCGCA  
1151 ACTCCAGGAC AATGATAAAA GAAGCCAATT TCTGGGGTGC TAACTTTGTA

```

1201 ATGAGTGGTT CTGACTGTGG CCACATTTTC ATCTGGGATC GGCACACTGC
1251 TGAGCATTTG ATGCTTCTGG AAGCTGATAA TCATGTGGTA AACTGCCTGC
1301 AGCCACATCC GTTTGACCCA ATTTTAGCCT CATCTGGCAT AGATTATGAC
1351 ATAAAGATCT GGTCAACATT AGAAGAGTCA AGGATTTTAA ACCGAAAACT
5 1401 TGCTGATGAA GTTATAACTC GAAACGAACT CATGCTGGAA GAAACTAGAA
1451 ACACCATTAC AGTTCCAGCC TCTTTCATGT TGAGGATGTT GGCTTCACTT
1501 AATCATATCC GAGCTGACCG GTTGGAGGGT GACAGATCAG AAGGCTCTGG
1551 TCAAGAGAAT GAAAATGAGG ATGAGGAATA ATAAACTCTT TTTGGCAAGC
1601 ACTTAAATGT TCTGAAATTT GTATAAGACA TTTATTATAT TTTTTTCTTT
10 1651 ACAGAGCTTT AGTGCAATTT TAAGGTATG GTTTTTGGAG TTTTCCCTT
1701 TTTTGGGAT AACCTAACAT TGGTTTGGAA TGATTGTGTG CATGAATTTG
1751 GGAGATTGTA TAAACAAAA CTAGCAGAAT GTTTTAAAA CTTTTTGCCG
1801 TGTATGAGGA GTGCTAGAAA ATGCAAAGTG CAATATTTTC CCTAACCTTC
1851 AAATGTGGGA GCTTGGATCA ATGTTGAAGA ATAATTTTCA TCATAGTGAA
15 1901 AATGTTGGTT CAAATAAATT TCTACACTTG CCAAAAAAAA AAAAAAAA
1951 AA

```

## BLAST Results

20

Entry HS702J19 from database EMBL:  
Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19

25 Score = 2043, P = 5.8e-252, identities = 425/445  
10 exons matching Bp 316-1932

Entry HS536148 from database EMBL:  
human STS WI-6347.

30 Score = 1203, P = 1.5e-47, identities = 247/252

Entry HS703H14 from database EMBLNEW:  
Human DNA sequence from clone 703H14 on chromosome 1q23.2-24.3

35 Score = 1307, P = 1.1e-51, identities = 263/265  
2 exons matching Bp 1-316

## Medline entries

40

93026383:

Bergsagel PL, Timblin CR, Eckhardt L, Laskov R, Kuehl WM.;  
Sequence and

45 expression of a murine cDNA encoding PC326, a novel  
gene expressed in plasmacytomas but not normal plasma cells.  
Oncogene  
1992 Oct;7(10):2059-64

50

## Peptide information for frame 1

55

ORF from 133 bp to 1578 bp; peptide length: 482  
Category: similarity to known protein  
Classification: Protein management

Prosites motifs: MYB\_1 (410-418)

```

5      1 MEVDTPAEQF LQPSTSSSTMS AQAHTSSSPT ESPHSTPLLS SPDSEQRQSV
      51 EASGHHTHHQ SDSPSSVVNK QLGMSLDEQ QDNNNEKLSP KPGTGEPVLS
     101 LHYTEGTTT STIKLNFTDE WSSIASSSRG IGSCHKSEGQ EESFVPQSSV
     151 QPPEGDSETK APEESSEDVT KYQEGVSAEN PVENHINITQ SDKFTAKPLD
     201 SNSGERNDLN LDRSCGVPEE SASSEKAKEP ETSDQTSTES ATNENNTNPE
     251 PQFQTEATGP SAHEETSTRD SALQDTDDSD DDPVLIPGAR YRAGPGDRRS
    10  301 AVARIQEFFR RRKERKEMEE LDTLNIRRL VKMVYKGHRN SRTMIKEANF
     351 WGANFVMSGG DCGHIFIWDR HTAEHMLLE ADNHVVNCLQ PHPFDPILAS
     401 SGIDYDIKIW SPLEESRIFN RKLADDEVITR NELMLEETRN TITVPASFML
     451 RMLASLNHIR ADRLEGDRSE GSGQENENED EE

```

15

# BLASTP hits

No BLASTP hits available

20

Alert BLASTP hits for DKFZphtes3\_11c22, frame 1

25

TREMBLNEW:HS06631\_1 gene: "H326"; Human (H326) mRNA, complete cds., N

= 1, Score = 278, P = 4e-22

PIR:S37694 gene PC326 protein - mouse, N = 1, Score = 265, P = 2.9e-20

30

PIR:T05676 hypothetical protein F20M13.40 - Arabidopsis thaliana, N =

1, Score = 240, P = 6.3e-18

35

>TREMBLNEW:HS06631\_1 gene: "H326"; Human (H326) mRNA, complete cds.

Length = 597

HSPs:

40

Score = 278 (41.7 bits), Expect = 4.0e-22, P = 4.0e-22

Identities = 63/148 (42%), Positives = 94/148 (63%)

Query: 335 YKGRNSRTMIKEANFWG--

45

ANFVMSGSDCGHIFIWDRHTAEHMLLEADNH-VVNCLQP 391

YKGRN+ T +K NF+G + FV+SGSDCGHIF+W++ + + + +E D

VVNCL+P

Sbjct: 428 YKGRNNAT-

VKGVNFYGPKEFVVSQSDCGHIFLWEKSSCQIIQFMEGDKGGVVNCLP 486

50

Query: 392 HPFDPILASSGIDYDIKIWSPLEESRIFNRKLADDEVITRNELMLEE-  
TRNTITVPASFML 450

HP P+LA+SG+D+D+KIW+P E+ L D VI +N+ +E + +

+ S ML

55

Sbjct: 487 HPHLPVLATSGLDHVDVKIWAPTAEASTELTGLKD-

VIKKNKRERDEDSLHQTDLFDHML 545

Query: 451 RMLASLNHIRADRLEGD-RSESGQENENEDE 481

-288-

SEQ EE  
SEG ..  
PRD CC

5

Prosites for DKFZphtes3\_11c22.1

10 PS00037 410->419 MYB\_1 PD0C00037

(No Pfam data available for DKFZphtes3\_11c22.1)

DKFZphtes3\_11d21

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5 group: signal transduction

DKFZphtes3\_11d21 encodes a novel 922 acid protein and contains the full coding sequence of the human Nedd-4-like ubiquitin-protein ligase.

10

The novel protein contains four WW domains. The WW/rsp5/WWP domain has been shown to bind proteins with particular proline-motifs, and thus resembles somewhat SH3 domains. It is frequently associated with other domains typical for proteins in signal transduction processes. There is also a ubiquitin-protein ligase activity reported. The protein is believed to play an important role in protein-degradation pathways.

15

20

The new protein can find application in diagnosis of diseases due to unnormal protein degradation like muscular dystrophy or multiple sclerosis as well as in modulating the half life of specific proteins and in expression profiling.

25

similarity to Nedd-4-like ubiquitin-protein ligase (Homo sapiens)

Sequenced by Qiagen

Locus: unknown

30

Insert length: 3382 bp

Poly A stretch at pos. 3362, polyadenylation signal at pos. 3345

35

1 ATTTTGGGAC ATGGCCACTG CTTACCAAG GTCTGATACT AGTAATAACC

51 ACAGTGGAAG GTTGCAGTTA CAGGTAAGT TTTCTAGTGC CAACTTAAA

101 AGAAAAAAGA ACTGGTTCGG AACAGCAATA TATACAGAAG TAGTTGTAGA

151 TGGAGAAATT ACGAAAACAG CAAAATCCAG TAGTTCTTCT AATCCAAAAT

201 GGGATGAACA GCTAACTGTA AATGTTACGC CACAGACTAC ATTGGAATTT

40

251 CAAGTTTGGG GCCATCGCAC TTTAAAAGCA GATGCTTTAT TAGGAAAAGC

301 AACGATAGAT TTGAAACAAG CTCTGTTGAT ACACAATAGA AAATTGGAAG

351 GAGTGAAAGA ACAATTAAAA CTTTCCTTGG AAAACAAGAA TGGCATAGCA

401 CAACTGGTG AATTGACAGT TGTGCTTGAT GGATTGGTGA TTGAGCAAGA

451 AAATATAACA AACTGCAGCT CATCTCCAAC CATAGAAATA CAGGAAAATG

45

501 GTGATGCCTT ACATGAAAAT GGAGAGCCTT CAGCAAGGAC AACTGCCAGG

551 TTGGCTGTTG AAGGCACGAA TGGAATAGAT AATCATGTAC CTACAAGCAC

601 TCTAGTCCAA AACTCATGCT GCTCGTATGT AGTTAATGGA GACAACACAC

651 CTTTCATCTCC GTCTCAGGTT GCTGCCAGAC CCAAAAATAC ACCAGCTCCA

701 AAACCACTCG CATCTGAGCC TGCCGATGAC ACTGTTAATG GAGAATCATC

50

751 CTCATTTGCA CCAACTGATA ATGCGTCTGT CACGGGTACT CCAGTAGTGT

801 CTGAAGAAAA TGCCTTGTCT CCAAATTGCA CTAGTACTAC TGTGGAAGAT

851 CCTCCAGTTC AAGAAATACT GACTTCCTCA GAAAACAATG AATGTATTCC

901 TTCTACCAGT GCAGAATTGG AATCTGAAGC TAGAAGTATA TTAGAGCCTG

951 ACACCTCTAA TTCTAGAAGT AGTTCTGCTT TTGAAGCAGC CAAATCAAGA

55

1001 CAGCCAGATG GGTGTATGGA TCCTGTACGG CAGCAGTCTG GGAATGCCAA

1051 CACAGAAACC TTGCCATCAG GGTGGGAACA AAGAAAAGAT CCTCATGGTA

1101 GAACCTATTA TGTGGATCAT AATACTCGAA CTACCACATG GGAGAGACCA

1151 CAACCTTTAC CTCCAGGTTG GGAAAGAAGA GTTGATGATC GTAGAAGAGT

```

1201 TTATTATGTG GATCATAACA CCAGAACAAAC AACGTGGCAG CGGCCTACCA
1251 TGGGAATCTGT CCGAAATTTT GAACAGTGGC AATCTCAGCG GAACCAATTG
1301 CAGGGAGCTA TGCAACAGTT TAACCAACGA TACCTCTATT CGGCTTCAAT
1351 GTTAGCTGCA GAAAATGACC CTTATGGACC TTTGCCACCA GGCTGGGAAA
5 1401 AAAGAGTGGG TTCAACAGAC AGGGTTTACT TTGTGAATCA TAACACAAAA
1451 ACAACCCAGT GGGAAGATCC AAGAACTCAA GGCTTACAGA ATGAAGAACC
1501 CCTGCCAGAA GGCTGGGAAA TTAGATATAC TCGTGAAGGT GTAAGGTACT
1551 TTGTTGATCA TAACACAAGA ACAACAACAT TCAAAGATCC TCGCAATGGG
1601 AAGTCATCTG TAACTAAAGG TGGTCCACAA ATTGCTTATG AACGCGGCTT
10 1651 TAGGTGGAAG CTTGCTCACT TCCGTTATTT GTGCCAGTCT AATGCACTAC
1701 CTAGTCATGT AAAGATCAAT GTGTCCCGGC AGACATTGTT TGAAGATTCC
1751 TTCCAACAGA TTATGGCATT AAAACCCCTAT GACTTGAGGA GGCCTTATA
1801 TGTAATATTT AGAGGAGAAG AAGGACTTGA TTATGGTGGC CTAGCGAGAG
1851 AATGGTTTTT CTTGCTTTCA CATGAAGTTT TGAACCCAAT GTATTGCTTA
15 1901 TTTGAGTATG CGGGCAAGAA CAACTATTGT CTGCAGATAA ATCCAGCATC
1951 AACCATTAAT CCAGACCATC TTTCACTATT CTGTTTCATT GGTCTGTTTA
2001 TTGCCATGGC ACTATTTTCA TGAAAGTTTA TCGATACTGG TTTCTCTTTA
2051 CCATTCTACA AGCGTATGTT AAGTAAAAAA CTTACTATTA AGGATTTGGA
2101 ATCTATTGAT ACTGAATTTT ATAACCTCCT TATCTGGATA AGAGATAACA
20 2151 ACATTGAAGA ATGTGGCTTA GAAATGTACT TTTCTGTTGA CATGGAGATT
2201 TTGGGAAAAG TTACTTCACA TGACCTGAAG TTGGGAGGTT CCAATATTCT
2251 GGTGACTGAG GAGAACAAG ATGAATATAT TGGTTTAATG ACAGAATGGC
2301 GTTTTTCTCG AGGAGTACAA GAACAGACCA AAGCTTTCCT TGATGGTTTT
2351 AATGAAGTTG TTCCTCTTCA GTGGCTACAG TACTTCGATG AAAAAGAATT
25 2401 AGAGGTTATG TTGTGTGGCA TGCAGGAGGT TGACTTGGCA GATTGGCAGA
2451 GAAATACTGT TTATCGACAT TATACAAGAA ACAGCAAGCA AATCATTTGG
2501 TTTTGGCAGT TTGTGAAAGA GACAGACAAT GAAGTAAGAA TGCGACTATT
2551 GCAGTTCGTC ACTGGAACCT GCCGTTTACC TCTAGGAGGA TTTGCTGAGC
2601 TCATGGGAAG TAATGGGCCT CAAAAGTTTT GCATTGAAAA AGTTGGCAAA
30 2651 GACACTTGGT TACCAAGAAG CCATACATGT TTTAATCGCT TGGATCTACC
2701 ACCATATAAG AGTTATGAAC AACTAAAGGA AAAACTTCTT TTTGCAATAG
2751 AAGAGACAGA GGGATTTGGA CAAGAATGAA TGTGGCTTCT TATTTTGGAG
2801 GAGCTCTTGC ATTTAAATAC CCCAGCCAAG AAAAATTGCA CAGATAGTGT
2851 ATATAAGCTG TTCATTCTGT ACAGTGAATT TTCCGAACCT CTCAAAGTAT
35 2901 GTTTTCCGTT CTTCACAGA AATATGCAAA ACAGTTCATC CTTTTCTACT
2951 TTATTTATTG TTCCCTTGAA ATGACTGACC AGGAAAAAGA TCATCCTTAA
3001 ATTTTGAAGC AAGTGAGAGA CTTTATTAAA AATACATATA TATCTATATA
3051 AACATATATG ATAGTGGCTC TAGTTTTATA GAGCTCCAAG TGTATTAAAC
3101 ATGACAGCCA TTCATTCTATA AAGATCTGGA TTTGCTTTAC CTTGTTAATA
40 3151 TTATCTAGGG GAAAAAGTGC AAATTGCTCC ATGTTCTTCT CTCCCTTATG
3201 TAACATCTCC TGAGGGTGTT TAGTTGCATG GCTGTTTACA AAGGTATTAA
3251 GGGCTTAGGC CAAATCTTAC TTTGAGTATG TTAATAAAAA AAAAATGCTG
3301 CTGGCTTTTC TGAAGACAGG TGCTTGAAC TGTGAGTTTG TTTTAAATAA
45 3351 ATACAATAGT TGAAAAAAA AAAAAAAA AA

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## BLAST Results

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50 No BLAST result

## Medline entries

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55

97313427:

Pirozzi G, McConnell SJ, Uveges AJ, Carter JM, Sparks AB, Kay BK, Fowlkes DM.; Identification of novel human WW domain-containing



proteins  
by cloning of ligand targets. J Biol Chem 1997 Jun  
6;272(23):14611-6

5

# Peptide information for frame 2

-----

10

ORF from 11 bp to 2776 bp; peptide length: 922

Category: known protein

Classification: Protein management

Prosite motifs: WW\_DOMAIN\_1 (355-380)

15

WW\_DOMAIN\_1 (387-412)

WW\_DOMAIN\_1 (462-487)

WW\_DOMAIN\_1 (502-527)

20

1 MATASPRSDT SNNHSGRLQL QVTVSSAKLK RKKNWFGTAI YTEVVVDGEI

51 TKTAKSSSSS NPKWDEQLTV NVTPQTTFLEF QVWSHRTLKA DALLGKATID

101 LKQALLIHNR KLERVKEQLK LSLENKNGIA QTGELTVVLD GLVIEQENIT

151 NCSSSPTIEI QENGDALHEN GEPSARTTAR LAVEGTNGID NHVPTSTLVQ

201 NSCCSYVVG DNTPSSPSQV AARPKNTPAP KPLASEPAD D TVNGESSSFA

25

251 PTDNASVTGT PVVSEENALS PNCTSTTVED PPVQEILTSS ENNECIPSTS

301 AELESEARSI LEPDTSNSRS SSAFEAAKSR QPDGCM DPVR QQSGNANTET

351 LPSGWEQRKD PHGRYYYVDH NTRTTTWERP QPLPPGWERR VDDRRRVYYV

401 DHNTRTTTWQ RPTMESVRNF EQWQSQRNQL QGAMQQFNQR YLYSASMLAA

451 ENDPYGPLPP GWEKRV DST D RYVFVNHN TK TTQWEDPRTQ GLQNEEPLPE

30

501 GWEIRY TREG VRYFVDHNTR TTTFKDPRNG KSSVTKGGPQ IAYERGFRWK

551 LAHFRYLCQS NALPSHV KIN VSRQTLFEDS FQQIMALKPY DLRRRLYVIF

601 RGEGLDYGG LAREWFFLLS HEVLNPMYCL FEYAGKNNYC LQINPASTIN

651 PDHLSYFCFI GRFIAMALFH GKFI DTGFSL PFYKRMLSKK LTIKDLESID

701 TEFYN SLIWI RDN NIEECGL EMYFSVDMEI LGKVTSHDLK LGGSN ILVTE

35

751 ENKDEYIGLM TEWRFSRGVQ EQTKAFLDGF NEVVPLQWLQ YFDEKELEV M

801 LCGMQEVDLA DWQRNTVYRH YTRNSKQIIW FWQFVKETDN EVRMRL LQFV

851 TGTCRLPLGG FAELMGSNGP QKFCIEKV GK DTWLPRSH TC FNRLDLPPYK

901 SYEQLKEKLL FAIEETEGFG QE

40

## BLASTP hits

No BLASTP hits available

45

Alert BLASTP hits for DKFZphtes3\_11d21, frame 2

No Alert BLASTP hits found

50

Pedant information for DKFZphtes3\_11d21, frame 2

-----

## Report for DKFZphtes3\_11d21.2

55

[[LENGTH]] 925  
[[MW]] 105650.58  
[[pI]] 5.60

[HOMOL] TREMBL:HSU96113\_1 product: "WWP1"; Homo sapiens  
 Nedd-4-like ubiquitin-protein ligase WWP1 mRNA, partial cds. 0.0  
 [FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae,  
 YER125w] 1e-149  
 5 [FUNCAT] 11.01 stress response [S. cerevisiae, YER125w] 1e-  
 149  
 [FUNCAT] 06.13.01 cytoplasmic degradation [S. cerevisiae,  
 YER125w] 1e-149  
 [FUNCAT] 03.10 sporulation and germination [S. cerevisiae,  
 10 YER125w] 1e-149  
 [FUNCAT] 06.07 protein modification (glycosylation, acylation,  
 myristylation, palmitylation, farnesylation and processing)  
 [S. cerevisiae, YER125w] 1e-149  
 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae,  
 15 YDR457w] 1e-78  
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YJR036c]  
 7e-39  
 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae,  
 YKLO10c] 8e-21  
 20 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKLO12w]  
 6e-05  
 [FUNCAT] 04.05.03 mrna processing (splicing) [S. cerevisiae,  
 YKLO12w] 6e-05  
 [FUNCAT] 30.01 organization of cell wall [S. cerevisiae,  
 25 YIRO19c] 3e-04  
 [FUNCAT] 30.90 extracellular/secretion proteins [S. cerevisiae,  
 YIRO19c] 3e-04  
 [FUNCAT] 01.05.01 carbohydrate utilization [S. cerevisiae,  
 YIRO19c] 3e-04  
 30 [BLOCKS] BP03746E  
 [BLOCKS] BP03761G  
 [BLOCKS] BL00514E Fibrinogen beta and gamma chains C-terminal  
 domain proteins  
 [BLOCKS] PR00731B  
 35 [BLOCKS] BP01566C  
 [BLOCKS] BL01159 WW/rsp5/WWP domain proteins  
 [BLOCKS] PR00403B  
 [BLOCKS] PR00403A  
 [BLOCKS] PF00632B  
 40 [BLOCKS] PF00632A  
 [EC] 6.3.2.19 Ubiquitin--protein ligase 1e-151  
 [PIRKW] ligase 1e-151  
 [PIRKW] transmembrane protein 2e-37  
 [PIRKW] leucine zipper 2e-28  
 45 [SUPFAM] WW repeat homology 1e-151  
 [SUPFAM] WD repeat homology 2e-28  
 [SUPFAM] ubiquitin ligase homolog 1e-151  
 [PROSITE] WW\_DOMAIN\_1 4  
 [PFAM] WW/rsp5/WWP domain containing proteins  
 50 [PFAM] C2 domain  
 [KW] Alpha\_Beta  
 [KW] LOW\_COMPLEXITY 1.41 %  
  
 55 SEQ FWD MATASPRSDTSNNHSGRLQLQVTVSSAKLKRKKNWFGTAIYTEVVVDGEITKTAKSS  
 SEG .....  
 PRD ccc

SEQ SSSNPKWDEQLTVNVTPQTTFEFQVWSHRTLKADALLGKATIDLKQALLIHNKRLERVKE  
SEG .....  
PRD ccc

5 SEQ QLKLSLENKNGIAQTGELTVVLDGLVIEQENITNCSSSPTIEIQENGDAHENGEPART  
SEG .....  
PRD hhhhhhccch

10 SEQ TARLAVEGTNGIDNHVPTSTLVQNSCCSYVVNGDNTSPSPSQVAARPKNTPAPKPLASEP  
SEG .....  
PRD hhhhhhcc

15 SEQ ADDTVNGESSFAPTDNASVTGTPVVSEENALSPNCTSTTVEDPPVQEI LTSSENNECIP  
SEG .....  
PRD ccc

20 SEQ STSAELESEARSILEPDTNSRSSSAFEAAKSRQPDGCM DPVRQQSGNANTETLP SGWEQ  
SEG .....  
PRD ccc

SEQ RKDPHGRTYYVDHNTRTTTWERPQPLPPGWERRVDDRRRVYYVDHNTRTTTWQRPTMESV  
SEG .....xxxxxxxxxxxxx.....  
PRD ccc

25 SEQ RNFEQWQSQRNQLQGAMQQFNQRYLYSASMLAENDPYGPLPPGWEKRV DSTDRVYFVNH  
SEG .....  
PRD hhhhhhhhhhhhhhhhhhhhhcc

30 SEQ NTKTTQWEDPRTQGLQNEEPLPEGWEIRY TREGVRYFVDHNTRTTT FKDP RNGKSSVTKG  
SEG .....  
PRD ccc

35 SEQ GPQIAYERGFRWKL AHFRYLQSNALPSHVKINVSRTLFEDSFQQIMALKPYDLRRRLY  
SEG .....  
PRD cccccchhhhhhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccccccc

40 SEQ VIFRGEGLDYGGLAREWFFLLSHEVLNPMYCLFEYAGKNNYCLQINPASTINPDHLSYF  
SEG .....  
PRD hhhccccccccccccchhhhhhhhhhhcccccccccccccccccccccccccccccccccc

SEQ CFIGRFIAMALFHGKFIDTGFSLPFYKRMLS SKLTIKDL ESIDTEFYNSLIWIRDNNIEE  
SEG .....  
PRD hhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhhhhhhhhhhccccccccchhhhhhheeecccccc

45 SEQ CGLEMYFSVDMEILGKVTSHDLKLGGSNILVTEENKDEYIGLMT EWRF SRGVQEQTKAFL  
SEG .....  
PRD chhhhhhhhhhhccchhhhhhhhhhhhhhhhhhh

50 SEQ DGFNEVVPLQWLQYFDEKELEVMLCGMQEVDLADWQRNTVYRHYTRNSKQIIWFQFVKE  
SEG .....  
PRD hhhhccccccccchhhhhhhhhhhhhhhhhccccccccccccccccccccccccchhhhhhhhhhhhhhh

55 SEQ TDNEVRMRLQFVTGTCRLPLGGFAELMG SNGPQKFCIEKVGKDTWLPRSHTCFNRLDLP  
SEG .....  
PRD hchhhhhhhhhhhhhhhhhcc

SEQ PYKSYEQ LKEKLLFAIEETEGFGQE  
SEG .....

5 Prosite for DKFZphtes3\_11d21.2

	PS01159	358->384	WW_DOMAIN_1	PD0C50020
	PS01159	390->416	WW_DOMAIN_1	PD0C50020
	PS01159	465->491	WW_DOMAIN_1	PD0C50020
10	PS01159	505->531	WW_DOMAIN_1	PD0C50020

Pfam for DKFZphtes3\_11d21.2

15

HMM\_NAME C2 domain

HMM

20	*LtVrIIeARNLWkMDMnGfSDPYVKVdMdPdpkDtkKWKtTiWNN-GL	
	L V++ +A+ +K++++G+ Y +V +D++	TKT

+++ +

Query	23	LQVTVSSAKLRKKNWFGTA-IYTEVVVDGE-----
ITKTAKSSSSS	63	

25

HMM NPVWNEEeFvFedIPyPd1qrkMLRFaVWDWDRFSRBDFIGHCi\*

NP W+ E+++ + + + L+F+VW + ++ + ++G ++

Query 64 NPKWD-EQLTVN---VTPQTT--LEFQVWSHRTLKADALLGKAT

101

30

HMM\_NAME WW/rsp5/WWP domain containing proteins

35	HMM	*LPsGWEeHWDpsGRpWYYWNHETkTTQWEpP*
		LPsGWE+++DP GR+ YY++H+T+TT+WEP
	Query	354 LPsGWEQRKDPHGRT-YYVDHNTRTTTWERP 383

50.09 386 415 1 31 dkfzphes3\_11d21.2 similarity to  
40 Nedd-4-like ubiquitin-protein ligase (Homo sapiens)

Alignment to HMM consensus:

Query		*LPsGWEeHWDpsGRpWYYWNHETkTTQWEpP*
		LP+GWE++ D+ R YY++H+T+TT+W++P
dkfzphes3	386	LPPGWERRVDDRRRV-YYVDHNTRTTTWQRP 415

45

Query 490 1 31 dkfzphes3\_11d21.2 similarity to  
Nedd-4-like ubiquitin-protein ligase (Homo sapiens)

Alignment to HMM consensus:

HMM		*LPsGWEeHWDpsGRpWYYWNHETkTTQWEpP*
		LP+GWE++ D + R Y++NH+TKTTQWE+P
50	Query	461 LPPGWEKRVDDSTDRV-YFVNHNTRTTQWEDP 490

38.62 501 530 1 31 dkfzphes3\_11d21.2 similarity to  
55 Nedd-4-like ubiquitin-protein ligase (Homo sapiens)

Alignment to HMM consensus:

Query		*LPsGWEeHWDpsGRpWYYWNHETkTTQWEpP*
		LP GWE +++ +G + Y+++H+T+TT+ ++P
dkfzphes3	501	LPEGWEIRYTRREGVR-YFVDHNTRTTTFKDP 530

**PAGE INTENTIONALLY LEFT BLANK**

5 group: testis derived

DKFZphtes3\_11e17 encodes a novel 573 amino acid protein without similarity to known proteins.

10 No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

15

unknown protein

Sequenced by Qiagen

20

Locus: unknown

Insert length: 2102 bp

Poly A stretch at pos. 2080, polyadenylation signal at pos. 2059

25

```

      1 GGCCTGGGGG GCTTCCCTGG GGGGCTTGTC GCCGGGGCCG CCTGGGCTTT
    51 CAGGTCTTCC GAGGCTGACA TTCACGTTTC ATTCTGCCAC ACTCGGGAAC
   101 GGTGATCGGG GAAGCATGGG GATCCGGGAG AAGCACCCAC AAAACTAGCA
   30 151 TCCTCCTGGA GGAGCTCGGG AATAGGATGA GTGATAATCC ACCCAGAATG
      201 GAAGTGTGTC CTTACTGTAA GAAGCCATTT AAACGATTAA AATCCCCTT
      251 GCCATACTGT AAGATGATAG GATCAACCAT ACCTACTGAT CAAAAAGTTT
      301 ATCAGTCCAA GCCAGCTACA CTCCCACGTG CTAAAAAGAT GAAAGGACCA
      351 ATCAAAGATT TAATTAAGC TAAAGGGAAA GAGTTAGAGA CAGAGAATGA
   35 401 AGAAAGAAAT TCTAAGTTGG TGGTGGACAA ACCAGAACAG ACAGTGAAGA
      451 CCTTTCCTCT GCCAGCTGTT GGTGTTGAAA GAGCAGCTAC TACAAAGGCA
      501 GATAAAGACA TCAAGAATCC AATCCAACCA TCCTTCAAAA TGTTAAAAAA
      551 TACTAAACCA ATGACTACTT TCCAAGAAGA AACCAGGCT CAGTTTTACG
      601 CATCAGAGAA AACCTCTCCT AAAAGAGAAC TTGCCAAGA TTTGCCTAAA
   40 651 TCAGGAGAAA GTCGATGTAA TCCTTCAGAA GCTGGAGCGT CTTTACTGGT
      701 TGGCTCAATA GAACCTTCTT TGTCAAATCA AGATAGAAAA TATTCCTCAA
      751 CTCTACCTAA TGATGTACAA ACTACCTCTG GTGATCTCAA ATTGGACAAA
      801 ATTGATCCCC AAAGACAGGA ACTTCTAGTA AAATTACTAG ATGTGCCTAC
      851 TGGTGATTGT CATATTTCTC CAAAGAATGT CAGTGATGGG GTTAAAAGGG
   45 901 TAAGAACATT ATTAAGCAAT GAGAGAGATT CCAAAGGCAG GGATCACCTC
      951 TCAGGAGTCC CTACTGATGT TACAGTTACT GAGACTCCAG AAAAGAACAC
   1001 AGAATCCCTC ATTTTAAGCC TTAATAAGAG CTCATTAGGT AAAATCCAAG
   1051 TCATGGAGAA ACAAGAGAAA GGACTTACCC TGGGAGTAGA GACGTGTGGG
   1101 AGCAAAGGAA ATGCAGAGAA AAGTATGTCT GCAACAGAAA AGCAGGAACG
   50 1151 GACTGTCATG AGCCATGGCT GTGAGAAGTT CAACACCAGG GATTCAGTCA
      1201 CAGGAAAGGA GTCTCAAGGG GAAAGACCAC ATTTAAGTTT GTTCATTCCG
      1251 AGGGAGACGA CTTACCAGTT TCATTCTGTA TCGCAGTCAA GTAGTCAAAG
      1301 TCTTGCTCTC CTAGCTACAA CATTTCTTCA AGAAAAGAAA GCAGAAGCCC
      1351 AGAATCATAA TTGTGTCCCT GATGTAAAGG CATTAATGGA GAGTCCCGAG
   55 1401 GGACAGTTAT CTCCTGGAGCC CAAATCTGAT AGTCAGTTCC AAGCATCACA
      1451 CACTGGGTGC CAGAGCCCTT TATGTTTCAGC CCAGCGTCAC ACTCCTCAGA
      1501 GCCCCTTCAC CAATCATGCT GCAGCTGCTG GCAGGAAGAC TCTTCGCAGC
      1551 TGCATGGGGC TGGAGTGGTT TCCAGAGCTC TATCCTGGTT ACCTTGACT
```

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1601 AGGGGTGTTG CCAGGGAAGC CTCAGTGTTG GAATGCAATG ACCCAGAAGC
1651 CACAACTTAT CAGTCCCCAG GGGGAAAGAC TCTCACAAGG CTGGATCAGG
1701 TGCAACACCA CCATAAGGAA GAGTGGATTG GGTGGCATCA CTATGCTCTT
1751 CACAGGATAC TTCGTCTGT GTTGTAGCTG GAGTTTCAGA CGTCTGAAAA
5 1801 AATTGTGCCG ACCCCTGCCC TGGAAGAGCA CAGTACCTCC ATGCATTGGT
1851 GTGGCGAAGA CGACTGGGGA TTGCCGCTCT AAAACATGTT TGGATTAGGA
1901 AGCACGTTTA AGTAGGAGAA GCCTTCGTGA CTTCTCTCTA GTGCCTTCGT
1951 GCCCTGTGTT GCCCACTGAA TTGCCCTGTA ACACCTAAGT GTAGTGGTAG
2001 CATTAAAGGA TAGCTTTTCA GCCCTCAAGG TTATCAGGAG CATTGTATC
10 2051 ACTGCTATAA ATAAAGTAGT ATCACTTGTC ATAAAAA AAAA
2101 AA

```

## BLAST Results

15

No BLAST result

20

## Medline entries

No Medline entry

25

## Peptide information for frame 3

```

30 ORF from 177 bp to 1895 bp; peptide length: 573
Category: putative protein
Classification: no clue

```

```

35 1 MSDNPPRMEV CPYCKKPFKR LKSHLPYCKM IGSTIPTDQK VYQSKPATLP
51 RAKKMKGPIK DLIKAKGKEL ETENEERN SK LVVDKPEQTV KTFPLPAVGL
101 ERAATTKADK DIKNPIQPSF KMLKNTKPM T FQEEETKAQF YASEKTS PKR
151 ELAKDLPKSG ESRCNPSEAG ASLLVGSIEP SLSNQDRKYS STLPNDVQTT
201 SGDLKLDKID PQRQELLVKL LDVPTGDCHI SPKNVSDGVK RVRTLLSNER
251 DSKGRDHLSG VPTDVTVTET PEKNTESLIL SLKMSSLGKI QVMEKQEKGL
40 301 TLGVETCGSK GNAEKSMSAT EKQERTVMSH GCENFNTRDS VTGKESQGER
351 PHLSLFIPRE TTYQFHSVSQ SSSQSLASLA TTFLQEKKA E AQNHNCVPDV
401 KALMESPEGQ LSLEPKSDSQ FQASHTGCQS PLCSAQ RHTP QSPFTNHAAA
451 AGRKTLRSCM GLEWFPELYP GYLGLGVLPG KPQCWNAMTQ KPQLISPQGE
501 RLSQGWIRC N TTIRKSGFGG ITMLFTGYFV LCCSWSFRR L KKL CRPLPWK
45 551 STVPPCIGVA KTTGDCRSKT CLD

```

## BLASTP hits

50

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3\_11e17, frame 3

55 No Alert BLASTP hits found

Pedant information for DKFZphtes3\_11e17, frame 3

## Report for DKFZphtes3\_11e17.3

5 [LENGTH] 573  
[MW] 63389.88  
[pI] 9.24  
[BLOCKS] BL00028 Zinc finger, C2H2 type, domain proteins  
[KW] Alpha\_Beta  
10 [KW] LOW\_COMPLEXITY 7.50 %

SEQ MSDNPPRMEVCPYCKPKFKRLKSHLPYCKMIGSTIPTDQKVYQSKPATLPRAKKMKGPIK  
SEG .....  
15 PRD cccccceeeccccccchhhhhhccccceeeccccceeeccccchhhhhhccccch  
  
SEQ DLIKAKGKELETENEERNNSKLVVDKPEQTVKTFPLPAVGLERAATTKADKDIKNPIQPSF  
SEG .....  
20 PRD hhhhhhccccchhhhhhheeeccccceeeccccchhhhhhccccccccccchh  
  
SEQ KMLKNTKPMTTTQEEETKAQFYASEKTSPKRELAIDLKSGESRCNPSEAGASLLVGSIEP  
SEG .....  
PRD hhhccccccchhhhhhccchhhhhhcccc  
  
25 SEQ SLSNQDRKYSSTLPNDVQTTSGDLKLDKIDPQRQELLVKLLDVPTGDCHISPKNVSDGVK  
SEG .....  
PRD cccccceeeccccccccccccccccccccccccccccccccccccchhhhhhccccccccccccccccchh  
  
30 SEQ RVRTLNSNERDSKGRDHLSGVPTDVTVTETPEKNTESLILSLKMSSLGKIQVMEKQEKGL  
SEG .....xxxxxxxxxxxxx.....  
PRD hhhhhhccccccccccccccccccccccccccccccccccccchhhhhhccccchhhhhhcccc  
  
SEQ TLGVETCGSKGNAEKSMSATEKQERTVM SHGCENFNTRDSVTGKESQGERPHLSLFI PRE  
SEG .....  
35 PRD eeeeeccccccccchhhhhhcc  
  
SEQ TTYQFHSVSQSSSQSLASLATTFLQEKKAQAQNHNCVPDVKALMESPEGQLSLEPKSDSQ  
SEG .....xxxxxxxxxxxxx.....  
40 PRD eeeeeccccccccchhhhhhcc  
  
SEQ FQASHTGCQSP LCSAQ RHTPQSPFTNHAAAAGRKTLRSCMGLEWFP ELYPGYLGLGVLP G  
SEG .....xxxxxxxxxxxxx.....  
PRD cccccccccccccccccccccccccccccccccccccchhhhhcchhhhhhcccccccccccccccccccc  
  
45 SEQ KPQCWNAMTQKPQLISPQGERLSQGWIRCNTTIRKSGFGGITMLFTGYFVLCCSWSFRL  
SEG xx.....  
PRD cccccccccccccccccccccccccccccccccccccchhhhhccccceeeccccccccccccccccccccchhhhh  
  
50 SEQ KKL CRPLPWKSTVPPCIGVAKTTGDCRSKTCLD  
SEG .....  
PRD hhhcc

(No Prosite data available for DKFZphtes3\_11e17.3)

(No Pfam data available for DKFZphtes3\_11e17.3)



5 group: testis derived

DKFZphtes3\_12d18 encodes a novel 1170 amino acid protein without similarity to known proteins.

10 The EST-distribution signifies an ubiquitous expression pattern. No informative BLAST results; No predictive prosite, pfam or SCOP motife.

15 The new protein can find application in studying the expression profile of testis-specific genes.

unknown protein

20 perhaps complete cds.

Sequenced by Qiagen

25 Locus: /map="13b.9 cR from top of Chr13 linkage group"

Insert length: 5469 bp

Poly A stretch at pos. 5449, polyadenylation signal at pos. 5420

```
30      1 AAGGACAGAG GACGAGATTT TGAACGACAA AGAGAAAAGA GAGACAAGCC
      51 AAGGTCTACT TCCCCAGCAG GACAGCATCA TTCTCCTATA TCTTCTAGAC
     101 ATCACTCATC TTCCTCACAA TCAGGATCAT CTATTCAAAG ACATTCTCCT
     151 TCTCCTCGTC GAAAAAGAAC TCCTTCACCA TCTTATCAGC GGACAETAAC
     201 TCCACCTTTA CGACGCTCTG CCTCTCCTTA TCCTTCACAT TCTTTGTCGT
35     251 CTCCCCAGAG AAAGCAGAGT CCTCCAAGAC ATCGCTCTCC AATGCGAGAG
     301 AAAGGGAGAC ATGATCATGA ACGAACTTCA CAGTCTCATG ATCGACGCCA
     351 CGAAAGGAGG GAAGATACTA GGGGCAAACG AGACAGAGAA AAGGACTCAA
     401 GAGAAGAACG AGAATATGAA CAGGATCAGA GCTCTTCTAG AGACCACAGA
     451 GATGACAGAG AACCTCGAGA TGGTCGGGAT CGGAGAGATG CCAGAGATAC
40     501 TAGGGACCGA AGGGAATAAA GAGACTCCAG AGACATGCGG GACTCAAGGG
     551 AGATGAGAGA TTATAGCAGA GATACCAAAG AGAGCCGTGA TCCCAGAGAT
     601 TCTCGGTCCA CTCGTGATGC CCATGACTAC AGGGACCGTG AAGGTGAGAG
     651 TACTCATCGA AAGGAGGATA CATATCCAGA AGAATCCCGG AGTTATGGCC
     701 GAAACCATTT GAGAGAAGAA AGTTCTCGTA CGGAAATAAG GAATGAGTCC
45     751 AGAAATGAGT CTCGAAGTGA AATTAGAAAT GACCGAATGG GCCGAAGTAG
     801 GGGGAGGGTT CCTGAGTTAC CTGAAAAGGG AAGTCGAGGC TCAAGAGGTT
     851 CTCAAATTGA TAGTCACAGT AGTAATAGCA ACTATCATGA CAGCTGGGAA
     901 ACTCGAAGTA GCTATCCTGA AAGAGATAGA TATCCTGAAA GAGACAACAG
     951 AGATCAAGCA AGGGATTCTT CTTTGGAGAG AAGACATGGA GAGCGAGACC
50    1001 GTCGTGACAA CAGAGAGAGA GATCAAAGAC CAAGCTCACC AATTCGACAT
     1051 CAGGGAAGGA ATGACGAGCT TGAGCGTGAT GAAAGAAGAG AGGAACGAAG
     1101 AGTAGACAGA GTGGATGATA GGAGAGATGA AAGGGCTAGA GAGAGAGATC
     1151 GGGAAACGAGA ACGAGACAGG GAGCGGGAGA GAGAGAGGGA ACGTGAACGG
     1201 GATCGGGAAA GAGAAAAAGA GAGAGAACTA GAAAGAGAGC GTGCTAGGGA
55    1251 ACGGGAGAGA GAAAGAGAAA AAGAGAGAGA TCGTGAAAGG GATAGAGACC
     1301 GAGACCACGA TCGAGAGCGG GAAAGAGAGA GGGAACGAGA CAGGGAAAAA
     1351 GAACGGGAAC GAGAAAGAGA AGAGAGAGAG AGGGAGAGAG AGCGAGAACG
     1401 GGAGAGAGAG CGAGAGCGAG AACGGGAACG AGAAAGAGCG AGAGAAAGGG
```

1451	ATAAAGAACG	AGAACGCCAA	AGGGATTGGG	AAGACAAAGA	CAAAGGACGA
1501	GATGACCGCA	GAGAAAAGCG	AGAAGAGATC	CGAGAAGATA	GGAATCCAAG
1551	AGATGGACAT	GATGAAAGAA	AATCAAAGAA	GCGCTATAGA	AATGAAGGGA
1601	GTCCCAGCCC	TAGACAGTCC	CCGAAGCGCC	GGCGTGAACA	TTCTCCGGAC
5 1651	AGTGATGCCT	ACAACAGTGG	AGATGATAAA	AATGAAAAAC	ACAGACTCTT
1701	GAGCCAAGTT	GTACGACCTC	AAGAATCTCG	TTCTCTTAGT	CCCTCGCACC
1751	TCACAGAAGA	CAGACAGGGT	AGATGGAAAG	AGGAGGATCG	TAAACCAGAA
1801	AGGAAAGAGA	GTTCAAGGCG	CTACGAAGAA	CAGGAACTCA	AGGAGAAAGT
1851	TTCTTCTGTA	GATAAACAGA	GAGAACAGAC	AGAAATCCTG	GAAAGCTCAA
10 1901	GAATGCGTGC	ACAGGACATT	ATAGGACACC	ACCAGTCTGA	AGATCGAGAG
1951	ACATCTGATC	GAGCTCATGA	TGAAAACAAG	AAGAAAGCAA	AAATTCAAAA
2001	GAAACCAATT	AAGAAAAAGA	AAGAGGATGA	TGTTGGAATA	GAGAGGGGTA
2051	ACATAGAGAC	AACATCTGAA	GATGGTCAAG	TATTTTCACC	AAAAAAAGGA
2101	CAGAAAAAGA	AAAGCATTGA	AAAAAAACGT	AAAAAATCCA	AAGGTGATTC
15 2151	TGATATTTCT	GATGAAGAAG	CAGCCCAGCA	AAGTAAGAAG	AAAAGAGGCC
2201	CACGGACTCC	CCCTATAACA	ACTAAAGAGG	AATTGGTTGA	AATGTGCAAT
2251	GGTAAGAATG	GTATTCTAGA	GGACTCCCAG	AAAAAAGAAG	ATACAGCATT
2301	CAGTGAAGTG	TCTGATGAGG	ATGTCCCTGA	CCGTACAGAG	GTGACAGAAG
2351	CAGAGCATAC	TGCCACCGCC	ACGACTCCTG	GTAGTACCCC	TTCTCCTCTA
20 2401	TCTTCTCTTC	TTCTCTCTCC	ACCGCCTGTG	GCTACTGCCA	CTGCTACAAC
2451	TGTGCCTGCA	ACTCTTGCTG	CCACTACTGC	TGCTGCCGCC	ACCTCTTTCA
2501	GCACATCTGC	CATCACTATT	TCCACCTCTG	CCACCCCCAC	CAATACCACC
2551	AATAATACTT	TTGCCAATGA	AGACTCACAC	AGAAAATGCC	ACAGAACACG
2601	AGTAGAAAAA	GTAGAGACGC	CTCACGTGAC	TATAGAAGAT	GCACAGCATC
25 2651	GCAAGCCTAT	GGATCAAAAAG	AGGAGCAGCA	GCCTCGGGAG	CAATCGGAGT
2701	AACCGTAGTC	ATACGTCTGG	TCGTCTTCGC	TCCCCATCCA	ATGATTCAGC
2751	CCATCGAAGT	GGAGATGACC	AAAGTGGTCG	AAAGAGAGTA	CTGCACAGTG
2801	GCTCAAGAGA	TAGAGAAAAA	ACAAAAAGCC	TGGAAATCAC	AGGAGAGAGA
2851	AAATCTAGGA	TTGATCAGTT	AAAGCGTGGA	GAACCCAGTC	GAAGTACTTC
30 2901	TTCAGATCGC	CAGGATTCAA	GAAGCCATAG	TTCAAGAAGA	AGTTCTCCAG
2951	AGTCAGATCG	ACAGGTCCAT	TCAAGATCTG	GGTCATTTGA	TAGCAGAGAC
3001	AGGCTTCAAG	AACGAGATCG	ATATGAACAC	GACAGAGAGC	GCGAGAGAGA
3051	GAGGAGAGAT	ACGAGGCAGA	GAGAATGGGA	CCGAGATGCT	GATAAAGATT
3101	GGCCACGCAA	CAGGGATCGA	GATAGATTGC	GAGAACGAGA	ACGAGAGAGA
35 3151	GAAACGAGACA	AAAGGAGAGA	CTTGGATAGG	GAAAGAGAGA	GACTAATTTT
3201	TGATTCTGTT	GAAAGGGACA	GAGACAGAGA	CAGAGACAGA	ACTTTTGAGA
3251	GTTCTCAAAT	AGAGTCTGTG	AAACGCTGTG	AAGCAAAACT	GGAAGGTGAA
3301	CATGAAAGGG	ATCTAGAAAG	CACTTCCCAG	GACTCTCTAG	CCTTGGATAA
3351	AGAGAGAATG	GATAAAGATC	TGGGATCTGT	GCAGGGATTT	GAAGATACAA
40 3401	ATAAATCCGA	GAGAACTGAG	AGTCTGGAAG	CAGGAGATGA	CGAGTCCAAG
3451	TTAGATGATG	CACATTCAAT	AGGCTCTGGT	GCTGGAGAAG	GATACGAGCC
3501	AATCAGTGAT	GACGAACTAG	ATGAAATTCT	GGCAGGTGAT	GCAGAAAAGA
3551	GGGAGGACCA	ACAGGATGAG	GAGAAGATGC	CAGATCCCTT	AGATGTGATA
3601	GATGTGGATT	GGTCTGGTCT	TATGCCAAAG	CATCCAAAAG	AACCACGAGA
45 3651	GCCTGGGGCT	GCACTCTTAA	AATTCACACC	TGGAGCTGTT	ATGCTAAGAG
3701	TTGGGATTTT	TAAAAAGTTG	GCAGGTTCTG	AACTCTTTGC	CAAAGTCAAA
3751	GAAACATGTC	AGAGACTTTT	AGAAAAACCC	AAAGGTAGTT	TCATTTTACT
3801	TTAACTATAT	AATGTCTGTT	AACCATTTAA	GATGCCATCT	GAAGGGGATT
3851	CTGATCTGTT	CTTATGTAGC	ACTTAACACT	GTGTAGAAAC	TATTTTTTGA
50 3901	GAAATCATTT	TATAATCATT	ATTTAACCCCT	CATGGTCAAA	GTTTCTCTTT
3951	AAAAATTTATT	TTGAGAAGAA	GAGTTATCCC	ACAGAAAAGT	TGGGAAAAGA
4001	GTACAATGAC	CTTTTTGTAT	GAAAATTACT	TATTAACAGG	CCAGGCGTGG
4051	TGTTGCAATG	CTGTAGTCAC	AGCTACTCAG	GGAGGTTGAG	GCAGCAGGAT
4101	TGCTGGAGCC	CAGGAAATTG	AGGCTGCAGT	GAGCCATGAT	TGAGCCACCA
55 4151	CACTCCAACC	TAGGTGACAG	AGCAAGACCC	TGTCTCAAAA	AAAAAAAAC
4201	AAATTAACCA	ATAAGTTCTA	ATATCAAAGT	GCTCAGTGGT	TTGCCCTTGG
4251	CTAAATGAAG	CAGAGCCAGG	AAAAACAGAC	TACATATTTT	TCATGTCTAA
4301	AGAAATTGGG	TATTTTGGCA	GCCCTTTCCC	CTAGACATCT	ACCCAAATGC

```

4351 AGGTGTGTAG GTTGAGTCTT TAACAAAGTG ATTAAGAGCT TGGTCTGTAA
4401 GGCCGGATGA TCTGGATTTT AGTAGGCACA CCACTTACTG GCTATTACTT
4451 AATCTGTGTG TTAGTGTGAT CATCTGTAAG TCAGGAATAA TCATACCACC
5 4501 AACTTCCTAT GGTAATTAGG AGCAAATGAG TTATTACAGG CAAAACACTT
4551 AGAACAGTTC CTGGCATATA GTAATACCCA ATAAATATTA ACTGCTACTT
4601 TGAAAAATATC CTATCACGCT GATTTTGTGAC CTCACTGCAG CAATTTTCAG
4651 TTATTCCAGA TTATCTAGCT TATGGATTCT GGTGGTAGGG GTTGTGTTGGT
4701 TTTGGTTTTC ACTGTCTCTG TCTCATCTAG TACCTACCTT AGTTTATTTT
4751 GCAACTTACT AATACTTTAT TAATGGGGAG GGACGAGTAG ATGGTAAAAA
10 4801 GAAGGAAAAAG GAGGTAAAAAG GTGAAAGGAA CAACATTAAT TAACAATTTT
4851 ACGTCATGTC CCTGGACATA AAAGTTTAGT TAGTATTAAA TTTTTCACCTA
4901 ATACAAAATA AAAAAATATT GTTTTATGAG TTTTATGAAT TCATGCCCTT
4951 CCTTTACTCT ATTAGCATAA GCAGTAAATT TTTTATTTT AATATAGCCC
5001 AATAAACCTA GAGTATACAT GTACAAAATA CATATAATTG TTAACGTGTA
15 5051 TTAACCGAAA AATGACCCAA GACTTAGTTC TTGCCCTACT GTATCTGCCT
5101 TGTGTTGGTTG GTTCTGTGAC CTTAAGCAAA TAACTCCTGT GAGCCTCAAT
5151 TTTATTTGTA AAGTGATGGA ATAAAACCCC TAAAATCTTA CCCACCTCTA
5201 AAGATATTTG TTTCTGTGAC CTTTGTCTAG TAGCATTTC AAGTTAAATC
5251 TGGTTTGATT TTGCTACCCA TGAAATACAG TTCGGCCCTT ACTTATTGAT
20 5301 GACTTAACCT AAACAGTGAA AATATGCACT GTAAAGGGTG GGGTGATGTG
5351 GCTTAACAAT CAGACTTCTT CTATTTTTCG TGCTATGGTG GTTGTATTAG
5401 AGAACTGATG TATTATCTTG AATAAAGACT TTGTCTTGTT TACTGCCCTA
5451 AAAAAAAAAA AAAAAAAAAA

```

25

## BLAST Results

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No BLAST result

30

## Medline entries

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35 No Medline entry

## Peptide information for frame 1

40

ORF from 292 bp to 3801 bp; peptide length: 1170

Category: similarity to unknown protein

Classification: no clue

45

50

55

```

1 MREKGRHDHE RTSQSHDRRH ERREDTRGKR DREKDSREER EYEQDQSSSR
51 DHRDDREPRD GRDRRDARDT RDRRELDRSR DMRDSREMRD YSRDTKESRD
101 PRDSRSTRDA HDYRDREGRD THRKEDTYPE ESRSYGRNHL REESSRTEIR
151 NESRNESRSE IRNDRMGRSR GRVPELPEKG SRGSRGSQID SHSSNSNYHD
201 SWETRSSYPE RDRYPERDNR DQARDSSFER RHGERDRRDN RERDQRPSSP
251 IRHQGRNDEL ERDERREERR VDRVDDRRDE RARERDRERE RDRERERERE
301 RERDREREKE RELERERARE REREREKERD RERDRDRDHD RERERERERD
351 REKERERERE ERERERERER ERERERERER ERARERDKER ERQRDWEDKD
401 KGRDDRREKR EEIREDRNPR DGHDERKSKK RYRNEGSPSP RQSPKRRREH
451 SPDSDAYNSG DDKNEKHRL SQQVVRQESR SLSPSHLTED RQGRWKEEDR
501 KPERKESSRR YEEQELKEKV SSVDKQREQT EILESSRMRA QDIIGHHQSE
551 DRETSDRAHD ENKKKAKIQK KPIKKKKEDD VGIERNIET TSEDGQVFSP
601 KKGQKKKSIE KKRKKS KGDS DISDEEAAQ SKKKRGPRTP PITTKHEELVE

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```

651 MCNGKNGILE DSQKKEDTAF SDWSDEDVPD RTEVTEAEHT ATATTPGSTP
701 SPLSSLLPPP PPVATATATT VPATLAATTA AAATSFSTSA ITISTSATPT
751 NTTNNTFANE DSHRKCHRT R VEKVEPHVT IEDAQHRKPM DQKRSSSLGS
801 NRSNRSHTSG RLRSPSND SA HRSQDDQSGR KRVLHSGSRD REKTKSLEIT
5 851 GERKSRIDQL KRGEP SRSTS SDRQDSRSHS SRRSSPESDR QVHSRSGSFD
901 SRDRLQERDR YEHDRE RERE RRDTRQREWD RDADKDWP RN RDRDRLRERE
951 RERERDKRRD LDRERERLIS DSV ERDRDRD RDRTFESSQI ESVKRCEAKL
1001 EGEHERDLES TSRDSLALDK ERMDKDLGSV QGFEDTNKSE RTESLEAGDD
1051 ESKLDDAHS L GSGAGEGYEP ISDDDELDEIL AGDAEKREDD QDEEKMPDPL
10 1101 DVIDVDWSGL MPKHPKEPRE PGAALLKFTP GAVMLRVGIS KKLAGESELF A
1151 KVKETCQRL L EKP KGSFILL

```

15 BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3\_12d18, frame 1

20 No Alert BLASTP hits found

Pedant information for DKFZphtes3\_12d18, frame 1

25

Report for DKFZphtes3\_12d18.1

```

30 [LENGTH] 1267
[MW] 150593.45
[pI] 9.22
[CHOMOL] TREMBL:AB020660_1 gene: "KIAA0853"; product:
"KIAA0853 protein"; Homo sapiens mRNA for KIAA0853 protein,
partial cds. 0.0
35 [BLOCKS] BL00422C Granins proteins
[BLOCKS] BL00803F
[BLOCKS] PR00308C
[BLOCKS] PR01089B
[BLOCKS] PR00049D
40 [BLOCKS] PR01083A
[BLOCKS] PR00545A
[BLOCKS] BL00048 Protamine P1 proteins
[BLOCKS] PF01140D
[BLOCKS] PR00833H
45 [KW] All_Alpha
[KW] LOW_COMPLEXITY 44.12 %

```

```

50 SEQ KDRGRD FERQREKRD KPRSTSPAGQHHSPISRRHHSSSSQSGSSIQRHSPSPRRKRT PSP
SEG .....
PRD cccccchhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccc

```

```

55 SEQ SYQRTLT PPLRRSASPYP SHSLSSPQRKQSPPRHRSPMREKGRHDHERTSQSHDRRHERR
SEG x.....
PRD cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccchhhhhc

```

```

SEQ EDTRGKRDR EKDSREEREYEQDQSSSRDHRDDREPRDGRDRRDARDTRDRREL RDSRDMR
SEG xx.xxxxxxxxxxxxxxxxxxxxxx.xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

```

PRD cccccccccccchhhhhhhhhccccccccccccccccccccchhhhhhhhhhhhhhhhhcccc

5 SEQ DSREMRDYSRDTKESRDPRDSRSTRDAHDYRDREGRDTHRKEDTYPEESRSYGRNHLREE  
SEG xxxxxxxxxxxx...xx  
PRD hhhhhhhcc

10 SEQ SSRTEIRNESRNESEIRNDRMGRSRGRVPELPEKSGSRGSRGSDIDSHSSNSNYHDSWE  
SEG .....xx  
PRD hhhhhhhcc

15 SEQ TRSSYPERDRYPERDNRDQARDSSFERRHGERDRRDNREDDQRPSSPIRHQGRNDELERD  
SEG .....xx  
PRD cchhhhhh

20 SEQ ERREERRVDRVDDRRDERARERDRERERDRERERERERERDREREKERELERERARERER  
SEG xxx  
PRD hhhhhhhhhccccccccchhh

25 SEQ EREKERDRERDRDRDHDRERERERERDREREKEREREERERERERERERERERERERERA  
SEG xxx  
PRD hhhhhhhhhccccccccchhh

30 SEQ RERDKERERQRDWEDKDKGRDDRREKREEIREDNRPRDGHDERKSKKRYRNEGSPSPRQS  
SEG xxxxxxxx-xx  
PRD hhhhhhhhhhhhhhhhhccccccccchhhhhhhhhhhccccccccccccchhhhhhcccccccccc

35 SEQ PKRRREHSPDSDAYNSGDDKNEKHRLLSQVVRPQESRSLSPSHLTEDRQGRWKEEDRKPE  
SEG xxxxx-.....  
PRD cccccccccccccccccccccchhhhhhhhhccccccccccccccccchhhhhhhhhhhcccc

40 SEQ RKESSRRYEEQELKEKVSSVDKQREQTEILESSRMRAQDIIGHHQSEDRETSDDRAHDENK  
SEG .....x  
PRD hhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhheeeccccccccccccccccch

45 SEQ KKAKIQKKPIKKKKEDDVGIERGNIETTSEDGQVFSPKKGQKKKSIEKKRKKSKGSDSDIS  
SEG xxxxxxxxxxxxxxxx.....xx  
PRD hhhhhhhhhccccccccccccccccccccceeeccccceeeccccccchhhhhhhhhhhcccccccc

50 SEQ DEEAAQQSKKKRGPRTPPITTKEELVEMCNGKNGILEDQKKEDTAFSDWSDDEDVPDRTE  
SEG xxx.....xx  
PRD hhhhhhhhhhhccccccccccccchhhhhhhccccccccceeeccccccccccccccccceee

55 SEQ VTEAHTATATTPGSTPSPLSSLLPPPPPVATATATTVPATLAATTAATAATSFSTSAITI  
SEG xxx  
PRD hhhhhhhhhccccccccccccccccccccceeeccccccccceeeccccchhhhhhhhhhhcccccccc

60 SEQ STSATPTNTTNTNFANEDSHRKCHRTRVEKVETPHVTIEDAQHRKPMQDKRSSSLGNSRS  
SEG xxxxxxxxxxxxxxxx.....xxxxxxxxxxxx  
PRD eccccccccccccccccccccchhhhhheeeccccceeecccccccccccccccccccccccc

65 SEQ NRSHTSGRLRSPSND SAHRSGDDQSGRKRVLHSGSRDREKTKSLEITGERKSRIDQLKRG  
SEG xxx.....  
PRD cccccccccccccccccccccccccccccccccceeeccccccccccccceeehhhhhhhhhhhhcc

70 SEQ EPSRSTSSDRQDSRSHSSRRSSPESDRQVHSRSGSFDSRDLQERDRYEHDRERERERRD  
SEG ..xx  
PRD cccccccccccccccccccccccccccccccccceeeccccccccchhhhhhhhhhhchhhhhhhhh

## 2.5

DKFZphtes3\_1417

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5 group: testis derived

DKFZphtes3\_1417 encodes a novel 815 amino acid protein without similarity to known proteins.

10 The mRNA is transcribed ubiquitously.  
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

15 The new protein can find application in studying the expression profile of testis-specific genes.

similarity to C.elegans B0412.3

20 see also DKFZphtes3\_17n3  
perhaps complete cds.

Sequenced by BMFZ

25 Locus: unknown

Insert length: 3522 bp

Poly A stretch at pos. 3456, polyadenylation signal at pos. 3437

30

```

      1 AACACATCGA CTTGTGTAAG AAAAAGATTG GAAGTGCGGA GCTGTCTTTT
    51 GAGCATGATG CATGGATGTC TAAACAATTC CAGGCCTTTG GAGATTTATT
   101 TGATGAAGCT ATTAAGTTAG GGTTAACAGC TATTCAAACCT CAGAATCCTG
   151 GTTTCTATTA CCAGCAGGCA GCATACTATG CCCAGGAGCG GAAACAGCTT
   35 201 GCAAAAACCC TCTGTAACCA CGAAGCTTCT GTAATGTATC CCAATCCTGA
      251 TCCCTTAGAA ACACAAACAG GCGTTCCTGA CTTTATGGA CAAAGATCAT
   301 GCGGACAAAG AATACTAAGT TTTGATCTTT CTGATCCTGA AAAAGAAAAG
   351 GTGGGAATTC TTGCCATTCA GCTGAAGGAG AGAAATGTTG TTCACTCTGA
   401 GATAATCATA ACTCTTCTGA GCAATGCTGT TGCACAGTTC AAGAAGTATA
   40 451 AGTGCCCGCG AATGAAAAGT CACCTAATGG TTCAGATGGG AGAGGAATAT
      501 TATTACGCAA AGGATTATAC CAAAGCTTTG AAGTTGCTGG ATTATGTGAT
      551 GTGTGATTAT CGGAGTGAAG GATGGTGGAC TCTGCTCACT TCTGTATTAA
   601 CTACAGCTCT GAAGTGCTCC TACCTCATGG CCCAATTAAA GGATTACATT
   651 ACTTACTCCC TAGAACTCCT TGGTAGAGCT TCAACTCTGA AAGATGACCA
   45 701 GAAGTCTCGG ATAGAAAAGA ACCTCATAAA TGTTTTAATG AATGAAAGTC
      751 CTGATCCAGA ACCCGACTGT GATATCTTAG CTGTGAAAAC TGCTCAGAAG
   801 CTGTGGGCAG ACCGAATTTT TCTGGCTGGC AGCAATATTT TCACAATAGG
   851 AGTACAGGAC TTTGTGCCAT TTGTGCAGTG CAAAGCCAAG TTTTCATGCCC
   901 CAAGTTTTCA TGTTGATGTT CCTGTTTCAAG TTGATATTTA TCTGAAGGCT
   50 951 GATTGTCCAC ATCCCATTAG GTTTTCCAAG CTCTGTGTCA GCTTTAATAA
  1001 TCAGGAATAC AACCAGTTCT GTGTAATAGA AGAAGCATCC AAAGCAAATG
  1051 AAGTTTTAGA AAATCTGACT CAAGGAAAGA TGTGCCTAGT TCCTGGCAAA
  1101 ACAAGAAAAC TGTTATTTAA GTTTGTTGCA AAAACTGAAG ATGTGGGAAA
  1151 GAAAATTGAG ATTACTTCAG TGGATCTTGC TCTGGGCAAT GAGACGGGAA
   55 1201 GATGTGTGGT TTAAATTGG CAGGGAGGAG GAGGAGATGC TGCTTCCTCC
      1251 CAAGAAGCCT TACAGGCAGC TCGGTCTTTC AAAAGGCGAC CTAAGCTACC
      1301 TGACAATGAA GTTCACTGGG ACAGCATTAT AATTCAGGCA AGCACAATGA
      1351 TCATATCCAG AGTCCCAAAC ATTTCTGTAC ATCTGCTACA TGAACCCCTT

```

1401 GCACTGACTA ATGAAATGTA TTGTTTGGTT GTGACTGTTC AGTCCCATGA  
1451 AAAGACCCAA ATCAGAGATG TGAAGCTCAC TGCTGGCTTA AAACCAGGAC  
1501 AGGATGCCAA TTAACTCAG AAGACTCACG TGACTCTTCA TGGACCAGAA  
1551 CTGTGTGATG AATCCTACCC GGCTTTACTC ACTGACATTC CTGTTGGAGA  
5 1601 CTTACATCCA GGGGAACAGC TGGAAAAAAT GTTGTATGTT CGCTGTGGAA  
1651 CAGTGGGTTC CAGAATGTTT CTTGTATATG TTTCTTACCT GATAAATACA  
1701 ACCGTTGAAG AAAAAGAAAT TGTGTTGCAAG TGTCAACAAG ATGAAACTGT  
1751 AACAATTGAA ACAGTCTTTC CATTTGATGT TGCAGTTAAA TTTGTTTCTA  
1801 CCAAGTTTGA GCACCTGGAA AGGGTTTATG CTGACATCCC CTTTCTGTTG  
10 1851 ATGACGGACC TCTTAAGTGC CTCACCCTGG GCCCTCACTA TTGTTTCCAG  
1901 TGAGCTCCAG CTTGCTCCAT CCATGACCAC AGTGGACCAG CTCGAGTCTC  
1951 AAGTGGACAA TGTTATCTTA CAGACTGGAG AGAGTGCTAG TGAATGCTTT  
2001 TGTCTTCAAT GCCCATCTCT TGGAAATATT GAAGGTGGAG TAGCAACCGG  
2051 GCATTATATT ATCTCTTGGA AAAGGACCTC AGCAATGGAG AATATCCCCA  
15 2101 TCATCACAAC TGTCACTACT CTGCCGCACG TGATTGTGGA GAATATCCCT  
2151 CTCCATGTGA ATGCAGATCT GCCGTCATTT GGGCGTGTCA GAGAGTCGTT  
2201 ACCTGTCAAG TATCACCTAC AGAATAAGAC CGACTTAGTT CAAGATGTAG  
2251 AAATTTCTGT GGAGCCCAGT GATGCCTTCA TGTCTCAGG TCTCAAACAG  
2301 ATTGATTAC GTATCCTCCC TGGCACGGAG CAGGAAATGC TATATAATTT  
20 2351 CTATCCTCTG ATGGCTGGAT ACCAGCAGCT GCCATCTCTC AACATCAACT  
2401 TGCTTAGATT TCCTAACTTC ACAAATCAGC TGCTCAGGCG TTTTATACCT  
2451 ACCAGTATTT TTGTCAAGCC ACAGGGTCGA CTCATGGATG ATACCTCTAT  
2501 TGCTGCTGCA TGATGTTCAA GACCGGCCCT TGGCTGTTGT TACAGAGATG  
2551 TTGGGCAGAG CTATGCAGGT GTTTCATTGT GAACTCTAGC TTTGATCATG  
25 2601 GTAAAAAGTT AACCTTTTCT ATTTTTTAAT GGATGTTATA CCAACTATTC  
2651 AGAGGAACTC ATACTTCAAA AATATTAGGA AAATCTGTCT TATAGTTTCT  
2701 CTAATAAATA TCTGAAATCT CAGTACGACA TGAAAGAATG TCAGACCATT  
2751 GTTATTGTTG AAAGTCATTT GATGAATGGT AAATTCTATG AAAAGTAAGT  
2801 GATTTGCATG TATAATATCA GGAAAAATTAA GCATCCCAAG TGTGACTGGA  
30 2851 CAAAGAGAGC AGATGCACCA GTGCCTGTGC CATAAAGTTC CGAATCCCCC  
2901 ATGTGTCTCT TTCAGAGCTG GCCAGACCGG AAATAAATCA TTCTCATAAA  
2951 TTCAGTGTGT ACTCAGAACA CATAACAAC AACATAGGGA GTTGTATGAC  
3001 TGATACGGAA AACTTCCAGA AAGTTTTAAT CAAAGCAGTT TAATTAAGGT  
3051 ATCAAAAATA TCTTTGCTTA CTATCAAGAA GTGTCAAATA GGTTCAGCTT  
35 3101 GCTGCCAAAA TATGGATCAT TTATGAAGCA GGTTCATATT TTAGAGGTGT  
3151 TAATAAAATC CTCATCGGAA AAGATCCAAA GTGCAAGGAT TTGATTATAA  
3201 ACATAATTTT CTAGACTGAA AGTTTTTGA AAAGATGCAG GGTCTGAGTC  
3251 AGGCCTTCTG GTTATATTGT GCAGTTTCAA AAGAACTATT TAAAACCTTT  
3301 GAAAACTCAT GTAAATAAAA ATCATAGGGT GAAAATTGTA TTTGTTAAAA  
40 3351 TACCTTAATA ATTTAAAATG ACCTGATTTT CTGGAAAATT TTATTATTCA  
3401 AAAGGTGGAG GCATTGTAAA AAGGAAATAG TGATGTAAAT AAACATGTTC  
3451 TCTTTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA  
3501 AAAAAAAAAA AAAAAAAAAA AA

45

## BLAST Results

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No BLAST result

50

## Medline entries

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55 No Medline entry



\_\_\_\_\_

Classification: no clue

25.

30 No BLASTP hits available

No Alert BLASTP hits found

\_\_\_\_\_

## 40

45

55

(No Pfam data available for DKFZphtes3\_1417.3)

DKFZphtes3\_15n14

-----

5 group: testis derived

DKFZphtes3\_15n14 encodes a novel 713 amino acid protein with weak similarity to the neurofilament triplet M protein of the rat.

10 Neurofilaments are the intermediate filaments specific to nervous tissue. They are probably essential to the tensile strength of the neuron, as well as to transport of molecules and organelles within the axon. Until now, ESTs of the novel mRNA could only be isolated from testes, germ cells and uterus.

15 No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

20

similarity to neurofilament triplet M protein - rat

few EST hits (6 of 9 hits from testis)

25 perhaps complete cds.

Sequenced by GBF

Locus: unknown

30

Insert length: 2389 bp

Poly A stretch at pos. 2328, polyadenylation signal at pos. 2306

```

35      1 TGGGCCCCAC CTCCTCAGCA CAACTTTCTG AAAAAGTGGC AGCGTAACAC
      51 AGCCCTGCGG AAGAAGCAGC AGGAAGCCCT CAGCGAACAC CTAAAGAAGC
     101 CAGTGAGTGA GCTGCTCATG CACACCGGGG AGACCTACAG ACGGATCCAG
     151 GAGGAGCGGG AGCTCATTGA CTGCACACTT CCAACCCGGC GTGATAGGAA
     201 AAGCTGGGAG AACAGTGGGT TCTGGAGTCG ACTGGAATAC TTGGGAGATG
40     251 AGATGACAGG TCTGGTCATG ACCAAGACAA AAAGTCAGCG TGGCCTCATG
     301 GAGCCCATCA CTCATATCAG GAAGCCCCAC TCCATCCGGG TGGAGACAGG
     351 ATTACCAGCC CAGAGGGACG CTTCATACCG CTACACCTGG GATCGGAGTC
     401 TGTTTCTGAT CTACCGACGC AAGGAGCTGC AGAGAATCAT GGAAGAGCTG
     451 GATTTTCAGCC AGCAGGATAT TGATGGCCTG GAGGTGGTGG GCAAAGGGTG
45     501 GCCCTTCTCG GCTGTTACTG TGGAAGACTA CACAGTGTTT GAAAGAAGTC
     551 AGGGAAGCTC CTCTGAAGAC ACAACATACT TAGGCACATT GGCCAGTTCC
     601 TCTGATGTCT CCATGCCTAT TCTCGGCCCT TCTCTGCTGT TCTGTGGGAA
     651 GCCAGCTTGC TGGATCAGAG GCAGTAATCC ACAGGACAAG AGGCAGGTTG
     701 GGATTGCTGC TCACTTGACC TTTGAAACCC TAGAAGGCGA GAAAACCTCC
50     751 TCAGAACTGA CTGTGGTCAA TAATGGCACC GTGGCCATTT GGTATGACTG
     801 GCGACGGCAG CACCAGCCGG ACACCTTCCA AGACCTTAAG AAAAACAGGA
     851 TGCAGCGATT TTACTTTGAC AACCAGGAAG GTGTGATTCT GCCTGGAGAA
     901 ATTAATAACAT TTACTTTCTT CTTCAAGTCT TTGACTGCTG GGGTCTTCAG
     951 GGAATTTTGG GAGTTTCGAA CCCATCCTAC TCTATTAGGA GGTGCTATAC
55    1001 TGCAGGTCAA TCTCCACGCG GTCTCCCTGA CCCAGGACGT TTTTGAGGAT
     1051 GAGAGGAAAG TACTGGAGAG CAAGCTGACT GCCCATGAGG CAGTCACCGT
     1101 CGTTCGCGAA GTGCTGCAGG AGCTGCTGAT GGGGGTCTTG ACCCCGGAGC
     1151 GCACACCATC ACCTGTGGAT GCCTATCTCA CCGAGGAAGA CTTGTTCCGG

```

1201 CACAGAAATC CTCCGCTGCA TTATGAGCAC CAAGTGGTGC AAAGCCTGCA  
 1251 CCAACTGTGG CGCCAGTACA TGACCCTGCC CGCCAAGGCT GAGGAGGCCA  
 1301 GGCCAGGGGA CAAGGAGCAC GTCAGCCCCA TAGCCACAGA GAAGGCCTCT  
 1351 GTGAATGCTG AGCTGTTACC ACGCTTTAGG AGCCCCATCT CCGAAACTCA  
 5 1401 AGTGCCCCGG CCTGAGAACG AGGCCCTCAG GGAATCCGGG TCCCAGAAGG  
 1451 CCAGAGTGGG GACCAAGAGT CCTCAGCGGA AGAGCATCAT GGAGGAGATC  
 1501 CTGGTGGAGG AAAGCCCAGA TGTGGACAGC ACCAAGAGCC CCTGGGAGCC  
 1551 GGATGGCCTT CCCCTGCTGG AGTGGAACTT CTGCTTGGAG GACTTCAGAA  
 1601 AGGCAGTGAT GGTGCTCCCT GATGAGAACC ACAGAGAGGA TGCCTTGATG  
 10 1651 AGGCTCAACA AAGCAGCCCT GGAGCTGTGC CAGAAGCCAA GGCCATTGCA  
 1701 GTCCAACCTC CTGCACCAGA TGTGTTTGCA GCTGTGGCGA GATGTGATTG  
 1751 ACAGCCTGGT GGGCCATTCC ATGTGGCTGA GGTCTGTGCT GGGCCTGCCT  
 1801 GAGAAGGAGA CCATCTATTT GAATGTGCCT GAAGAGCAAG ATCAAAAATC  
 1851 ACCTCCTATC ATGGAAGTGA AGGTACCTGT GGGGAAAGCT GGGGAAGGAGG  
 15 1901 AGCGGAAAGG AGCAGCCCAG GAAAAGAAGC AACTGGGGAT CAAAGACAAA  
 1951 GAAGACAAGA AAGGAGCCAA GCTGCTCGGG AAAGAGGACC GTCCCAACAG  
 2001 CAAGAAGCAC AAGGCAAAGG ATGACAAGAA AGTCATAAAA TCTGCAAGTC  
 2051 AGGACAGGTT TTCTTTGGAA GACCCTACCC CTGACATCAT CCTCTCTTCT  
 2101 CAAGAACCCA TAGACCCCTT GGTGATGGGG AAATACACCC AGAGGCTGCA  
 20 2151 CAGTGAGGTC CGTGGGCTGC TGGACACCCT GGTGACCGAC CTGATGGTCC  
 2201 TGGCTGATGA GCTCAGCCCC ATAAAGAATG TCGAGGAGGC TTTGCGCCTC  
 2251 TGCAGGTGAC TCTCGGGCCC AAGCAACCTT CTGGAACACG GGTAAATAAA  
 2301 TAAATCAATA AAGAACCTTC AAGTTTCTAC TAAAAAATAA AAAAAAATAA  
 2351 AAAAAAATAA AAAAAAATAA AAAAAAATAA GGGCGGCCG

## BLAST Results

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30 No BLAST result

## Medline entries

-----

35 No Medline entry

## Peptide information for frame 1

-----

ORF from 118 bp to 2256 bp; peptide length: 713

Category: putative protein

45 Classification: Cell structure/motility

1 MHTGETYRRI QEERELIDCT LPTRRDRKSW ENSGFWSRLE YLGDEMTGLV  
 51 MTKTKTQRL MEPITHIRKP HSIRVETGLP AQRDASYRYT WDRSLFLIYR  
 101 RKELQRIMEE LDFSQQDIDG LEVVGKGWPF SAVTVEDYTV FERSQGSSE  
 50 151 DTTYLGTLAS SSDVSMPIG PSLLFCGKPA CWIRGSPQD KRQVGIAAHL  
 201 TFETLEGEKT SSELTVVNG TVAIWYDWRR QHQPDTFQDL KKNRMQRFYF  
 251 DNREGVILPG EIKTFTFFFK SLTAGVFREF WEFRTHTPTLL GGAILQVNLH  
 301 AVSLTQDVFE DERKVLESKL TAHEAVTVVR EVLQELLMGV LTPERTPSPV  
 351 DAYLTEEDLF RHRNPPLHYE HQVVQSLHQL WRQYMTLPK AEEARP GDKE  
 55 401 HVSPIATEKA SVNAELLPRF RSPISETQVP RPENEALRES GSQKARVGTK  
 451 SPQRKSIMEE ILVEESPDVD STKSPWEPDG LPLLEWNLCL EDFRKAVMVL  
 501 PDENHREDAL MRLNKALEL CQKPRPLQSN LLHQMCLQLW RDVIDSLVGH  
 551 SMWLRSVLGL PEKETIYLVN PEEQDQKSP IMEVKVPVGK AGKEERKGAA

601 QEKKQLGIKD KEDKKGAKLL GKEDRPNSKK HKAKDDKKVI KSASQDRFSL  
651 EDPTPDILS SQEPIDPLVM GKYTQRLHSE VRGLDLTLVT DLMVLADELS  
701 PIKNVEEARL LCR

5

## BLASTP hits

No BLASTP hits available

10

Alert BLASTP hits for DKFZphtes3\_15n14, frame 1

No Alert BLASTP hits found

15

Pedant information for DKFZphtes3\_15n14, frame 1

## Report for DKFZphtes3\_15n14.1

20

[[LENGTH]] 713  
[[MW]] 81780.53  
[[pI]] 6.00  
[[BLOCKS]] PF00878C  
25 [[BLOCKS]] BLO0690C DEAH-box subfamily ATP-dependent helicases  
proteins  
[[KW]] Alpha\_Beta  
[[KW]] LOW\_COMPLEXITY 4.07 %

30

SEQ MHTGETYRRIQEERELIDCTLPTRDRKSWENSGFWSRLEYLGDEMTGLVMTKTKTQRL  
SEG .....  
PRD ccchhhhhhhhhhhhhhhhhhhccccchhhhhhhcccccccccccccccccccccccccccc

35

SEQ MEPITHIRKPHSIRVETGLPAQRDASYRYTWDRSLFLIYRRKELQRIMEELDFSQQDIDG  
SEG .....  
PRD cce

40

SEQ LEVVGKGWPFSAVTVEDYTVFERSQGSSSEDTTYLGTASSSDVSMPILGPSLLFCGKPA  
SEG .....  
PRD eeeeecc

45

SEQ CWIRGSNPQDKRQVGIAAHLTFETLEGEKTSSSELTVVNNGTVAIWYDWRRQHQPDTFQDL  
SEG .....  
PRD eeeccccccccchhhhhhhhhhhheeeccccccccccccccccccccccccccccccccchhh

50

SEQ KKNRMQRFYFDNREGVILPGEIKTFTFFFKSLTAGVREFWEFRTHPTLLGGAILQVNLH  
SEG .....  
PRD hhhhhhhhhccchhhhhhhh

55

SEQ AVSLTQDVFEDEKRVLESKLTAEAVTVVREVLQELLMGVLTPERTPSPVDAYLTEEDLF  
SEG .....  
PRD hhhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccccccccccccc  
55 SEQ RHRNPPLHYEHQVVQSLHQLWRQYMTLPKAAEEARPGDKEHVSPiateKASVNAELLPRF  
SEG .....  
PRD cccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccccccccccc

SEQ RSPISSETQVPRPENEALRESGSQKARVGTKSPQRKSIMEEILVEESPDVDSTKSPWEPDG  
SEG .....  
PRD cccccccccccccchhhhhccccccccccccccccchhhhhhhhhhhcccccccccccccccc

5 SEQ LPLLEWNLCLEDFRKAVMVLPDENHREDALMRLNKAALCQKPRPLQSNLLHQMCLQLW  
SEG .....  
PRD cccccchhhhhhhhhhhhhccccccccchhhhhhhhhhhhhhhhhhhccccccchhhhhhhhhhhhh

10 SEQ RDVIDSLVGHSMWLRSVLGLPEKETIYLVNVEEQDQKSPPIMEVKVPVGKAGKEERKGAA  
SEG .....  
PRD hhhhhhhhhccchhhhhhhccccccccccccccccccccccccccccccccccccchhhhhhhhh

15 SEQ QEKKQLGIKDKEDKKGAKLLGKEDRPNSKKHKAKDDKKVIKSASQDRFSLEDPTPDIIIS  
SEG .....xxxxxxxxxxxxxxxxxxxxxxxx.....  
PRD hhhhhhhccccccccchhhhhhhcc

20 SEQ SQEPIDPLVMGKYTQRLHSEVRGLLDTLVTDLMVLADELSPKKNVEEALRLCR  
SEG .....xxxxxxxxxxxxxxxx.....  
PRD cccccccceechhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccchhhhhhhccc

(No Prosite data available for DKFZphtes3\_15n14.1)

(No Pfam data available for DKFZphtes3\_15n14.1)

25

DKFZphtes3\_1bb5

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5 group: cell structure and motility

DKFZphtes3\_1bb5 encodes a novel 268 amino acid protein with similarity to various tropomyosins.

10 Tropomyosins play regulatory roles in cellular structure and transport.

The new protein can find application in modulating cell structure and motility as well as modulationg cellular transport.

15

weak similarity to KIAAD774

perhaps complete cds.

20

Sequenced by BMFZ

Locus: unknown

25 Insert length: 1316 bp

Poly A stretch at pos. 1247, polyadenylation signal at pos. 1232

```

30  1 TGCTAAAATG GAATTAGAGA GAAGCATAGA CATCAGCAGA AGACAGAGTA
    51 AGGAGCACAT ATGTAGAATT ACAGATCTAC AAGAGGAATT AAGACACAGA
   101 GAGCATCACA TCTCTGAATT GGATAAGGAG GTTCAGCACC TTCATGAGAA
   151 TATAAGTGCC CTAACCAAAG AACTGGAATT TAAGGGGAAA GAAATTCTCA
   201 GAATACGAAG TGAATCTAAC CAACAGATAA GGTTGCATGA ACAAGATTTA
   251 AACAAGAGAC TTGAAAAAGA GTTGGATGTC ATGACAGCAG ACCACCTCAG
   301 AGAGAAAAAT ATCATGCGGG CAGATTTTAA TAAGACTAAC GAGCTACTCA
   351 AGGAAATAAA TGCCGCTTTA CAAGTGTTCAT TAGAAGAAAT GGAAGAAAAA
   401 TATCTAATGA GAGAATCAAA ACCAGAAGAT ATACAGATGA TTACAGAATT
   451 AAAAGCCATG CTTACAGAAA GAGACCAGAT CATAAAGAAA CTAATTGAGG
   501 ATAATAAGTT TTATCAGCTG GAATTAGTCA ATCGAGAAAC TAACTTCAAC
   40  551 AAAGTGTTTA ACTCAAGTCC TACTGTTGGT GTTATTAATC CATTGGCTAA
   601 GCAAAAGAAG AAGAATGATA AATCACCAAC AAACAGGTTT GTGAGTGTTC
   651 CCAATCTAAG TGCTCTGGAA TCTGGTGGAG TGGGCAATGG ACATCCTAAC
   701 CGCCTGGATC CCATTCCTAA TTCTCCAGTC CACGATATTG AGTTCAACAG
   751 CAGCAAACCA CTTCCACAGC CAGTGCCACC TAAAGGGCCC AAGACATTTT
   45  801 TGAGGTATCA GTAAGATGCA TGTGCATGAG CTCAAGGAAC ATGACTACTG
   851 GAGTTTCCAT TACACATTGT TGCCTGCCCT GTAATTTTCC CCAAAGACGT
   901 CCTGCTCAGA GTGAAGCTTC TCCAGTGGCT TCTCCAGATC CCCAGCGCCA
   951 GGAGTGTTT GCGCGGTACT TCACATTCTG AAAGAATTGT GTTGGCACAG
  1001 CTCTGTATAG ACTGTTACTA AGAGCATGAC TTTATACAGA TTGTTATGTA
   50 1051 AATAGGCTTT CCTATGTCAA ACACTGTGAA TGAGAAAGTA TTTGTCTCTC
  1101 CAACTTGAAA ATGCACTGTA TTTCTGTGA TATTTATTGG AATCATTCTA
  1151 TAAGGTACTA TATTATGTGT GTAATTATAA CTGTTATTTT TATTTGAGAT
  1201 GGAAGAGTCT TTAACCTTTG TAATTACTGC ATAATAAATT TTGTTAGAAT
  1251 CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
   55 1301 AAAAAAAAAA AAAAAA
```

BLAST Results

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No BLAST result

5

Medline entries

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No Medline entry

10

Peptide information for frame 2

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15

ORF from 8 bp to 811 bp; peptide length: 268

Category: similarity to known protein

Classification: Cellular transport and traffic

20

1 MELERSIDIS RRQSEHICR ITDLQEEELRH REHHISELDK EVQHLHENIS  
 51 ALTKELEFKG KEILRIRSES NQQIRLHEQD LNKRLKELD VMTADHLREK  
 101 NIMRADFNKT NELLKEINAA LQVSLEEMEE KYLMRESKPE DIQMITELKA  
 151 MLTERDQIIK KLIEDNKFYQ LELVNRETNF NKVFNSSPTV GVINPLAKQK  
 201 KKNDKSPTNR FVSPNLSAL ESGGVGNHGP NRLDPIPNSP VHDIEFNSSK  
 251 PLPQPVPPKG PKTFLRYQ

25

BLASTP hits

30

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3\_16b5, frame 2

35

No Alert BLASTP hits found

Pedant information for DKFZphtes3\_16b5, frame 2

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40

Report for DKFZphtes3\_16b5.2

45

[[LENGTH]] 270  
 [[MW]] 31493.09  
 [[pI]] 6.90  
 [[HOMOL]] PIR:A57013 early endosome antigen 1 - human 1e-05  
 [[FUNCAT]] 03.19 recombination and dna repair [[S. cerevisiae,  
 Y0L034w]] 1e-05  
 [[FUNCAT]] 03.22 cell cycle control and mitosis [[S. cerevisiae,  
 YFR031c]] 2e-05  
 [[FUNCAT]] 30.10 nuclear organization [[S. cerevisiae, YFR031c]]  
 2e-05  
 [[FUNCAT]] 11.04 dna repair (direct repair, base excision repair  
 and nucleotide excision repair) [[S. cerevisiae, YKR095w]] 5e-05  
 [[FUNCAT]] 30.04 organization of cytoskeleton [[S. cerevisiae,  
 YDR356w]] 7e-05  
 [[FUNCAT]] 09.10 nuclear biogenesis [[S. cerevisiae, YDR356w]]  
 7e-05

50

55



[illegible]

50 (No Pfam data available for DKFZphtes3\_1665.2)

55 group: testis derived

DKFZphtes3\_1b3 encodes a novel 1663 amino acid protein without similarity to known proteins.

5 The novel protein is glutamine rich and contains a cell attachment RGD motif. According to the low number of ESTs and their origin the protein seems to be expressed ubiquitously at low levels.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

10 The new protein can find application in studying the expression profile of testis-specific genes.

15 putative protein

perhaps complete cds.

Sequenced by BMFZ

20 Locus: unknown

Insert length: 5411 bp -

Poly A stretch at pos. 5354, polyadenylation signal at pos. 5340

25

```

      1 GGCGGCCAGG TGGAGGACCT GAGCAAGCAG CTCAAGCGTG TGGACGGCCA
      51 GGTGCAGGGC ATCGCCACGC ACGTGCAGCA CTTCTCCCAG GCCAGCGGGC
     101 TTGACCTGGC CGCGCTAGAG TGGCCGGAGG AGCAGGAGGT GGGCGTGCGG
     30 151 GCGTTCGATA GGGTGC GGAC TGGGAGTATC ATGAAGGACG CCGCCGAGGA
     201 GCTCAGCTTT GCCAGGGTAC TTTTACAGCG GGTGATGAA CTAGAGAAGC
     251 TATTCAAAGA TCGGGAGCAA TTCCTGGAAC TAGTCAGCCG GAAGCTGAGT
     301 TTGGTTCCTG GTGCAGAAGA AGTCACCATG GTCACCTGGG AAGAGCTGGA
     351 GCAGGCGATT ACGGACGGCT GGAGAGCCTC ACAAGCGGGC TCAGAAACAC
     401 TTATGGGATT TTCTAAGCAC GGAGGGTTCA CTTCTTAAAC ATCACCTGAA
     451 GGGACTCTAA GCGGAGACTC TACCAAGCAA CCAAGTATTG AGCAGGCTCT
     501 GGATTCTGCC AGTGGTCTTG GCCCGGATCG GACTGCATCA GGATCTGGTG
     551 GCACAGCACA CCCCTCTGAT GGGGTTTCCA GTAGGGAACA AAGCAAGGTC
     601 CCCTCTGGTA CTGGGAGACA GCAGCAGCCG AGGGCCCGTG ATGAAGCTGG
     40 651 CGTGCCACGA CTCCATCAGT CTTCTACATT CCAATTCAAA TCAGACTCAG
     701 ATCGTCACAG GAGTAGAGAG AAGCTTACCT CGACACAACC AAGAAGAAAT
     751 GCACGTCCTG GTCCAGTTCA ACAGGACTTA CCCTTGGCCA GAGACCAGCC
     801 CAGTAGTGTG CCCGCTAGCC AGAGTCAGGT CCATCTAAGG CCAGATCGTC
     851 GTGGGTTAGA ACCAACTGGC ATGAATCAGC CTGGATTAGT GCCTGCTAGC
     45 901 ACTTACCCAC ATGGTGTGGT ACCCCTCAGC ATGGGTGAGC TTGGTGTGCC
     951 ACCACCTGAA ATGGATGATC GGGAAATTGAT ACCATTTGTC GTGGATGAGC
    1001 AACGTATGTT GCCACCATCA GTACCTGGCA GAGACCAGCA AGGATTGGAA
    1051 CTACCTAGCA CAGACCAACA TGGTCTGGTT TCAGTCAGTG CATATCAGCA
    1101 TGGTATGACA TTTCTGGCA CAGACCAACG CAGTATGGAA CCACTTGGCA
    50 1151 TGGATCAGCG TGGATGTGTA ATATCAGGCA TGGGTCAGCA AGGACTAGTA
    1201 CCCCCTGGTA TAGACCAGCA AGGATTGACA TTGCCTGTCT TCGATCAACA
    1251 TGGCCTGGTT CTACCTTTTA CAGACCAGCA TGGTTTGGTA TCACCTGGTT
    1301 TGATGCCAAT TAGTGCAGAT CAGCAAGGTT TTGTGCAGCC CAGTTTGGAA
    1351 GCAACTGGCT TCATACAACC TGGCACAGAG CAGCATGATT TGATCCAGTC
    55 1401 TGGCAGATTT CAGCGTGCTT TGGTGCAGCG TGGTGCATAT CAGCCTGGCT
    1451 TGGTCCAACC TGGTGCAGAT CAGCGTGGTT TGGTCCGGCC TGGGAATGGAT
    1501 CAGTCTGGTT TGGCCCAACC TGGTGCAGAT CAGCGTGGTT TGGTCTGGCC
    1551 TGGGAATGGAT CAGTCTGGTT TGGCCCAACC TGGTAGAGAT CAGCATGGTT

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	1601	TGATCCAGCC	TGGCACAGGT	CAGCATGATT	TGGTCCAATC	TGGCACAGGT
	1651	CAGGGTGTCT	TGGTACAGCC	TGGTGTAGAT	CAGCCTGGCA	TGGTCCAACC
	1701	TGGCAGATTT	CAGCGTGCTT	TGGTGCAGCC	TGGTGCATAT	CAGCCTGGCT
	1751	TGGTCCAACC	TGGTGCAGAT	CAGATTGATG	TGGTGCAACC	TGGTGCAGAT
5	1801	CAGCATGGTT	TGGTACAATC	TGGTGCAGAT	CAGAGTGATT	TGGCTCAACC
	1851	TGGTGCAGTT	CAGCATGGTT	TGGTCCAACC	TGGAGTAGAT	CAGCGTGGTT
	1901	TGGCACAACC	TCGTGCAGAT	CATCAGCGTG	GTTTGGTCCC	ACCTGGTGCA
	1951	GATCAGCGTG	GTTTGGTCCA	ACCTGGTGCA	GATCAGCATG	GTTTGGTCCA
	2001	ACCTGGAGTG	GATCAGCATG	GTTTGGCACA	ACCTGGTGAA	GTTCAGCGTA
10	2051	GTTTGGTGCA	ACCTGGTATA	GTTTGGTGGT	GTTTGGTGCA	ACCTGGTGCA
	2101	GTTTGGTGGT	GTTTGGTGCA	ACCTGGTGCA	GTTTGGTGGT	GTTTGGTCCA
	2151	ACCTGGAGTG	GATCAGCGTG	GTTTGGTCCA	ACCTGGTGCA	GTTTGGTGGT
	2201	GTTTGGTCCA	ACCTGGTGCA	GTTTGGTGGT	GTTTGGTCCA	ACCTGGTGCA
	2251	GATCAGCGTG	GTTTGGTCCA	ACCTGGAGTG	GATCAGCGTG	GTTTGGTGCA
15	2301	ACCTGGAGTG	GATCAGCGTG	GTTTGGTCCA	ACCTGGAGTG	GATCAGCGTG
	2351	GTTTGGTCCA	ACCTGGTGCA	GATCAGCGTG	GTTTGGTCCA	GATCAGCGTG
	2401	GGTCAGCTGG	GTATGGTGCA	GCCTGGAGTG	GGTCAGCAAG	GTATGGTGCA
	2451	ACCTCAGGCA	GATCCACATG	GCCTGGTACA	ACCTGGTGCC	TATCCTCTTG
	2501	GTTTGGTACA	ACCTGGTGCA	TATTTGCATG	ATTTATCTCA	ATCTGGGACA
20	2551	TATCCACGTG	GTCTGGTGCA	GCCAGGAATG	GATCAGTATG	GTTTGGGACA
	2601	ACCTGGTGCA	TATCAGCCAG	GCTTGATAGC	ACCAGGCACA	AAGCTTCGTG
	2651	GCTCTTCAAC	ATTCCAGGCA	GATTCTACAG	GTTTATATATC	AGTACGTCCA
	2701	TATCAACATG	GTATGGTACC	TCCTGGCAGA	GAACAATACG	GCCAGGTGTC
	2751	ACCACTCCTA	GCCAGTCAAG	GTTTGGCATC	ACCTGGTATA	GATCGAAGGA
25	2801	GTTTGGTACC	ACCAGAAACT	TATCAGCAAG	GTTTGGTATA	TCCTGGCACA
	2851	GACCAGCACA	GCCCAATACC	ACTGAGTACA	GGTTTGGGAT	CTACACACCC
	2901	AGATCAACAG	CATGTGGCAT	CACCTGGCCC	AGGTGAGCAT	GACCAGGTAT
	2951	ACCCAGATGC	AGCTCAGCAT	GGCCATGCTT	TCTCTCTCTT	TGACAGTCAT
30	3001	GATTCAATGT	ATCCTGGTTA	TCGTGGCCCA	GGGTATCTAA	GTGCTGATCA
	3051	GCATGGCCAG	GAAGGTTTGG	ATCCAAATAG	AACACGAGCC	TCGGACCGAC
	3101	ATGGAATTCC	TGCCCAGAAAG	GCCCCAGGCC	AAGATGTAC	TCTTTTCAGG
	3151	AGTCCAGACT	CCGTGACCCG	AGTCTTATCA	GAAGGGAGCG	AAGTCTCGAG
	3201	TGAAGTCCTG	AGTGAGCGAC	GCAATTCACT	GCGTAGAATG	AGTTCTAGTT
	3251	TCCCCACGGC	AGTGGAGACA	TTTCATCTGA	TGGGAGAGCT	CAGTAGCCTC
35	3301	TATGTGGGGC	TAAAGGAGAG	TATGAAGGAT	CTGGATGAGG	AGCAGGCCGG
	3351	CCAAACCGAC	TTGGAGAAGA	TCCAGTTCCT	GCTGGCACAG	ATGGTCAAAA
	3401	GGACCATACC	TCCTGAACTG	CAGGAGCAGC	TGAAGACCGT	AAAGACGCTA
	3451	GCCAAAGAAG	TTTGGCAGGA	GAAAGCAAAA	GTGGAAAGGC	TGCAGAGGAT
	3501	CCTGGAAGGG	GAAGGGAATC	AAGAAGCAGG	GAAGGAACTG	AAAGGTGGAG
40	3551	AGCTGAGATT	GCAGCTGGGT	GTCTCAGAG	TCACCGTGGC	TGACATAGAA
	3601	AAGGAGCTGG	CCGAGTTGAG	GGAGAGCCAA	GACAGGGGCA	AGGCTGCCAT
	3651	GGAAAATTCT	GTCTCTGAAG	CCTCCCTTTA	CCTGCAGGAC	CAGTTGGACA
	3701	AGCTCAGGAT	GATCATTGAG	AGCATGCTGA	CCTCCTCCTC	CACGCTCCTG
	3751	TCCATGAGCA	TGGCCCCGCA	CAAGGCCAC	ACCTTGGCTC	CTGGCCAGAT
45	3801	CGACCCCTGAG	GCCACCTGTC	CAGCCTGCAG	CCTGGATGTG	AGCCATCAGG
	3851	TCAGCACGCT	GGTGCGGCGC	TATGAGCAAC	TCCAAGACAT	GGTCAACAGC
	3901	CTGGCCGTCT	CCCGACCTC	CAAGAAGGCC	AAGCTCCAGA	GACAGGACGA
	3951	GGAGCTGCTG	GGCCGTGTGC	AGAGTGCCAT	CCTGCAGGTG	CAGGGTGACT
	4001	GCGAGAAGCT	CAACATCACC	ACCAGCAACC	TCATCGAGGA	CCATCGGCAG
50	4051	AAACAGAAGG	ACATTGCTAT	GCTGTACCAG	GGTCTGGAGA	AGCTCGAAAA
	4101	GGAAAAGGCC	AACAGGGAGC	ACCTGGAGAT	GGAGATCGAT	GTGAAAGCCG
	4151	ACAAGAGTGC	TCTGGCCACC	AAAGTGAGCC	GTGTCCAGTT	TGATGCCACC
	4201	ACGGAGCAGC	TGAACCATAT	GATGCAGGAG	CTGGTGGCCA	AGATGAGCGG
	4251	GCAGGAGCAG	GACTGGCAGA	AGATGCTGGA	CAGGCTGCTC	ACAGAGATGG
55	4301	ACAACAAGCT	GGACCGCCTG	GAGCTGGACC	CAGTGAAGCA	GTTGCTGGAG
	4351	GATCGGTGGA	AATCGCTGCG	ACAGCAGCTC	AGGGAGCGCC	CCCCACTCTA
	4401	CCAGGCAGAC	GAGGCGGCTG	CCATGCGGAG	GCAGCTCCTG	GCACATTTCC
	4451	ACTGCCCTCTC	ATGTGACCGG	CCCTTGGAGA	CACCTGTGAC	TGGACATGCC

4501 ATCCCCGTGA CCCCCGCGGG TCCAGGCCTA CCTGGGCACC ATTCCATCCG  
 4551 CCCCTACACG GTGTTTGAAC TGGAGCAGGT CCGGCAGCAT AGCCGCAACC  
 4601 TCAAGCTGGG CAGCGCCTTC CCTCGGGGTG ACCTGGCGCA GATGGAGCAG  
 4651 AGCGTGGGGC GCCTGCGCTC CATGCACTCC AAGATGCTGA TGAACATTGA  
 5 4701 GAAGGTGCAG ATCCACTTCG GGGGCTCCAC CAAGGCCAGC AGCCAGATAA  
 4751 TCCGCGAGCT GCTGCACGCC CAGTGCCTGG GCTCCCCCTG CTACAAACGG  
 4801 GTGACAGATA TGGCTGATTA CACCTACTCA ACTGTGCCCC GCGCTGCGG  
 4851 GGGCAGCCAC ACCCTCACCT ACCCTACCA CCGCAGCCGC CCGCAGCACC  
 4901 TTCCCCGGGG CCTGTATCCT ACTGAAGAGA TCCAGATTGC CATGAAGCAT  
 10 4951 GATGAGGTGG ACATCTTGGG CCTGGATGGC CACATTTACA AGGGACGGAT  
 5001 GGACACAAGG CTGCCAGGCA TCCTCCGAAA AGACAGCTCA GGGACCTCAA  
 5051 AGCGCAAGTC CCAGCAGCCC AGGCCCCACG TGCACAGGCC GCCATCCCTC  
 5101 AGCAGCAATG GCCAGCTGCC CTCTCGGCCA CAGAGCGCCC AGATTTCCGC  
 5151 TGGCAACACC TCAGAAAGAT AGACCTTCCT CCGAGGGCCG TCTCTCCAG  
 15 5201 CCGAACACAG CCCACCCGCC CAGCTCCGCC TCGGTGGCAA ACAGGGGGCT  
 5251 GGAGAGGCAC GTGGACATGC CTCCTGGGGA GGGGCTCGAG GAGCCCACGC  
 5301 GGGGGCCGCG GTCCAGCACC GCTCAGTGAG CGGAGGTGTA AATAAACATT  
 5351 CAGGAGGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA  
 5401 AAAAAAAAAA A

## BLAST Results

25 No BLAST result

## Medline entries

30 No Medline entry

## Peptide information for frame 1

35 ORF from 181 bp to 5169 bp; peptide length: 1663  
 Category: putative protein  
 40 Classification: no clue  
 Prosite motifs: RGD (1482-1484)

1 MKDAAEELSF ARVLLQRVDE LEKLFKDREQ FLELVSRKLS LVPGAEEVTM  
 45 51 VTWEELEQAI TDGWRASQAG SETLMGFSKH GGFTSLTSPE GTLSGDSTKQ  
 101 PSIEQALDSA SGLGPDR TAS GSGGTAHPSD GVSSREQSKV PSGTGRQQQP  
 151 RARDEAGVPR LHQSSTFQFK SDSDRHRSRE KLTSTQPRRN ARPGPVQQDL  
 201 PLARDQPVSSV PASQSQVHLR PDRRGLEPTG MNQPGLV PAS TYPHGVVPLS  
 251 MGQLGVPPPE MDDRELIPFV VDEQRMLPPS VPGRDQQGLE LPSTDQHGLV  
 50 301 SVSAYQHGMT FPGTDQRSME PLGMDQRCV ISGMGQQGLV PPGIDQQGLT  
 351 LPVVDQHGLV LPFTDQHGLV SPGLMPISAD QQGFVQPSLE ATGFIQPGTE  
 401 QHDLIQSGRF QRALVQPGAY QPGLVQPGAD QRGLVRPGMD QSGLAQPGAD  
 451 QRGLVWPGMD QSGLAQPGRD QHGLIQPGTG QHDLVQSGTG QGVLVQPGVD  
 501 QPGMVQPGRF QRALVQPGAY QPGLVQPGAD QIDVVQPGAD QHGLVQSGAD  
 55 551 QSDLAQPGAV QHGLVQPGVD QRGLAQPRAD HQRGLVPPGA DQRGLVQPGA  
 601 DQHGLVQPGV DQHGLAQPGV VQRSLVQPGI VQRGLVQPGA VQRGLVQPGA  
 651 VQRGLVQPGV DQRGLVQPGA VQRGLVQPGA VQHGLVQPGA DQRGLVQPGV  
 701 DQRGLVQPGV DQRGLVQPGM DQRGLIQPGA DQPGLVQPGA GQLGMVQPGI

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751 GQQGMVQPPA DPHGLVQPGA YPLGLVQPGA YLHDLSSQSGT YPRGLVQPGM
801 DQYGLRQPGA YQPGLIAPGT KLRGSSTFQA DSTGFISVRP YQHGMPVPPGR
851 EQYGVVSPLL ASQGLASPGI DRRSLVPPET YQQGLMHPGT DQHSPIPLST
901 GLGSTHPDQQ HVASPGPGEH DQVYPDAAQH GHAFSLFDSSH DSMYPGYRGP
5 951 GYLSADQHGQ EGLDPNRTRA SDRHGIPAQK APGQDVTLFR SPDSVDRVLS
1001 EGSEVSSEVL SERRNSLRRM SSSFTAVET FHLMGELSSL YVGLKESMKD
1051 LDEEQAGQTD LEKIQFLLAQ MVKRTIPPEL QEQLKTVKTL AKEVWQEKAK
1101 VERLQRILEG EGNQEAGKEL KAGELRLQLG VLRVTVADIE KELAELRESQ
1151 DRGKAAMENS VSEASLYLQD QLDKLRMIIE SMLTSSSTLL SMSMAPHKAH
10 1201 TLAPGQIDPE ATCPACSLDV SHQVSTLVRR YEQLQDMVNS LAVSRPSKKA
1251 KLQRQDEELL GRVQSAILQV QGDCEKLNIT TSNLIEDHRQ KQKDIAMLYQ
1301 GLEKLEKEKA NREHLEMEID VKADKSALAT KVSrvQFDAT TEQLNHMMQE
1351 LVAKMSGQEQ DWQKMLDRL TEMDNKLDRL ELDPVKQLLE DRWKSRLRQQL
1401 RERPPLYQAD EAAAMRRQLL AHFHCLSCDR PLETPVTGHA IPVTPAGPGL
15 1451 PGHHSIRPYT VFELEQVRQH SRNLKLGSAF PRGDLAQMEQ SVGRLRSMHS
1501 KMLMNIQKVQ IHFGGSTKAS SQIIRELLHA QCLGSPCYKR VTDMAQYTYS
1551 TVPRRCGGSH TLTPYHRSR PQHLPRGLYP TEEIQIAMKH DEVQILGLDG
1601 HIYKGRMDTR LPGAIRKQSS GTSKRKSQQP RPHVHRPPSL SSNGQLPSRP
1651 QSAQISAGNT SER
20

```

## BLASTP hits

25 No BLASTP hits available

Alert BLASTP hits for DKFZphtes3\_16p3, frame 1

No Alert BLASTP hits found

30

Pedant information for DKFZphtes3\_16p3, frame 1

## Report for DKFZphtes3\_16p3.1

35

```

[LENGTH] 1723
[MW] 187354.98
[pI] 6.19
40 [HOMOL] TREMBL:AF025461_4 gene: "M01D1.5"; Caenorhabditis
elegans cosmid M01D1.1e-47
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae,
YDL058w] 8e-07
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S.
45 cerevisiae, YDL058w] 8e-07
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YOR216c]
2e-04
[FUNCAT] 11.04 dna repair (direct repair, base excision repair
and nucleotide excision repair) [S. cerevisiae, YKR095w] 0.001
50 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKR095w]
0.001
[BLOCKS] PRO1098C
[BLOCKS] BP02308D
[BLOCKS] PRO0543H
55 [BLOCKS] PRO0210G
[BLOCKS] PRO0210E
[BLOCKS] BP04236A
[PIRKW] RNA binding 3e-06

```

[illegible]

SEQ TYPHGVVPLSMGQLGVPPPEMDDRELIPFVVDEQRMLPPSVPGRDQQGLELPSTDQHGLV  
SEG .....  
PRD .....  
COILS .....  
5 .....

SEQ SVSAYQHGMTFPGTDQRSMEPLGMDQRGCVISGMGQQGLVPPGIDQQGLTLPVVDQHGLV  
SEG .....  
PRD .....  
COILS .....  
10 .....

SEQ LPFTDQHGLVSPGLMPISADQQGFVQPSLEATGFIQPGTEQHDLIQSGRFQRALVQRGAY  
SEG .....  
PRD .....  
COILS .....  
15 .....

SEQ QPGLVQPGADQRGLVRPGMDQSGLAQPGADQRGLVWPGMDQSGLAQPGRDQHGLIAPGTG  
SEG .....  
PRD .....  
COILS .....  
20 .....

SEQ QHDLVQSGTGQGVLVQPGVDQPGMVQPGRFQRALVQPGAYQPGLVQPGADQIDVVQPGAD  
SEG .....  
PRD .....  
COILS .....  
25 .....

SEQ QHGLVQSGADQSDLAQPGAVQHGLVQPGVDQRGLAQPRADHQRGLVPPGADQRGLVQPGA  
SEG .....  
PRD .....  
COILS .....  
30 .....

SEQ DQHGLVQPGVDQHGLAQPGEVQRSLVQPGIVQRGLVQPGAVQRGLVQPGAVQRGLVQPGV  
SEG .....  
PRD .....  
COILS .....  
35 .....

SEQ DQRGLVQPGAVQRGLVQPGAVQHGLVQPGADQRGLVQPGVDQRGLVQPGVDQRGLVQPGM  
SEG .....  
PRD .....  
COILS .....  
40 .....

SEQ DQRGLIAPGADQPGLVQPGAGQLGMVQPGIGQQGMVQPADPHGLVQPGAYPLGLVQPGA  
SEG .....  
PRD .....  
COILS .....  
45 .....

SEQ YLHDLQSGTYPRGLVQPGMDQYGLRQPGAYQPGLIAPGTKLRGSSTFQADSTGFISVRP  
SEG .....  
PRD .....  
COILS .....  
50 .....

SEQ YLHDLQSGTYPRGLVQPGMDQYGLRQPGAYQPGLIAPGTKLRGSSTFQADSTGFISVRP  
SEG .....  
PRD .....  
COILS .....  
55 .....

```

.....
SEQ  YQHGMVPPGREQYGVSPLLASQGLASPGIDRRSLVPPETYQQGLMHPGTDQHSPIPLST
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS
.....

SEQ  GLGSTHPDQQHVASPGPGEHDAQVYPDAAQHGHAFLFDSHDSMPYGPYRGPYLSADQHGG
SEG  .....
PRD  ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
COILS
.....

SEQ  EGLDPNRTRASDRHGIPAQKAPGQDVTLFRSPDSVDRVLSEGSEVSSEVLSERRNSLRMR
SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.
PRD  cccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhhcccccc
COILS
.....

SEQ  SSSFPTAVETFHLMGELSSLYVGLKESMKDLDEEQAGQTDLEKIQFLLAQMVKRTIPPEL
SEG  .....
PRD  cccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhcchhh
COILS
.....

SEQ  QEQLKTVKTLAKEVWQEKAKVERLQRILEGEGNQEAGKELKAGELRLQLGVLRVTVADIE
SEG  .....
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS
.....cccccccccccccccccccccccccccccccccccccc

SEQ  KELAELRESQDRGKAAMENSVSSEASLYLQDQLDKLRMIIESMLTSSSTLLSMSEMAPHKAH
SEG  .....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS
CCCCCCCCC.....

SEQ  TLAPGQIDPEATCPACSLDVSHQVSTLVRRYEQLQDMVNSLAVSRPSKKAKLQRQDEELL
SEG  .....
PRD  hhccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS
.....

SEQ  GRVQSAILQVQGDCEKLNITTSNLIEDHRQKQKDIAMLYQGLEKLEKEKANREHLEMEID
SEG  .....
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS
.....

SEQ  VKADKSALATKVSrvQFDATTEQLNHMMQELVAKMSGQEQDWQKMLDRLLTEMQNKLDRL
SEG  .....
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS
.....

SEQ  ELDPVKQLLEDRWKSLRQQLRERPPPLYQADEAAAMRRQLLAHFHCLSCDRPLETPVTGHA

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5

10

15

20

.....

COILS . . . . .

30

PD0C00016

35

(No Pfam data available for DKFZphtes3\_16p3.1)

DKFZphtes3\_17i21

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5 group: transmembrane protein

DKFZphtes3\_17i21 encodes a novel 224 amino acid protein without similarity to known proteins.

10 The novel protein contains 2 transmembrane regions. ESTs can be found in testis, retina and brain.  
No informative BLAST results; No predictive prosite, pfam or SCOP motif.

15 The new protein can find application in studying the expression profile of testis-specific genes and as a new marker for testicular cells.

20 unknown protein

Pedant: contains signal peptide(frame 1) and TRANSMEMBRANE 2 (frame 2)

25 perhaps complete cds.

Sequenced by GBF

Locus: unknown

30

Insert length: 1518 bp

Poly A stretch at pos. 1480, polyadenylation signal at pos. 1454

```

35      1 GCCAGACAGC TAGGTGTCAT TCAGGGCTGG TGTCTCTGT CCAGGCCATC
      51 ATGGCCTCCA CTGCCGGCTA CATCGTCTCC ACCTCCTGCA AGCACATCAT
     101 TGATGACCAA CACTGGCTGT CCTCTGCCTA CACGCAATTT GCTGTGCCCT
     151 ACTTCATCTA CGACATCTAC GCCATGTTCC TCTGTCACTG GCACAAGCAC
     201 CAGGTCAAAG GGCATGGAGG GGACGACGGA GCGGCCAGAG CCCCGGGCAG
40     251 CACGTGGGCC ATAGCGCGTG GCTACCTGCA CAAGGAGTTC CTCATGGTGC
     301 TCCACCATGC CGCCATGGTG CTGGTGTGCT TCCCACTCTC AGTGGTGTGG
     351 CGACAGGGTA AGGGAGACTT CTTTCTGGGT TGCATGTTGA TGGCAGAGGT
     401 CAGCACGCCC TTCGTCTGCC TTGGCAAGAT CCTCATCCAG TACAAGCAGC
     451 AGCACACACT GCTGCACAAG GTGAACGGGG CCCTGATGCT GCTCAGCTTC
45     501 CTCTGCTGCC GGGTGCTGCT CTTTCCCTAC CTGTA CTGGG CCTACGGGCG
     551 CCATGCCGGC CTGCCCCCTG TGGCCGTGCC CCTGGCCATC CCTGCCCCAG
     601 TCAACCTGGG CGCTGCGCTG CTCCTGGCCC CTCAGCTCTA CTGGTTCTTC
     651 CTCATCTGCC GTGGGGCCTG CCGCCTCTTC TGGCCCCGCT CCGGGCCGCC
     701 CCGGGCCTGC CAGGCCCAGG ACTGAGGCCG GGGGCCGGGA CCCTCCCCCT
50     751 CCCCACCCCC ACCCCCGTGG AGACAGGGCT CTGGGGCTGA TGGCTGGGGT
     801 TGGGAGCCAG GGTCTCTTTG CCCGGACAAC CCCAGGACTG ACGATGACCC
     851 CGAAAGGGAA GAGGCCCCAT CTCTCGGGGA CTGAGGGGGT GGAGAGAGGG
     901 GACCTCTTCC CCCTACTCTG CCCCCTTCCT GCACACCCTT GCGCTGGAGG
     951 AGGGGAGGGG GCACCGCCTC CCACCCACTG AGGGCAGGAG GGCTTGTGGG
55    1001 GAGGGACACC AACAGGGTTT CAAGGGGACC AGGAGTCAGA ATGTGGGGAG
     1051 ACGCCTCTGC CAAGGCCATC CCAGCCCCTA TGCTGCCATC CCCCAGGGCT
     1101 CCCCATCACC CGAGAGGAGA GGACGCCCCA ACTAACCCCC GCTGGCCCCC
     1151 GGGCCTCCCG AGTGGCCGGC TGCAACCACG GCTCCTCTCC AGGGTAGGCC

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1201 AGCTTGAGGA ATCTTATTTA TTTTATTTAT TTACCCAAAT TTGAACTAGT  
 1251 CTGTTGGGTT GGGGGAAGGA GGTGGCTGCT ACCCCCAAGC CTTCCCAGTG  
 1301 CTGACAACCC CGGGGGCAGG CGAGGGCGCC CAGTCCCTCA CCATCGGCTG  
 1351 CACATCGCGC CCTCGGGCCC TGCCATGTCC CTGGTGCTAC TGACCTCTCA  
 5 1401 AGGCTTCCTC CAATCTGGGG TCGGGGGACC CTGGGAGGTG CTTTACAGAC  
 1451 CGCTAATAAA AGACGATCTG CGTGAACGCC AAAAAAAAAA AAAAAAAAAA  
 1501 AAAAAAAAAA AAAAAAAAAA

# 10 BLAST Results -----

No BLAST result

# 15 Medline entries -----

No Medline entry

# 20 Peptide information for frame 3 -----

25 ORF from 51 bp to 722 bp; peptide length: 224  
 Category: putative protein  
 Classification: Transmembrane proteins unclassified

30 1 MASTAGYIVS TSCKHIIDDQ HWLSSAYTQF AVPYFIYDIY AMFLCHWHKH  
 51 QVKGHGDDG AARAPGSTWA IARGYLHKEF LMVLHHAAMV LVCFPLSVVW  
 101 RQGGKDDFFLG CMLMAEVSTP FVCLGKILIQ YKQQTLLHK VNGALMLLSF  
 151 LCCRVLLFPY LYWAYGRHAG LPLLAVALAI PAHVNLGAAL LLAPQLYWFF  
 201 LICRGACRLF WPRSRPPAC QAQD

35

# BLASTP hits

40 No BLASTP hits available

Alert BLASTP hits for DKFZphtes3\_17i21, frame 3

No Alert BLASTP hits found

45

Pedant information for DKFZphtes3\_17i21, frame 3  
 -----

# 50 Report for DKFZphtes3\_17i21.3

55 [LENGTH] 224  
 [MW] 25224.11  
 [pI] 9.03  
 [HOMOL] TREMBLNEW:AF181646\_1 gene: "BcDNA.GH12326";  
 product: "BcDNA.GH12326"; Drosophila melanogaster BcDNA.GH02340  
 (BcDNA.GH02340) mRNA, complete cds. 9e-20  
 [BLOCKS] PRO0632H

[[BLOCKS]] PRO0904A  
 [[BLOCKS]] BL01243C  
 [[KW]] TRANSMEMBRANE 2  
 [[KW]] LOW\_COMPLEXITY 6.25 %

5

SEQ MASTAGYIVSTSCKHIIDDQHWLSSAYTQFAVPYFIYDIYAMFLCHWHKHQVKGHGGDDG  
 SEG .....  
 PRD cccccccccccccccccccccchhhhhhhhhhhheeehhhhhhhhhhhhhhhhhhhhcccccccc  
 MEM .....

10

SEQ AARAPGSTWAIARGYLHKEFLMVLHHAAMVLVCFPLSVVWRQGGKGDFFLGCMLEAEVSTP  
 SEG .....  
 PRD cccccccccccccccccchhhhhhhhhhhhhhhhhhhccccccccccccccccchhhhhhhhhhhccc  
 MEM .....MMMMMMMMMMMMMMMMMM.....

15

SEQ FVCLGKILIQYKQQTLLHKVNGALMLLSFLCCRVLLFPYLYWAYGRHAGLPLLAVPLAI  
 SEG .....xxxxxxxxxxxxxx  
 PRD ccchhhhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhheeeccceeecccccccccccccccccc  
 MEM .....MMMMMMMMMMMMMMMMMM.....

20

SEQ PAHVNLGAALLLAPQLYWFFLICRGACRLFWRPSRPPACQAAQD  
 SEG xx.....  
 PRD cchhhhhhhhhhhhhcccccccccccccccccccccccccccccccccccccc  
 MEM .....

25

(No Prosite data available for DKFZphtes3\_17i21.3)

30 (No Pfam data available for DKFZphtes3\_17i21.3)

DKFZphtes3\_18n14

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5 group: transcription factors

DKFZphtes3\_18n14 encodes a novel 377 amino acid protein with similarity to human giantin.

10 Giantin is discussed as an autoantigen in rheumatoid arthritis. The novel protein contains a leucine zipper and a putative Helix-loop-helix DNA-binding domain. Therefore it might be a novel transkription factor. Most EST hits are from testis and germ cells.

15 The new protein can find application in modulation of gene expression and in expression profiling.

20 unknown protein

see DKFZphtes3\_30i23  
wrong orientation  
perhaps complete cds.

25 Sequenced by MediGenomix

Locus: /chromosome="16"

30 Insert length: 5282 bp  
Poly A stretch at pos. 5242, polyadenylation signal at pos. 5227

```

      1 CCGGCACCCG GAGCTCCTGG GCACACGGCA TTGGCAGGGG CCGCTTCGGC
35    51 AGAGTGATGA CTGATGATGA GTCCGAGAGC GTCCTCTCCG ACTCCCATGA
      101 AGGGTCGGAG CTGGAGCTGC CTGTTATCCA GCTGTGCGGG CTGGTGGAGG
      151 AGCTCAGCTA TGTAAACTCT GCTCTCAAAA CTGAGACTGA GATGTTTGAG
      201 AAATATTACG CTAAACTGGA GCCCAGGGAT CAGCGACCTC CACGATTATC
      251 AGAAATTAAA ATATCAGCAG CAGATTATGC ACAGTTTCGA GGCAGGCGTA
40    301 GATCCAAATC CCGGACAGGT ATGGACCGTG GGGTAGGCCT GACTGCCGAC
      351 CAAAAACTTG AGCTGGTACA AAAAGAGGTT GCGGACATGA AGGATGACTT
      401 ACGACACACA AGGGCAAATG CGGAACGCGA CCTGCAGCAT CACGAGGCGA
      451 TCATTGAGGA GGCTGAAATT CGATGGAGTG AAGTTTCGAG AGAAGTGCAT
      501 GAGTTTGAAA AAGATATTCT AAAAGCCATA TCCAAGAAGA AAGGGAGTAT
45    551 TTTGGCCACT CAGAAAGTGA TGAAATACAT TGAGGACATG AACCGCCGGA
      601 GGGATAATAT GAAGGAGAAA TTACGTTTGA AAAATGTTTC TCTCAAAGTT
      651 CAGAGGAAAA AAATGCTTTT ACAATTGAGG CAGAAGGAAG AGGTGAGTGA
      701 GGCCCTTCAC GATGTTGATT TTCAGCAGTT GAAGATAGAG AACGCTCAAT
      751 TTCTTGAGAC AATTGAAGCA AGGAATCAAG AACTGACCCA GCTAAAGCTG
50    801 TCATCTGGAA ACACTCTGCA GGTTCCTCAAT GCCTACAAAA GCAAGCTTCA
      851 CAAGGCAATG GAAATATACC TCAATCTGGA CAAGGAGATC TTGCTGAGAA
      901 AAGAGCTACT TGAAAAAATT GAAAAAGAAA CACTACAAGT AGAGGAGGAC
      951 CGGGCCAAAG CCGAGGCAGT GAATAAGAGG CTCCGGAAGC AGCTGGCCGA
100   1001 GTTCCGGGCA CCACAGGTGA TGACTTACGT CCGGGAGAAG ATCTTAAATG
55   1051 CGGACCTGGA GAAGAGCATC AGGATGTGGG AAAGGAAAGT GGAGATAGCA
      1101 GAGATGTCCT TAAAAGGCCA TCGTAAGGCT TGGAATCGAA TGAATAAAC
      1151 CAATGAGCAG TTGCAGGCAG ATTACCTTGC TGGGAAGTAG CCAGAGGCAG
      1201 GCCACGGCTT ACAGACCACT ACATGACCTA TAAAAGTAAT CAGCTCCTTT

```

1251 CTAGTCACGG GCTCCTCTCA CTGTTCCCTG TCTGCCTGGT GTTCCCAACC  
 1301 CCCCACCCAG GCTGAGTATC ATCTCCTGGG CCACATCTGC CCATGGGGAG  
 1351 TGTTTTCACA GCCTGGCCCC TGGAAGTGT ACCACTGAAA GAACCACAGG  
 1401 GCACTCTAAT GGTTTGACAC TTGTTAGCCA GCATTTAGTT CACAAGCATA  
 5 1451 GTGAAAGTGA CCTTCCCACA CCTGGGAGAG GGATAGAGGA GGGAGAGCCA  
 1501 GCCCAGTGTA TGCCATGGGC TTATCCGTGG CAGCCCCAGT GTGCAACTAT  
 1551 CAAAAACAGA CATCAAAACA GCATGGTGAA TGCCTGGCAC TCAGCATTCT  
 1601 CAGTTTACTC TTCAGTTTGG TGGGGTAGCT CCTGGACTAG ATACTGCTGC  
 1651 AAAAGAAAAAC AAGCACGAAG GAAACCAAGA TGATTTCTTC GGGCTGATAC  
 10 1701 AACCTGTTCT GACCTGCAAA AATCCTACCT TCCCCACCT CCCCACGTA  
 1751 ATAGTCATAG TATAAGGGTT GTACAGACGC CTCAGGAGAC CTGCCTGATT  
 1801 CCTTTACATC CTTCTCCCTA ACATCTAGAC TATCTCTAGA GCTGTTTCTT  
 1851 AGTCGTGAAT GCGTGATGGT CTTCTTTTGT CCCTGCAAGT ATGATCCAAC  
 1901 ATGGCCCAGT TCAGAATCAG AATATGTCTT CTGTGTCATG GTGGCATTTG  
 15 1951 GTCCATGGTG GGAGAAAGAA ATCAACTTTT CCCAGTGGTG GAGTGAGGAC  
 2001 AGGGGAGGGG CGGCCCTCTC AGCCTTGGAT GTGATCCATT TGCTGTAGTC  
 2051 TTCCACCTTG GTGTACAGAA ACAGGCCAGG GCACGTCTCA CCACCGAAGT  
 2101 TCAGGACTCC TCTCAGAACC CACAGATCGA ACTGCTGTAG CTGGCACATC  
 2151 ATTGGGCTTC CTGGGTCCCC CTGTGATAAA AGACAGAAGG CTTCAAGTCT  
 20 2201 TAGAAAAACT AGTTTTTGT GTAAATCTAT CCTTGTCGAA TATACTGTTT  
 2251 GTTCTAGAAA TGTTTTACGC TGGTTCTCAC TGGAAATGGG GCAAATTATA  
 2301 GGATACAATT TCAAATCTAG GCAGCCACCA CCACAAATTC CAACAAGATG  
 2351 ACTTTTCTCT TTATTATGCA AATTAGCTGT GGACTTCTGC TGATTGCCTA  
 2401 TAGCTTCTCT GTTCATATTT CATTTTCTTG CCCCTTTCCA GTCCTTTGGC  
 25 2451 CAAACCTTCC CTCTCTTCTG GCTTCTCATT CCTGAAATGT TGGTGTTTGT  
 2501 TTCTGTTTTG TCCTGAAATG CTCACATTTT CCCTTCTCTG CCTTGCTTCA  
 2551 ACCCTTAGTG TAAGCCACTT CTTGCCACCT GGCAACTGCT TACCAGCCTG  
 2601 GCTGGCCGTG CTCTGGGTCT TCCCTACTCC CAATGGAGCA GTCCTCTGGG  
 2651 ACTTGGAAT TCTGCCACAT ACACCTTATC TAACCTAAAG TGACGGAGTA  
 30 2701 GAAGCTTGGC ATCATTAGCT AGATATGGGA CCCTGGCAAG TGACCAAATC  
 2751 CTCTCTGAGC CAAGGTGGGA ACACAGTTAA TGCTGTAAAC ACGTGCTGAG  
 2801 CACAGCACAG TGCTGGGCAC ACAGCAAACA CTCAATAGAA TATTAGCTAC  
 2851 CATCATCCTG ATGTCGCTAT AAAGGCCAGC ATTTTCTGA AAAGTTGGGG  
 2901 AAAATGGGAA AAGCAACAAG GCAACTAGTA GGTATCACTT ACCTTACCTG  
 35 2951 CCCAGACCCC ACACCCCTAG GTCTCCTCTC AAAGGAATTC CTGCCCCCTC  
 3001 CATGGCCCCA CTTGGTCCGA GAAGGGGGTG GTCATCCCCA GGCTAGCCAG  
 3051 CCACCTCTGA CCTGTGTGGC CTGCCCTGGT GGAAGGCCCCA GGCAATTACA  
 3101 TGTTGCTCTC GCAGTTTGGG CTGAGACATG GAATGGGGCC GCAATTAACA  
 3151 ACAGGAAACA ATCTGAACAG ACTGAACCAC GAGCAGCAGA AAGGCAGAAG  
 40 3201 AGCAGCCGCT TCAGCCCCTT ACCATCCGAG ACCTGGGTGT GTGGTCTGTC  
 3251 TTGGTCACTC TCTCTGTCTC TCTTCTCTC TTTCTTTCTC TGTCCCCAAG  
 3301 GCTGGAGTGC AGTGGTGCAA TCTTGGCTCA CTGCAACCTC CACCTCTGGG  
 3351 ATTCAAGCAA TTCTCCCACC TCAGCCTCTC GAGTAGCTGG GGCTACAGCT  
 3401 ATGCGCCACC ATGCCCAGCT AATTTTTTTT TTTTTTTTTT GAGATGGAGT  
 45 3451 CTTGCTCTGT CCCCATGCT GGAGTGCACT GGCATGATCT CGGCTCGCTG  
 3501 CAACCTCCTC CTCCTGGGTT CAAGCGATT TCCTACCTCA GCCTCCCCAG  
 3551 TAGCTGGGAT TACAGGCGCC CACCACCACA CCTGGCTAAT TTTTATTTTT  
 3601 AGTAGAGATG GGGTTTCAAC ATGTTGGCCA GGCTGGTCTC GAACTCCTGA  
 3651 CCTCATGATC CACCCGCTC GGCCTCCCCA AGTGTGGGA TTACAGGCGT  
 50 3701 GAGCCACTGC ACCCGGCTA ATTTCTGTAT TTTTAGTAGA GATGGGGTTT  
 3751 CACGATGTTG GCCAGGCTGG TCTTAATCTA ACTTCAAGTG ATCTGCCCCG  
 3801 CTCGCCCTCT CAAAGTGCTG GGATTAGGCA TGAACCTACCA TGCCCAGTGG  
 3851 GGTATTCTCT TTCAATAAAG CTCCTCTTTT CCAAGGAAGC CACACCAGAA  
 3901 CAGAGATGAA GACCAGTGGG AAAACATGGG AGCAACTCCG TGGGCAGGCC  
 55 3951 AGCGGGGAGG CCATGCTGCA AAGCTGCCGT GATTCCTGG TGATCTCTCA  
 4001 GCAGGCCAAG GCCAGACATG TGAGGAAGGC CTTGAGGACT TCATTCTGTG  
 4051 CCTCTCCTTG GATGGAAGGG GGTGCTTTAG TGTGGCACTC CTGACTTTTC  
 4101 AATTGACTGG TGAAGAGGCC CTTGTGTGCA CCTCACTATG TCTGCCTAGG

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4151 TCATGGGGGC TCCCTGGCCA AGAATGACGT GGTCCCCCT TTCATCAGTC
4201 CGATTGCGAG TTTGTCTTAA CTGTAGTGGT ATAGCCAGAG CAAGAAAAAG
4251 AATGTGATTT AGGACAAATG ATTGGATGAG TGATTGGTAG ATGTCCTCAG
4301 CTATGGCGTG GTTTTGCAAG TCACTGTTCC ACCCACCTGG GCACAGCATA
5 4351 TACGCTTTT CTCTTCCCCA TAATCCCCTA GGGGCTGCGA CTTCTGAAGC
4401 ACAAGAGGCA GAGGCGAACA GCTCCAGGTG CCCCTCTGGA GCTACCCCTAC
4451 CTCATCTCCC AAGGGAGCGG CCACAGCCCA GAGTGGGGTC TTTCAATTTG
4501 TGATCTTTTC CCTTGACATT CAGCAAAAGC CCTGACAGTG GTAGAATAAA
4551 GGCAGGATGG GTGAGTGCAG AGTGATTCTG CTTTTGTTGG GTTTCAGGGA
10 4601 AACCCTAGAG CAGATTCTGA ACCTGGTGGT TGATTCTACA TGTGGGAATT
4651 GTGGCTTTGA AGACCTCTGG ACATGAGAAC ATATTTCCAA GACAGAGGAT
4701 TCTATGGGGA CGGGTCACCA TTAAATGGTG TGCAAGCATA ATTCTGTTCA
4751 AAAATGAAGG CATGTTTAGA GGTGTGTCAC AGTTAAAAAC CAACCTGAAC
4801 TTTGCAGTTA GATTTTAAAA GATGGTCAGT TAGAGTAGAA ATAGCTTAGA
15 4851 ATATTCATT GAGTCTAAGA TACAGTTAGA AATCAACATC TTTGAAATTA
4901 GGGTGTGTCT TTTAATCAGT TGATGTCAGA GTTTAACGGG CAGCATTTTT
4951 TTCTTTCTTG GGATTACAAA AAATGATGGT GCATTCTATA ATTGGCAGCA
5001 TCTTAGATCT GAGGAAGTAT GATACTTGTG TGACGGAATG GTTGACGGCA
5051 GAATTTTGTG AAAAAGCTAT ATCTTCACTG TATTTTAAAC CATTATCTAA
20 5101 TTTAAGAAAT TGTTAAGATC CCCCACCTGG CAGAGGACCC AGTACAAAAT
5151 AGGCACTCAA TAGATGTTAC ACCAACTTTG GAAGGGCAAA CATATTTCTT
5201 AATGAGAGGC AGTCCTTCAT GTTTTGCAAT AAAATGACTT TTAACAAAAA
5251 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA

```

25

## BLAST Results

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No BLAST result

30

## Medline entries

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35 No Medline entry

40

## Peptide information for frame 3

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ORF from 57 bp to 1187 bp; peptide length: 377

Category: putative protein

Classification: no clue

45 Prosite motifs: LEUCINE\_ZIPPER (19-40)

```

1 MTDDSESSEVL SDSHEGSELE LPVIQLCGLV EELSYVNSAL KTETEMFEKY
51 YAKLEPRDQR PPRLSEIKIS AADYAQFRGR RRSKSRTGMD RGVGLTADQK
50 101 LELVQKEVAD MKDDLRLHTRA NAERDLQHHE AIIEEAEIRW SEVSREVEHF
151 EKDILKAISK KKGSLATQK VMKYIEDMNR RRDNMKEKLR LKNVSLKVQR
201 KKMLLQLRQK EEVSEALHDV DFQQLKIENA QFLETIEARN QELTQLKLSS
251 GNTLQVLNAY KSKLHKAMEI YLNLDKIILL RKELLEKIEK ETLQVEEDRA
301 KAEAVNKRRLR KQLAEFRAPQ VMTYVREKIL NADLEKSIRM WERKVEIAEM
55 351 SLKGHRKAWN RMKITNEQLQ ADYLAGK

```

No BLASTP hits available

No Alert BLASTP hits found

10

[illegible]



.....{

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COILS
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.....
```

15

20 PS00029 37->59 LEUCINE\_ZIPPER PD0C00029

25

30

RRR NM E+ R++++ + + +++++ +E L V+

Query 198 RRR-DNMKEKLR LKNVSLKVQRKKMLLQL-RQKEEVSEA-  
LHDVDFQQL 243

Query 244 KIENAQFLE 252

DKFZphtes3\_l9p12

-----

5 group: testis derived

DKFZphtes3\_l9p12 encodes a novel 664 amino acid protein without similarity to known proteins.

10 No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

15

unknown protein

Sequenced by MediGenomix

20

Locus: unknown

Insert length: 2161 bp

Poly A stretch at pos. 2086, no polyadenylation signal found

25

```

      1 CCCGAGCCAG CAACCCTGAG GGGCGGCCGG GCAGCGCCGC CACCATGTTC
    51 CTGGGCACCG GGGAGCCGGC CTTGGACACG AGTCACCTTA TCTCTCTAAG
   101 CCGAGCGTCC CTGACCCCGC AGAAGCTGTG GCTGGGAACC GCAAAGCCAG
   30 151 GAAGTCTGAC CCAGGCCCTG AACTCACCCC TCACCTGGGA GCATGCGTGG
   201 ACTGGCGTCC CCGGCGGCAC TCCTGACTGT CTGACAGACA CCTTCAGAGT
   251 GAAGAGGCCA CATCTCAGGC GCTCTGCCAG CAACGGTCAT GTCCCTGGGA
   301 CTCCTGTCTA CAGAGAAAAA GAAGATATGT ATGACGAGAT TATTGAGTTA
   351 AAGAAGTCAT TGCACGTGCA GAAGAGCGAC GTGGACCTGA TGAGAACGAA
   35 401 GCTCCGGCGC CTGGAGGAGG AAAACAGCAG GAAGGACCGG CAGATAGAGC
   451 AGCTCCTGGA TCCCAGCCGC GGCACGGATT TTGTTCCGGAC TCTGGCAGAG
   501 AAAAGGCCCG ATGCCAGTTG GGTCAATTAAC GGGCTGAAGC AGAGGATCCT
   551 GAAGCTGGAA CAGCAGTGCA AGGAGAAGGA CGGCACCATC AGCAAACCTCC
   601 AGACCGATAT GAAGACTACC AACCTGGAAG AGATGCGGAT CGCCATGGAG
   40 651 ACATACTACG AGGAGGTGCA TCGTCTCCAG ACCCTCTTGG CAAGTTCTGA
   701 AACCACCGGA AAGAAGCCCC TGGGGGAGAA GAAGACGGGC GCCAAAAGGC
   751 AGAAGAAGAT GGGCAGTGCC CTCCTGAGCT TGTCCCGGAG TGTCCAGGAG
   801 CTCACGGAAG AGAACCAGAG CCTGAAGGAG GACCTGGACC GCGTGCTGAG
   851 CACCTCCCCA ACCATCTCCA AGACACAGGG TTATGTGGAG TGGAGCAAGC
   45 901 CCCGGCTGCT GAGGCGCATT GTGGAGCTGG AGAAGAAACT AAGTGTGATG
   951 GAGAGCTCAA AATCACACGC CGCAGAGCCA GTCAGATCAC ACCCGCCAGC
  1001 CTGCCTTGCA TCCAGCTCTG CGCTGCACAG ACAGCCACGA GGGGACCGCA
  1051 ACAAGGACCA CGAGCGTCTC CGAGGGGCTG TGAGAGACCT GAAGGAAGAG
  1101 CGGACCGCGC TGCAGGAGCA GCTGCTGCAG AGAGATTTGG AGGTGAAGCA
  50 1151 GCTCCTGCAG GCGAAGGCCG ACCTGGAGAA GGAGCTGGAG TGC GCGAGGG
  1201 AGGGCGAGGA GGAGAGGAGA GAGCGAGAGG AGGTTTTGAG AGAGGAGATT
  1251 CAGACACTTA CCAGCAAGCT CCAAGAATTG CAAGAAATGA AGAAAGAAGA
  1301 GAAAGAGGAT TGCCCGGAAG TTCCTCATAA GGCCCAAGAG CTCCAGCTC
  1351 CCACTCCCA GAGCAGGCAC TGCGAGCAAG ACTGGCCGCC GGATTCCAGC
  55 1401 GAGGAGGGGC TCCGCGGGCC CCGCTCCCCC TGCTCTGATG GGAGAAGAGA
  1451 CGCCGCGGCC AGAGTCCTGC AGGCCCAGTG GAAGGTGTAC AAGCACAAGA
  1501 AAAAAAAGGC TGTTCCTGGAT GAGGCGGCTG TGGTGCTTCA GGCAGCTTTC
  1551 AGGGGACATC TCACGCGGAC AAAGCTCTTA GCAAGCAAAG CACATGGCTC
```

```

1601 AGAGCCACCC AGCGTGCCAG GCCTCCCAGA CCAGAGCTCT CCTGTGCCCC
1651 GCGTTCCGAG CCCCATCGCC CAGGCCACGG GCAGCCCTGT GCAGGAGGAG
1701 GCCATCGTCA TCATCCAGTC CGCTCTGCGG GCACACCTGG CCCGGGCCAG
1751 GCACAGTGCT ACCGGTAAAA GAACCACCAC CGCAGCTTCT ACCAGGAGGA
5 1801 GATCGGCTTC AGCCACACAC GGGGACGCCT CCTCCCCACC CTTCTCGCA
1851 GCTCTTCCTG ACCCCTCTCC CTCAGGGCCA CAGGCCTTGG CACCTCTACC
1901 TGGGGATGAC GTCAACTCCG ATGATTCCGA CGATATTGTC ATTGCACCGT
1951 CTCTGCCAC GAAGAACTTT CCAGTTTAGG TCCCCGTCAC TGTCTCCACG
2001 CCGTGATGGC AGCGCTGCCG AGGACATAGG AACCACGACT GGAAAGATAA
10 2051 TTTATCGTGT TAGGAGAAGA ACGATGATAC CTACTTAAAA AAAAAAAAAA
2101 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2151 AAAAAAAAAA A

```

15

## BLAST Results

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No BLAST result

20

## Medline entries

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No Medline entry

25

## Peptide information for frame 3

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30

ORF from 45 bp to 1976 bp; peptide length: 644  
 Category: similarity to unknown protein  
 Classification: unclassified  
 Prosite motifs: RGD (332-334)

35

40

45

50

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1 MFLGTGEPAL DTSHLISLSR ASLTPQKLWL GTAKPGSLTQ ALNSPLTWEH
51 AWTGVPGGTP DCLTDTFRVK RPHLRRSASN GHVPGTPVYR EKEDMYDEII
101 ELKKSLSHVQK SDVDLMRTKL RRLEEENSRL DRQIEQLLDP SRGTDVVRTL
40 151 AEKRPDASWV INGLKQRIK LEQQCKEKDG TISKLTDMK TTNLEEMRIA
201 METYYEEVHR LQTLASSET TGKKPLGEKK TGAKRQKKMG SALLSLRSV
251 QELTEENQSL KEDLDRVLST SPTISKTDGY VEWSKPRLLR RIVELEKKLS
301 VMESKSHAA EPVRSHPPAC LASSALHRQ PRGDRNKDHE RLRGAVRDLK
351 EERTALQEQ LQRDLEVKQL LQAKADLEKE LECAREGEEE RREREVLRE
45 401 EIQLTSLKLQ ELQEMKKEEK EDCPEVPHKA QELPAPTPSS RHCEQDWPPD
451 SSEEGLPRPR SPCSDGRRDA AARVLQAQWK VYKHKKKKAV LDEAAVVLQA
501 AFRGHLTRTK LLASKAHGSE PPSVPLPDQ SSPVPRVPSP IAQATGSPVQ
551 EEAIVIIQSA LRAHLARARH SATGKRTTTA ASTRRRSASA THGDASSPPF
601 LAALPDPSPS GPQALAPLPG DDVNSDDSDD IVIAPSLPTK NFPV

```

## BLASTP hits

55 No BLASTP hits available

Alert BLASTP hits for DKFZpHtes3\_19p12, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphtes3\_19p12, frame 3

5

Report for DKFZphtes3\_19p12.3

10 [LENGTH] 644  
 [MW] 71810.41  
 [pI] 8.80  
 [HOMOL] TREMBL:AB028946\_1 gene: "KIAA1023"; product:  
 "KIAA1023 protein"; Homo sapiens mRNA for KIAA1023 protein,  
 partial cds. 0.0  
 15 [FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae,  
 YDL058w] 2e-07  
 [FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S.  
 cerevisiae, YDL058w] 2e-07  
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YLR309c]  
 20 3e-06  
 [FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae,  
 YDR356w] 2e-05  
 [FUNCAT] 09.10 nuclear biogenesis [S. cerevisiae, YDR356w]  
 2e-05  
 25 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae,  
 YDR356w] 2e-05  
 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae,  
 YJR134c] 4e-05  
 [BLOCKS] DM013541  
 30 [BLOCKS] BL00627B GHMP kinases ATP-binding domain proteins  
 [BLOCKS] BL00326C Tropomyosins proteins  
 [BLOCKS] BL01160B Kinesin light chain repeat proteins  
 [BLOCKS] BL00820D Glucoamylase proteins region proteins  
 [BLOCKS] BP04417C  
 35 [BLOCKS] BL00412B Neuromodulin (GAP-43) proteins  
 [EC] 3.6.1.32 Myosin ATPase 3e-08  
 [PIRKW] tandem repeat 3e-08  
 [PIRKW] transmembrane protein 2e-07  
 [PIRKW] muscle contraction 3e-08  
 40 [PIRKW] actin binding 3e-08  
 [PIRKW] ATP 3e-08  
 [PIRKW] thick filament 3e-08  
 [PIRKW] alternative splicing 7e-07  
 [PIRKW] coiled coil 3e-08  
 45 [PIRKW] P-loop 3e-08  
 [PIRKW] heptad repeat 2e-07  
 [PIRKW] methylated amino acid 3e-08  
 [PIRKW] hydrolase 3e-08  
 [PIRKW] Golgi apparatus 2e-07  
 50 [SUPFAM] myosin heavy chain 3e-08  
 [SUPFAM] myosin motor domain homology 3e-08  
 [SUPFAM] alpha-actinin actin-binding domain homology 8e-06  
 [SUPFAM] plectin 8e-06  
 [SUPFAM] ribosomal protein S10 homology 8e-06  
 55 [SUPFAM] giantin 2e-07  
 [PROSITE] RGD 1  
 [KW] All\_Alpha  
 [KW] LOW\_COMPLEXITY 14.60 %

[KW] COILED\_COIL 15.22 %

5 SEQ MFLGTGEPALDTSHLISLSRASLTPQKLWLGTAKPGSLTQALNSPLTWEHAWTGVPGGTP  
SEG .....  
PRD ccc  
COILS  
.....

10 SEQ DCLTDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIEELKKSLSHVQKSDVDLMRTKL  
SEG .....  
PRD cccccchhh  
COILS  
.....CCCCCCCCCCCCCCCCCCCCCCCCCCCC

15 SEQ RRLEEENS RKDRQIEQLLDP SRGTD FVRTLA EKRPDASWVINGLKQRILKLEQCKEKDG  
SEG .....  
PRD hhh  
COILS  
20 CCCCCC.....

SEQ TISKLQTD MKTTNLEEMRIAMETYYEEVHRLQTLASSETTGKKPLGEKKTGAKRQKKMG  
SEG .....  
PRD hhh  
25 COILS  
.....CCCC

SEQ SALLSLSRSVQELTEENQSLKEDLDRVLSTSP TISK TQGYVEWSKPRLLRRIVELEKKLS  
SEG .....  
PRD hhh  
30 COILS  
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.....

SEQ VMESSKSHAAEPVRSHPPACLA SSSALHRQPRGDRNKDHERLRGAVRDLKEERTALQEQ L  
SEG .....  
PRD hhh  
35 COILS  
.....

40 SEQ LQRDLEVKQLLQAKADLEKELE CAREGEEERRERE EVLREEIQTLTSKLQELQEMKKEEK  
SEG .....xx  
PRD hhh  
COILS  
.....CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

45 SEQ EDCPEVPHKAQELPAPT PSSRHCEQDWPPDSSEGLPRPRSPCSDGRRDAAARVLQAAQWK  
SEG x.....x  
PRD hhh  
COILS  
50 CCCCCC.....

55 SEQ VYKHKKKKAVLDEAAVVLQAAFRGHLTRTKLLASKAHGSEPPSVGPLDQSSPVPRVPSP  
SEG xxxxxxxx.....  
PRD hhh  
COILS  
.....

SEQ IAQATGSPVQEEAIVIIQSALRAHLARARHSATGKRTTTAASTRRRRSASATHGDASSPPF

SEG .....xx.....  
PRD cccccccccceeehhhhhhhhhhhhhhhhhhccccceeehhhhhhhhhhccccccccce  
COILS

5

SEQ LAALPDPSPSGPQALAPLPGDVVNSDDSDDIVIAPSLPTKNFPV  
SEG .....xxxxxxxxxxxxx.....  
PRD eee  
COILS .....

10

Prosites for DKFZphtes3\_19p12.3

15 PS00016 332->335 RGD PD0C00016

(No Pfam data available for DKFZphtes3\_19p12.3)

5 group: transmembrane protein

DKFZphtes3\_20h12 encodes a novel 1204 amino acid protein without similarity to known proteins.

10 The novel protein contains 1 transmembrane region and two leucine zippers.  
No informative BLAST results; No predictive prosite, pfam or SCOP motive.

15 The new protein can find application in studying the expression profile of testis-specific genes and as a new marker for testicular cells.

20 putative protein

perhaps complete cds.  
Pedant: TRANSMEMBRANE 1

25 Sequenced by MediGenomix

Locus: unknown

Insert length: 5894 bp

30 Poly A stretch at pos. 5874, no polyadenylation signal found

```

      1 CTCTGCCTTT CCTCTCGCAG CCACCCCTTCC TCTCAGACCA GTACGGTGGC
      51 CGACGGGAGT CAGACGCTGG GGATGAATGA AGGATCAACA AACAGTAATA
35    101 ATGACTGAAT GTACAAGTCT TCAGTTTGTC AGCCCTTTTG CTTTGTAGGC
      151 AATGCAGAAG GTGGATGTTG TTTGCCTGGC ATCTTTAAGT GATCCAGAAT
      201 TAAGACTTCT TCTGCCCTGT TTGGTACGGA TGGCACTTTG TGCACCTGCT
      251 GACCAGAGCC AAAGCTGGGC TCAGGATAAG AAATCATCC TTCGCTTCT
      301 TTCTGGAGTG GAAGCTGTCA ACTCCATTGT TGCATTGTTG TCCGTGGACT
40    351 TTCATGCTTT AGAACAAGAT GCCAGCAAAG AACAGCAGCT TAGGCATAAA
      401 CTTGGAGGAG GCAGTGGAGA GAGCATCCTG GTATCACAGC TTCAGCATGG
      451 ACTGACGTTA GAGTTTGAAC ACAGTGATTC ACCTCGTCGA TTGCGTCTTG
      501 TGCTTAGTGA ACTGTTGGCA ATTATGAACA AGGTGTCTGA GTCCAACGGA
      551 GAATTTTTTT TCAAGTCTTC TGAACTTTTT GAGAGTCCAG TATATTTGGA
45    601 GGAAGCTGCA GATGTACTTT GTATTTTACA AGCAGAGCTC CCTTCCTTGC
      651 TCCCTATAGT TGATGTAGCT GAAGCTTTGC TACATGTTAG AAATGGTGCC
      701 TGGTTCTTGT GTCTCTTGGT GGCCAATGTT CCTGATAGTT TTAATGAAGT
      751 TTGTAGGGGC CTGATAAAAA ATGGAGAACG ACAAGATGAA GAAAGTCTTG
      801 GAGGAAGGCG CAGGACAGAT GCCTTACGCT TCTTGTGTAA AATGAATCCT
50    851 TCTCAGGCCC TCAAGGTCCG AGGCATGGTG GTGGAAGAAT GTCACCTGCC
      901 AGGCCTTGGT GTGGCTTTGA CATTGGATCA TACTAAAAAT GAAGCTTGTG
      951 AGGATGGAGT GAGTGACTTG GTTTGTTTTG TAAGTGGTTT GCTTCTTGGA
     1001 ACAATGCGA AAGTCCGGAC TTGGTTTGGG ACTTTTATCC GAAATGGACA
     1051 GCAGAGAAAA AGAGAGACCA GCAGTTCTGT CCTTTGGCAG ATGAGAAGGC
55    1101 AGCTTCTTCT GGAGTTGATG GGCATTCTTC CCACAGTAAG AAGCACCCGA
     1151 ATTGTGGAAG AAGCTGATGT GGATATGGAG CCCAATGTGT CTGTGTATTC
     1201 GGGGCTGAAA GAAGAGCATG TTGTGAAAGC CAGTGCACCTC TTACGTCTGT
     1251 ACTGTGCTTT GATGGGGATC GCTGGACTCA AACCAACTGA AGAAGAAGCT
```

	1301	GAGCAATTAC	TGCAGTTGAT	GACGAGCCGT	CCTCCTGCTA	CGCCAGCTGG
	1351	GGTTCGCTTT	GTTTCACTTT	CCTTTTGTAT	GCTACTGGCC	TTTTCTACAC
	1401	TTGTCAGTAC	ACCTGAACAG	GAGCAGCTGA	TGGTGGTGTG	GCTAAGTTGG
	1451	ATGATAAAAG	AAGAAGCGTA	TTTTGAGAGT	ACTTCAGGCG	TCTCTGCTTC
5	1501	TTTTGGGGAG	ATGTTATTAT	TGGTGGCTAT	GTACTTTCAC	AGCAACCAGC
	1551	TTAGTGCTAT	CATTGACCTG	GTCTGTTCCA	CTTTGGGGAT	GAAGATTGTA
	1601	ATTAAGCCAA	GCTCCTTGAG	CAGGATGAAG	ACAATCTTCA	CACAGGAAAT
	1651	TTTTACTGAG	CAGGTTGTCA	CAGCTCATGC	AGTTCGGGTC	CCTGTCACCA
	1701	GCAACCTGAG	TGCCAACATT	ACTGGATTTT	TGCCTATTCA	TTGTATTTAC
10	1751	CAGCTTCTCA	GGAGCCGTTT	CTTTACCAAG	CACAAAGTGT	CAATAAAAGA
	1801	TTGGATTTAT	AGACAGCTGT	GTGAAACCTC	TACTCCACTT	CATCCTCAAT
	1851	TACTTCCTTT	GATTGATGTG	TACATAAATT	CTATACTTAC	TCCTGCGTCG
	1901	AAATCTAATC	CAGAAGCCAC	AAATCAGCCA	GTCACAGAAC	AGGAGATACT
	1951	CAATATTTTC	CAAGGAGTCA	TTGGGGGTGA	CAACATCCGC	CTTAATCAGC
15	2001	GTTTCAGTAT	CACAGCACAG	CTTTTGGTGC	TCTACTATAT	ACTGTCTTAT
	2051	GAAGAGGCTC	TTCTAGCAAA	CACGAAGACT	TTAGCTGCCA	TGCAAAGAAA
	2101	GCCCCAAATCA	TATTCTTCTT	CTTTAATGGA	TCAGATTCTT	ATCAAATTCC
	2151	TTATTGACAC	GGCTCAAGGG	CTGCAGCAGG	AGTTGGGAGG	GTTGCATTCA
	2201	GCTTTACTAC	GTCTCCTTGC	TACTAACTAC	CCACATTTAT	GTATTGTGGA
20	2251	TGACTGGATT	TGTGAAGAAG	AAATCACAGG	GACTGATGCC	CTGCTACGGC
	2301	GAATGCTCCT	GACTAATAAT	GCTAAAAATC	ATTCTCCCAA	ACAACCTCAA
	2351	GAAGCATTTC	CAGCTGTCCC	AGTAAATCAC	ACACAAGTGA	TGCAGATTAT
	2401	AGAACACTTG	ACTCTACTCT	CTGCCAGTGA	ACTTATACCA	TATGCGGAAG
	2451	TGTTAACATC	CAATATGAGC	CAGCTATTGA	ATTCAGGGGT	TCCACGGAGA
25	2501	ATTCTGCAAA	CAGTCAATAA	ACTATGGATG	GTTCTTAATA	CTGTGATGCC
	2551	TAGAAGGCTA	TGGGTAATGA	CGGTAAATGC	ACTTCAGCCT	TCAATAAAGT
	2601	TTGTACGACA	ACAAAAGTAT	ACTCAGAATG	ACCTGATGAT	AGATCCTCTC
	2651	ATTGTCCTAA	GGTGTGATCA	GAGGGTTCAC	AGATGCCCCC	CACTGATGGA
	2701	TATTACCCTA	CACATGTTGA	ATGGATATCT	TCTTGCATCT	AAAGCCTACC
30	2751	TTAGTGCTCA	TCTGAAGGAA	ACAGAGCAAG	ATAGGCCTTC	CCAGAATAAT
	2801	ACAATTGGTT	TAGTTGGACA	AACTGATGCT	CCGGAAGTTA	CCAGGGAAGA
	2851	ATTGAAAAAT	GCATTACTGG	CCGCTCAGGA	TAGTGCAGCT	GTCCAGATTCT
	2901	TCTTAGAGAT	TTGCCTACCT	ACTGAAGAGG	AGAAAGCAAA	TGGTGTCAAT
	2951	CCAGATAGCT	TGTTAAGAAA	TGTTCAAAGT	GTTATTACCA	CCAGCGCTCC
35	3001	AAATAAGGGA	ATGGAGGAAG	GAGAAGACAA	TTTGCTCTGT	AACCTTCGAG
	3051	AAGTTCAGTG	CCTTATCTGT	TGTCTCTTGC	ACCAAATGTA	CATTGCAGAT
	3101	CCCAACATTG	CTAAGCTTGT	TCACTTTCAG	GGTTATCCAT	GTGAACTTTT
	3151	GCCTCTGACG	GTCGCAGGTA	TTCCATCTAT	GCACATCTGT	CTAGATTTCA
	3201	TACCTGAGCT	TATTGCACAG	CCAGAACTTG	AGAAACAGAT	ATTTGCTATC
40	3251	CAGTTGCTTT	CTCACTTGTG	TATACAATAT	GCATTACCAA	AGTCACTTAG
	3301	TGTGGCTCGT	TTAGCTGTCA	ATGTCAATGG	AACTTTGTTA	ACAGTTTTAA
	3351	CACAGGCTAA	GCGGTATGCT	TTTTTTATGC	CAACTCTGCC	AAGTTTTGGTC
	3401	TCTTTTTGTC	GAGCATTTC	TCCATTGTAT	GAGGATATTA	TGTCTTTGCT
	3451	GATCCAAATA	GGGCAAGTTT	GTGCCTCTGA	TGTTGCCACT	CAGACAAGAG
45	3501	ACATTGATCC	AATTATTACA	CGTCTTCAAC	AAATAAAGGA	GAAACCAAGT
	3551	GGATGGTCTC	AAATCTGTAA	AGATTCACTT	TATAAAAATG	GATCCAGGGA
	3601	CACTGGAAGC	ATGGATCCTG	ATGTACAGCT	CTGTCACTGT	ATTGAAAGAA
	3651	CAGTAATTGA	AATAATAAAT	ATGAGTGTTA	GTGGAATTTA	AAACAAAATT
	3701	TAAAACAACA	AAAAGTTGTT	TGCTGCATAT	ACCCAACATG	AATCTGCATA
50	3751	TTAGTAACAA	CTCTAAACTG	AATGGGAACA	GTAAGTATT	GTCTTGGAAAT
	3801	CACTAAAACA	ATTCAATTCA	ACATGAGTAT	AGTTTAGAAC	TTTATGAGAA
	3851	TTATGCTTGC	TTGTTTCTGA	TTGGCACATC	TTTGGATCTA	CTTTGCTGAT
	3901	ATGTTTCTAT	TGTAGCAGCT	GAGCTTTTTT	TTTTTCCACT	GGGAACACAT
	3951	GTAAGAAACT	CATTATTGGA	AAGGGAATTT	GGCCTTGTAT	TTAGCTTTTG
55	4001	AAGTGAAGAC	TGCCATGCCCT	TTAATTTCTT	ATAAAAATGA	GTCTGTGGGT
	4051	AGCCCTAGTG	TTTATTTTAA	CTGTGAGCTT	GTAACAGAAT	GTGACAAAGA
	4101	TGCAAAGATG	GGAGAGGAAA	AAAGGGTAAA	GGGAAAGGAG	AATTAAGGAA
	4151	ATAATAGGAG	TTAAAAACAC	AAGTAGAAAT	CTCAAAGATT	TGCAGTGCAA



4201 GTAATAGTAA TGCAAGTTGG AATTCTAGTT CTCAAGAAAG AGTATTGAGA  
4251 AGACTTTTAA AAAGGCAAGT AGCTTTTGTA AATGATTTCT GTGGAAATAC  
4301 AGATGAGGAT TTAAAGATTT CACATATTTG CTTCAATTTT TATTAATATA  
4351 TGAAGCCATA TGTTTAAAGA GATACTTGAA TAATTTGGAA TTTTAAGATA  
5 4401 CTGGTGTAAG AGTGTTTACA GAAACATCTT TGTTCAAAGA AGAACCTGAG  
4451 AGATCTCATT TAGTTTTATG TTTTAAATTT ATTTTATATA TGCTTTATTA  
4501 ACTTACCTAA TGCTCAGAGG GGGGAAATAT GTATCAAATT AAATGAAGGT  
4551 AGAGCAATAA AACCCACTGG ATTAAGAGAGC TCTTGGTTTG TCATCAGGAT  
4601 TATAATTCAT ATCTTACTTT GAGAAGATCT TTGAGTAAGA AAATGCAGTG  
10 4651 TTTGAACCTG AGGAAAAGTT AAAGTGTAAG AAATATTGTC TTGCCGAAGG  
4701 ATTTTGCAGT CCTCTGTCAG TAACCTCCAT TGATTAGGCA GACATATTCA  
4751 GGTAAACCTT AATCATTAAA AAAAAATTAT CAATGTAGAA AGTAATTTCC  
4801 TTTTTTCTCT CTGAGATATA CCTCAATCAC ACACTTCCCC ACCCCCACTT  
4851 GAAACAGACC TCTTCACTTG TGTTTTTTTT TTTTTTTTCC TGAGGTGGAG  
15 4901 TCTTCCCCTG TTGCCCAGGC TGGAGTGCAG TGGGATGATC TTGGCTCACT  
4951 GCAACTTCTG CCACCTGGGT TCAAGGGATT CTCGTGCCTC AACCTCCTGA  
5001 GTAGCTGGGA CTGCAGGCAC GCGCCACCTG TATTTTTGTA TTTTTAGTAG  
5051 AGACGGGGGT TTGCCATGTT GCCCAGACTG GTTTTGAACCT CCTGGCCTCA  
5101 GGTGATCTGC CCACCTTGGC CTCCCAAAGT GCTGGGATTA CAGGTGTGAG  
20 5151 CCACCGCACC TGGCCAGACC GCTTCACTTG TAAAAGAAAT TAGGCTAATA  
5201 AGAAGGTGTA GTTTTTGAGA AATGAAATTT AACTTTAGCC TTTTCACTAG  
5251 TAAATAGTCA CATCTCATTT TCTTCCTTTG TAAAATGGGG TTAATACTGG  
5301 CCCTACCTCA TATTCTATGA GAATGAGTTT GTAGCTGTTT CAAATCATGA  
5351 AGTGCAAGT ATCACATGTG ATAGAATATT TATAACTTTT TATTAGATGC  
25 5401 TTAATGTTCA ATTAAGTAAT TTTGATGTGA AAAATAAAAG TAATAAAAGT  
5451 ATCTTAAAAA TAGCATAAGA ATTTTCATAT TTTTAAACAA GGCAGTTTTG  
5501 TAGTCCCTTA AGATTAAATA CAACTGCTCC TTTTTTTTTT AAAGTGGGC  
5551 CTTGCGATAT TTTGTGTGAA TAGATATGCC CTAGGAGTTC AGAAAAAGTT  
5601 AAAAGTATGT TTTCTAATTA AATGCAGTGC ACATTCCTGG ATCAATATTC  
30 5651 AAAGACTGGT CATAACCTGC TGTGTTAAAA TAATCACATA TGCTCTTTTT  
5701 CATCAGATTT GTTGATGATG TAAATAAAAT GTGTAAATAT ATTAGTAAAT  
5751 GTTAATATTC ATGTATTTTA AGTTAAGGTT ATAAAATTTG TCACAATGTG  
5801 TTTTTTTTATT CAAGTGAAAA CAGATGTGTG CAGCTATTTT GAATATTGGT  
5851 TTATAAACAT TCATATTCTT TATCAAACAA AAAAAAAAAA AAAA

## BLAST Results

40 No BLAST result

## Medline entries

45 No Medline entry

50 Peptide information for frame 2

ORF from 77 bp to 3688 bp; peptide length: 1204

Category: putative protein

55 Classification: unclassified

Prosites motifs: LEUCINE\_ZIPPER (167-184)

LEUCINE\_ZIPPER (692-709)

```

1 MKDQQTIVIMT ECTSLQFVSP FAFEAMQKVD VVCLASLSDP ELRLLLPCLV
5 51 RMALCAPADQ SQSWAQDKKL ILRLLSGVEA VNSIVALLSV DFHALEQDAS
101 KEQQLRHKLK GSGGESILVS QLQHGLTLEF EHS DSPRRLR LVLSELLAIM
5 151 NKVSESNGEF FFKSSELFES PVYLEEAADV LCILQAE LPS LLPIVDVAEA
201 LLHVRNGAWF LCLLVANVPD SFNEYCRGLI KNGERQDEES LGGRRRTDAL
251 RFLCKMNPSQ ALKVRGMVVE ECHLPGLGVA LTL DHTKNEA CEDGVSDLVC
301 FVSGLLLG TN AKVRTWFGTF IRNGQQRKRE TSSSVLWQMR RQLLLELMGI
351 LPTVRSTRIV EEADV DMEPN VSVYSGLKEE HVVKASALLR LYCALMG IAG
10 401 LKPTEEEEAEQ LLQLM TS RPP ATPAGVRFVS LSFCMLLAFS TLVSTPEQEQ
451 LMVVWLSWMI KEEAYFESTS GVSASFGEML LLVAMYFHSN QLSAIIDLVC
501 STLGMKIVIK PSSLSRMKTI FTQEIFTEQV VTAHAVRVPV TSNLSANITG
551 FLPIHCIYQL LRSRSFTKHK VSIKDWIYRQ LCETSTPLHP QLLPLIDVYI
601 NSILTPASKS NPEATNQPV T EQEILNIFQG VIGGDNIRLN QRF SITAQLL
15 651 VLYYILSYEE ALLANTKT LA AMQRKPKSYS SSLMDQIPIK FLIRQAQGLQ
701 QELGGLHSAL LRLLATNYPH LCIVDDWICE EEITGTDALL RRMLLTNNAK
751 NHSPKQLQEA FSAVPVNHTQ VMQIIIEH TL LSASELIPYA EVLTSNMSQL
801 LNSGVPRRIL QTVNKLWMVL NTVMPRRLWV MTVNALQPSI KFVRQQKYTQ
851 NDL MIDPLIV LRCDQRVHRC PPLMDITLHM LNGYLLASKA YLSAHLKETE
20 901 QDRPSQNN TI GLVGQTD APE VTREELKNAL LAAQDSA AVQ ILLEICLPTE
951 EEKANGVNP D SLLRNVSQSVI TTSAPNKGME EGEDNLLCNL REVQCLICCL
1001 LHQMYIADPN IAKLVHFQGY PCELLPLTVA GIPSMHICLD FIPELIAQPE
1051 LEKQIFAIQL LSHLCIQYAL PKSLSVARLA VNVMG TLLTV LTQAKRYAFF
1101 MPTLPSLV SF CRAFTPLYED IMSLLIQIGQ VCASDVATQT RDIDPIITRL
25 1151 QQIKEKPSGW SQICKDSSYK NGRSDTGSM D PDVQLCHCIE RTVIEIINMS
1201 VSGI

```

30

## BLASTP hits

No BLASTP hits available

35

Alert BLASTP hits for DKFZphtes3\_20h12, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphtes3\_20h12, frame 2

40

## Report for DKFZphtes3\_20h12.2

```

45 [LENGTH] 1204
[MW] 134347.53
[pI] 5.75
[HOMOL] TREMBL:CEZC37b_3 gene: "ZC37b.b"; Caenorhabditis
elegans cosmid ZC37b 2e-22
[PROSITE] LEUCINE_ZIPPER 2
50 [KW] TRANSMEMBRANE 1
[KW] LOW_COMPLEXITY 2.57 %
[KW] COILED_COIL 2.33 %

55 SEQ MKDQQTIVIMTECTSLQFVSPFAFEAMQKVDVVCLASLSDPELRLLLPCLVRMALCAPADQ
SEG .....
PRD cccceeeeeeeccceecchhhhhhhhhheeeeeeeccchhhhhhhchhhhhhhhhccccc

```

COILS

MEM .....

5 SEQ SQSWAQDKKLILRLLSGVEAVNSIVALLSVDFHALEQDASKEQQLRHKLGGGSGESILVS  
SEG .....  
PRD hhhhhhhhhhhhhhhhhccccccccccccccccchhhhhhhhhhhhhhhhhccccceeeec  
COILS

10 MEM .....

SEQ QLQHGLTLEFEHSDSPRRLRLVLSELLAIMNKVSESNGEFFFKSSELFESPVYLEEAADV  
SEG .....xxxxxxxxxxxxx.....  
PRD cccccceeeecccccchhhhhhhhhhhhhhhhhhhccccccccccccccccchhhhhhhhh  
COILS

15 MEM .....

20 SEQ LCILQAEPLSLLPIVDVAEALLHVRNGAWFLCLLVANVPDSFNEVCRGLIKNGERQDEES  
SEG .....  
PRD hhhhhhccccchhhhhhhhhhhhhhhhhhhccchhhhhheeeccccccccchhhhhcccccccccc  
COILS

25 MEM .....

SEQ LGGRRRTDALRFLCKMNPSQALKVRGMVVEECHLPGLGVALTDHTKNEACEDGVSDLVC  
SEG .....  
PRD ccccchhhhhhhhhhhccccceeeeeeeeeeeeeccccccccceeeccccccccccccccccceee  
COILS

30 MEM .....

35 SEQ FVSGLLLGTNAKVRTWFGTFIRNGQQRKRETSSSVLWQMRQQLLLELMGILPTVRSTRIV  
SEG .....  
PRD eeccccccccceeeeeeeeeeeecchhhhhccccchhhhhhhhhhhhhhhhhccccceeeeee  
COILS

MEM .....

40 SEQ EEADVDMEPNVSVYSGLKEEHVVKASALLRLYCALMGIAGLKPTEEAEQQLQMTSRPP  
SEG .....  
PRD eeccccccccceeeccccchhhhhhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhhhcccc  
COILS

45 MEM .....

50 SEQ ATPAGVRFVSLSFCLLAFSTLVSTPEQQLMVVWLSWMIKEEAYFESTSGVSASFGEML  
SEG .....  
PRD cccceeeeeehhhhhhhhhhhccccccchhhhhhhhhhhhhhhhhhhccccccccchhhhhh  
COILS

MEM .....MMMMMMMMMMMMMMMM.....

55 SEQ LLVAMYFHSNQLSAIIDLVCSTLGMKIVIKPSSLSRMKTIFTQEIFTEQVVTAHAVRVPV  
SEG .....  
PRD hhhhhhccchhhhhhhhhhhhhhhccccceeeccccchhhhhhhhhhhhhhhhhhhheeeec  
COILS

.....

MEM .....  
5 SEQ TSNLSANITGFLPIHCIYQLLRSRSTKHKVSIKDWIYRQLCETSTPLHPQLPLIDVYI  
SEG .....  
PRD cccccceeeeeehhhhhhhhhhhhhccccccchhhhhhhhhccccccccccccceeee  
COILS .....  
MEM .....  
10 SEQ NSILTPASKSNPEATNQPVTQEILNIFQGVIGGDNIIRLNQRFSSITAQLLVLYILSYEE  
SEG .....  
PRD eccccccccccccccccchhhhhhhhhhhccccccceeeehhhhhhhhhhhhhhhhhhh  
COILS .....  
15 MEM .....  
20 SEQ ALLANTKTAAAMQKPKSYSSSLMDQIPIKFLIRQAQGLQELGGLHSALLRLLATNYPH  
SEG .....xxxxxxxxxxxxxxxxxxxxx.....  
PRD hhhhhhhhhhhhhhhccccccccccccchhhhhhhhhhhhhhhhhhhccccchhhhhhhhhcccc  
COILS .....CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.....  
MEM .....  
25 SEQ LCIVDDWICEEEITGTDALLRRMLLTNNAKNHSPKQLQEAFAVPVNHTQVMQIEHLTL  
SEG .....  
PRD eeeecceeeeeechhhhhhhhhhhhhhhccccccccchhhhhhhhhhhccccchhhhhhhhhhh  
COILS .....  
30 MEM .....  
35 SEQ LSASELIPYAEVLTSNMSQLLNSGVPRRILQTVNKLWMLNTVMPRRLWMTVNALQPSI  
SEG .....  
PRD hhhhhhhhhhhccccchhhhhccccchhhhhhhhhhhhhhhhhccccchhhhhhhccccch  
COILS .....  
40 MEM .....  
45 SEQ KQVVRQKQYTDNDLMIDPLIVLRCDQVRVHRCPLMDITLHMLNGYLLASKAYLSAHLKETE  
SEG .....  
PRD hhhhhhhccccccccccccceeeecccccccccccccceeeccccccchhhhhhhhhhhhhhhhh  
COILS .....  
MEM .....  
50 SEQ QDRPSQNNITIGLVGTDAPEVTREELKNALLAAQDSAQVQILLEICLPTEEEKANGVNP  
SEG .....  
PRD cccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccccccccc  
COILS .....  
55 MEM .....  
60 SEQ SLLRNVQSVITTSAPNKGMEEGEDNLLCNLREVQCLICLLHQMYIADPNIAKL VHFQGY  
SEG .....  
PRD cccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccccccccc  
COILS .....  
MEM .....

30 Prosite for DKFZphtes3\_20h12.2

```

PS00029      167->189    LEUCINE_ZIPPER      PD0C00029
PS00029      692->714    LEUCINE_ZIPPER      PD0C00029

```

35 (No Pfam data available for DKFZphtes3\_20h12.2)

5 group: testis derived

DKFZphtes3\_21k14 encodes a novel 558 amino acid protein without similarity to known proteins.

10 No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

15

unknown protein

perhaps complete cds.

20

Sequenced by LMU

Locus: unknown

25 Insert length: 2547 bp

Poly A stretch at pos. 2506, polyadenylation signal at pos. 2479

```

30  1  GGCCACGTTT  AGCGGACACG  GGAGCAAGAT  GGCATTCCG  GGCAGGCAGT
    51  ATGGGCTTAT  TTTGCCAAAG  AAAACACAGC  AGTTGCACCC  TGTTTTGCAA
   101  AAACCATCAG  TGTTTGGGAA  TGATTCTGAT  GATGATGATG  AGACCTCTGT
   151  GAGTGAAAAGC  CTTCAGAGGG  AAGCTGCTAA  GAAGCAGGCC  ATGAAACAGA
   201  CCAAACCTGGA  AATCCAGAAG  GCCCTTGCA  AAGATGCTAC  TGTGTATGAA
   251  TATGACAGTA  TTTATGATGA  AATGCAGAAA  AAAAAGGAGG  AAAATAATCC
   301  CAAATTGCTT  TTGGGGAAAG  ACAGAAAGCC  CAAGTATATT  CACAACCTGC
   351  TAAAAGCAGT  TGAGATCAGA  AAAAAGGAAC  AGGAAAAAAG  AATGGAAAAA
   401  AAAATACAGA  GAGAACGAGA  AATGGAAAAA  GGGGAGTTTG  ATGATAAAGA
   451  AGCATTTGTG  ACATCTGCAT  ATAAGAAAAA  ACTGCAAGAG  AGAGCTGAAG
   501  AAGAAGAAAG  AGAAAAGAGG  GCTGCTGCAC  TGGAAAGCATG  TTTGGATGTA
   551  ACCAAGCAGA  AAGATCTCAG  TGGATTTTAT  AGGCACCTAT  TAAATCAAGC
   601  AGTTGGTGAA  GAGGAAGTAC  CTAAATGCAG  CTTTCGTGAA  GCCAGATCTG
   651  GTATAAAGGA  AGAAAAATCA  AGGGGCTTCT  CCAATGAAGT  AAGTTCAAAA
   701  AACAGAATAC  CACAAGAGAA  ATGCATTCTT  CAAACTGATG  TGAAAGTAGA
   751  GGAAACCCCA  GATGCAGACA  GTGACTTCGA  TGCTAAGAGC  AGTGCAGGATG
   801  ATGAAATAGA  AGAACTAGA  GTGAACTGCA  GAAGGGAAAA  GGTTCATAGAG
   851  ACCCCTGAGA  ATGACTTCAA  GCACCACAGG  AGTCAAAACC  ACTCTCGGTC
   901  ACCTAGTGAA  GAAAGAGGGC  ACAGTACCAG  GCACCACACG  AAAGGATCAC
   951  GAACGTCGAG  AGGACATGAG  AAAAGGGAAG  ATCAGCACCA  GCAGAAGCAA
  1001  TCCAGAGACC  AAGAGAACCA  TTACACTGAC  CGTGATTACC  GGAAAGAAAG
  1051  GGATTCTCAT  AGGCACAGAG  AGGCCAGTCA  TAGAGATTCC  CATTGGAAGA
  1101  GGCATGAACA  GGAAGATAAA  CCAAGGGCGA  GGGACCAAAG  AGAAAGAAGT
  1151  GACAGAGTAT  GGAAAAGGGA  GAAAGATAGG  GAGAAATATT  CCCAAAGAGA
  1201  ACAAGAAAGA  GATAGACAAC  AAAATGATCA  GAACCGACCC  AGTGAGAAAG
  1251  GAGAGAAGGA  AGAGAAAAGC  AAAGCAAAGG  AAGAGCATAT  GAAAGTAAGG
  1301  AAGGAAAGAT  ATGAAAATAA  TGATAAATAC  AGAGATAGAG  AAAAACGAGA
  1351  GGTAGGTGTT  CAGTCTTCAG  AAAGAAATCA  AGACAGAAAG  GAAAGCAGCC
  1401  CAAATTCTAG  GGCAAAGGAT  AAATTTCTTG  ACCAAGAAAG  ATCCAACAAA
  1451  ATGAGAAACA  TGGCAAAGGA  CAAAGAAAGA  AACCAAGAGA  AACCTCTAA
```

```

1501 TTCTGAATCA TCACTGGGAG CAAAACACAG ACTCACAGAG GAAGGGCAAG
1551 AGAAGGGTAA AGAACAAAGAG AGACCACCTG AGGCAGTGAG CAAGTTTGCA
1601 AAGCGGAACA ATGAAGAAAC TGTAAATGTCA GCTAGAGACA GGTACTTGGC
1651 CAGGCAGATG GCGCGGGTTA ATGCAAAGAC CTATATTGAG AAAGAAGATG
5 1701 ATTGATGGCT ACCCCAAGAG AAAGATTTAA GGAAGCACAG AAAACTGTAA
1751 TTCCTGGAAC CTGCTGCGTA AAACCATAAA GGAGTGTGTT ACCAGTAGTT
1801 TGGAGGGCAT TTTTAAATTT ATTTTCAAAA TTTTAAGTTA AAAGTCAGTC
1851 TTACAGCTTG GATGTTTGGA TGTGGATGTT TGGCTGAATT TATATATAGT
1901 GTGTACTCAT CAATACCACA TTCTTTGTTG TATTCAAGAA CCGTTAAGAG
10 1951 TGTGCTAATT CCCTGTAGGT ACATAATGAG GAAAATTTGC TCCACTACAA
2001 CCATTAAAAA ATAATTTTGG CCAGATACGG TAGCTCGTGC CTGTAATACC
2051 AACATTTTGG GAGGCCAAGG CAGAAGGATA TTGAGGCTAG GCATTCAAGA
2101 CCAGCCTAGG CAGGATAATA AGACCTTGTC TCTATTTAAA AAACAAAAAG
2151 CCTAGCATGG TAGTCCATGC CTGTAGTCCC AGCTGTTTGA GAGGCTGAGG
15 2201 CAAGAAGATC ACTTGAGCCT AGGAATTTGA TGTTACAGTG AGGTATGATC
2251 ATGCCACTGC ACTCCAACCT GGGCAACAGA ATGAGACCCT GTCTCTAAAA
2301 AATTTTTTTT AAATAAATAA TTTAACTCTT CTAATAATGT TTTGTTGCAG
2351 GAAATGTATT TCAGATAAAA TATGGATTTG AAAAACAGAA AATATACTTT
2401 ATGTTCTGAA ATTTGTATTT AAGTATAAAA TGTGAATCAT CTTGTCTAAA
20 2451 TAGCTTACAG CATAGTTGGC TTAAATGAAA ATAAAATGAT ATGCTTATAC
2501 ATTTGGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAG

```

## BLAST Results

25

No BLAST result

## Medline entries

30

No Medline entry

## Peptide information for frame 2

35

```

40 ORF from 29 bp to 1702 bp; peptide length: 558
Category: similarity to unknown protein
Classification: Nucleic acid management

```

```

45 1 MAIPGRQYGL ILPKKTQQLH PVLQKPSVFG NDSDDDDETS VSESLQREAA
51 KKQAMKQTKL EIQKALAEDA TVEYDSIYD EMQKKKEENN PKLLLKGDRK
101 PKYIHNLLKA VEIRKKEQEK RMEKKIQER EMKGEFDDK EAFVTSAYKK
151 KLQERAEEEE REKRAAALEA CLDVTQKQDL SGFYRHLLNQ AVGEEVVPKC
201 SFREARSGIK EEKSRGFSNE VSSKNRIPQE KCILQTDVKV EENPDADSD
251 DAKSSADDEI EETRVNCRRE KVIETPENDF KHHRSQNHRS SPSEERGHST
50 301 RHHTKGSRTS RGHEKREDQH QQKQSRDQEN HYTDYRKE RDSHRHREAS
351 HRDSHWKRHE QEDKPRARDQ RERSDRVWKR EKDRKYSQR EQERDRQQND
401 QNRPSEKGEK EEKSKAKEEH MKVRKERYEN NDKYRDREKR EVGVQSSERN
451 QDRKESSPNS RAKDKFLDQE RSNKMRNMAK DKERNQEKPS NSESSLGAKH
501 RLTEEGQEKG KEQERPPEAV SKFAKRNNEE TVMSARDRYL ARQMARVNAK
55 551 TYIEKEDD

```

## BLASTP hits

No BLASTP hits available

5 Alert BLASTP hits for DKFZphtes3\_21k14, frame 2

No Alert BLASTP hits found

10 Pedant information for DKFZphtes3\_21k14, frame 2  
-----

## Report for DKFZphtes3\_21k14.2

15 [LENGTH] 567  
 [MW] 67262.89  
 [pI] 8.96  
 [HOMOL] TREMBL:AC006233\_14 gene: "F12K2.14"; Arabidopsis  
 thaliana chromosome II BAC F12K2 genomic sequence, complete  
 20 sequence. 3e-11  
 [FUNCAT] 04.99 other transcription activities [S. cerevisiae,  
 YKR092c] 1e-05  
 [FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKR092c]  
 1e-05  
 25 [FUNCAT] 06.07 protein modification (glycosylation, acylation,  
 myristylation, palmitylation, farnesylation and processing)  
 [S. cerevisiae, YKL201c] 1e-04  
 [BLOCKS] PF00748F  
 [BLOCKS] BL01182E Glycosyl hydrolases family 35 proteins  
 30 [EC] 2.7.1.37 Protein kinase 7e-06  
 [EC] 5.99.1.2 DNA topoisomerase 4e-06  
 [PIRKW] phosphotransferase 7e-06  
 [PIRKW] pre-mRNA splicing 1e-06  
 [PIRKW] citrulline 3e-06  
 35 [PIRKW] tandem repeat 3e-06  
 [PIRKW] DNA binding 4e-06  
 [PIRKW] DNA replication 4e-06  
 [PIRKW] isomerase 4e-06  
 [PIRKW] ATP 3e-06  
 40 [PIRKW] phosphoprotein 1e-06  
 [PIRKW] calcium binding 3e-06  
 [PIRKW] alternative splicing 7e-06  
 [PIRKW] P-loop 3e-06  
 [PIRKW] EF hand 3e-06  
 45 [PIRKW] hair 3e-06  
 [SUPFAM] DEAD/H box helicase homology 3e-06  
 [SUPFAM] unassigned Ser/Thr or Tyr-specific protein kinases 4e-  
 06  
 [SUPFAM] calmodulin repeat homology 3e-06  
 50 [SUPFAM] unassigned ribonucleoprotein repeat-containing proteins  
 1e-06  
 [SUPFAM] unassigned DEAD/H box helicases 3e-06  
 [SUPFAM] trichohyalin 3e-06  
 [SUPFAM] protein kinase homology 4e-06  
 55 [SUPFAM] eukaryotic type I DNA topoisomerase 4e-06  
 [SUPFAM] ribonucleoprotein repeat homology 1e-06  
 [KW] All\_Alpha  
 [KW] LOW\_COMPLEXITY 22.75 %



5 SEQ ATFSGHGSKMAIPGRQYGLILPKKTQQLHPVLQKPSVFGNDSDDDDDETSVSESLQREAAK  
SEG .....xxxxxxxxxxxxxxxx.....  
PRD cccccccccccccccccceccccccccccccccccccccccccccccchhhhhhhhhh

10 SEQ KQAMKQTKLEIQKALAEDATVYEYDSIYDEMOKKKEENNPKLLLKGKDRPKYIHNLLKAV  
SEG .....xxxxxxxxxxxxxxxx.....  
PRD hhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhhhhchhhhhhhccccchhhhhhhhhh

15 SEQ EIRKKEQEKMEKKIQREREMEKGEFDDKEAFVTSAYKKKLQERAEEREKRAAALEAC  
SEG xxx.....  
PRD hhhhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

20 SEQ LDVTKQKDLSGFYRHLLNQAVGEEVPKCSFREARSGIKEEKSRGFSNEVSSKNRIPQEK  
SEG .....  
PRD hhhhhhhccchhhhhhhhhhhhhccccccccccccchhhhhhhhhhhhhhhhhhhhhhhh

25 SEQ CILQTDVKVEENPDADSDFDAKSSADDEIEETRVNCRREKVIETPENDFKHHRSQNHRS  
SEG .....xxxxxxxxxxxxxxxx.....  
PRD hhhhhhhhhhhccccchhhccc

30 SEQ PSEERGHSTRHHTKGSRTSRGHEKREDQHQKQSRDQENHYTDRDYRKERDSHRHREASH  
SEG .....  
PRD cccccchhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhchh

35 SEQ RDSHWKRHEQEDKPRARDQRERSDRVWKREKDREKYSQREQERDRQQNDQNRPSEKGEKE  
SEG .....xxxxxxxxxxxxxxxx.....  
PRD hhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccccchh

40 SEQ EKSKAKEEHMKVRKERYENNDKYRDREKREVGVSSESNQDRKESSPNSRAKDKFLDQER  
SEG xxxxxxxxxxx.....  
PRD hhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhchhhhhhhhhhhhhhhhhh

45 SEQ SNKMRNMAKDKERNQEKPSNSESSLGAKHRLTEEGQEKGKEQERPPEAVSKFAKRNEET  
SEG .....xxxxxxxx.....  
PRD hhhhhhhhhhhhhhhhhccccchhhhhccccchhhhhhhhhhhhhccccchhhhhhhccccch

50 SEQ VMSARDRYLARQMARVNAKTYIEKEDD  
SEG .....  
PRD hhhhhhhhhhhhhhhhhchhhhhcccc

(No Prosite data available for DKFZphtes3\_21k14.2)

(No Pfam data available for DKFZphtes3\_21k14.2)

5 group: testis derived

DKFZphtes3\_22i11 encodes a novel 580 amino acid protein with  
similarity to RCC1-like G exchanging factor RLG, UVR8 (UVB-  
10 resistance protein) of Arabidopsis thaliana and to the murine  
retinitis pigmentosa GTPase regulator.

No informative BLAST results; No predictive prosite, pfam or SCOP  
motife.

15 The new protein can find application in studying the expression  
profile of testis-specific genes.

Homo sapiens chromosome 7q22 sequence, ORF4, extension  
20 differences to genmodel of ORF4,  
differential splicing

Sequenced by LMU

25 Locus: /map="7q22"

Insert length: 2236 bp

30 Poly A stretch at pos. 2197, polyadenylation signal at pos. 2180

```

1  ACAATGCTCA GATCGGGAGG TGGAGCCAAT CAGGTCCAAC CAAGAGGAGG
51  GGACACCGGC ACTCCACTAG CAGGAAAACG GGCCGAGGGA CCGCAAGCAG
101 GGGGTGCCTA GTCCTCGTCC CCCAAAGACC AATCGTAAGC CAGATACAGG
35 151 CGAGTGACTG TCAAGAAGGC CAATTAGAGC CTCCGAAGGG AATCTGGACC
201 TGCCTCTTCT CTGAGGGGACG GCTCTACCTA CCAATAGCAT GGGCGAGAAG
251 GCGGTCCCTT TGCTAAGGAG GAGGCGGGTG AAGAGAAGCT GCCCTTCTTG
301 TGGCTCGGAG CTTGGGGTTG AAGAGAAGAG GGGGAAAGGA AATCCGATTT
351 CCATCCAGTT GTTCCCCCA GAGCTGGTGG AGCATATCAT CTCATTCTCT
40 401 CCAGTCAGAG ACCTTGTTGC CCTCGGCCAG ACCTGCCGCT ACTTCCACGA
451 AGTGTGCGAT GGGGAAGGCG TGTGGAGACG CATCTGTGCG AGACTCAGTC
501 CGCGCCTCCA AGATCAGGGT TCTGGAGTCC GGCCCTGGAA GAGAGCTGCC
551 ATTCTGAACT ACACGAAGGG CCTGTATTTC CAGGCATTTG GAGGCCGCCG
601 CCGATGTCTC AGCAAGAGCG TGGCCCCCTT GCTAGCCCAC GGCTACCGCC
45 651 GCTTCTTGCC CACCAAGGAT CACGTCTTCA TTCTTGACTA CGTGGGGACC
701 CTCTTCTTCC TCAAAAATGC CCTGGTCTCC ACCCTCGGCC AGATGCAGTG
751 GAAGCGGGCC TGTGCTATG TTGTGTTGTG TCGTGGAGCC AAGGATTTTG
801 CCTCGGACCC AAGGTGTGAC ACAGTTTACC GTAAATACCT CTACGTCTTG
851 GCCACTCGGG AGCCGCAGGA AGTGGTGGGT ACCACCAGCA GCCGGGCGTG
50 901 TGA CTGTGTT GAGGTCTATC TGCAGTCTAG TGGGCAGCGG GTCTTCAAGA
951 TGACATTCCA CCACTCAATG ACCTTCAAGC AGATCGTGCT GGTGGTTCAG
1001 GAGACCCAGC GGGCTCTACT GCTCCTCACA GAGGAAGGAA AGATCTACTC
1051 TTTGGTAGTG AATGAGACCC AGCTTGACCA GCCACGCTCC TACACGGTTC
1101 AGCTGGCCCT GAGGAAGGTG TCCCACTACC TGCCTCACCT GCGCGTGGCC
55 1151 TGCATGACTT CCAACCAGAG CAGCACCTC TACGTCACAG ACCAGGGGGG
1201 AGTGTATTTT GAGGTGCATA CCCAGGGGT GTATCGCGAT CTCTTTGGGA
1251 CCCTTCAAGC CTTTGACCCC CTGGACCAGC AGATGCCGCT TGCTCTCTCA
1301 CTGCCTGCCA AGATCCTATT CTGTGCTCTT GGCTACAACC ACCTTGGCCT
```

```

1351 GGTGGATGAA TTTGGCCGAA TCTTCATGCA AGGAAATAAC AGATACGGGC
1401 AGCTAGGAAC AGGGGACAAA ATGGACCGAG GGGAAACCCAC ACAGGTTTGT
1451 TACCTGCAGC GGCCCATCAC CCTGTGGTGC GGCCTCAACC ACTCCCTGGT
1501 GCTGAGCCAG AGCTCAGAGT TCAGCAAGGA GCTGCTGGGC TGC GGCTGTG
5 1551 GGGCTGGGGG CCGCCTCCCA GGCTGGCCCA AGGGGAGTGC CTCCTTCGTC
1601 AAGCTCCAAG TCAAGGTCCC TCTGTGTGCC TGTGCCCTCT GTGCCACCAG
1651 GGAGTGCCTA TACATCCTGT CCAGCCACGA CATTGAGCAG CACGCCCCCT
1701 ATCGCCACCT GCCAGCCAGC AGGGTGGTGG GGA CTCTGA GCCCAGCCTG
1751 GGGGCCAGAG CACCCAGGA CCCC GGGGGG ATGGCCAGG CCTGCGAGGA
10 1801 GTACCTCAGC CAGATCCACA GTTGCCAAAC GTTG CAGGAC CGCACGGAGA
1851 AGATGAAGGA GATCGTAGGG TGGATGCCCC TGATGGCCGC ACAGAAGGAC
1901 TTCTTCTGGG AGGCCCTGGA CATGCTGCAG AGGGCTGAAG GAGGCGGGGG
1951 TGGTGTAGGG CCCCCAGCCC CTGAGACCTA ATCCCCCTCA TGCTAGCCTA
2001 GTCCCTGGAG GAGGGAGTCC GGCCCCAGGC CAGGGACTAA GGAGCAATGA
15 2051 CCATTGTGCA CATGCGTGTG GGAAGGGGTT GCTAGGGGGT GGGGACGGCT
2101 AACCAGGGTA AGAATGTTCA GGGGGCTGCC CAGGAGGGGC CCCCACCTG
2151 ACTATCATGG ACAAGAGATT TGATGGATAG AATAAAAGGC TGCAGCGAAA
2201 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAG

```

20

## BLAST Results

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Entry AF053356 from database EMBL:

25 Homo sapiens chromosome 7q22 sequence, complete sequence.

Score = 2952, P = 0.0e+00, identities = 666/729

10 exons

30

## Medline entries

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No Medline entry

35

## Peptide information for frame 2

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40

ORF from 239 bp to 1978 bp; peptide length: 580

Category: similarity to unknown protein

Classification: no clue

```

45 1 MGEKAVPLLR RRRVKRSCPS CGSELGVEEK RGKGNPISIQ LFPPELVEHI
51 ISFLPVRDLV ALGQTCRYFH EVCDGEGVWR RICRRLSPRL QDQSGSVRPW
101 KRAAILNYTK GLYFQAFGGR RRCLSKSVAP LLAHGYRRFL PTKDHVFILD
151 YVGTLLFFLKN ALVSTLGQMQ WKACRYVVL CRGAKDFASD PRCDTVYRKY
201 LYVLATREPQ EVVGTSSRA CDCVEVYLQS SGQRVFKMTF HHSMTFKQIV
50 251 LVGQETQRAL LLLTEEGKIY SLVVNETQLD QPRSYTVQLA LRKVSHYLP
301 LRVACMTSNQ SSTLYVTDAQ GVFVHTPG VYRDLFGTLQ AFDPLDQAMP
351 LALSIPAKIL FCALGYNHGL LVDEFGRIFM QGNNRYGQLG TGDKMDRGE
401 TQVCYLQRP I TLWCGLNHS LVSQSSEFSK ELLGCGCGAG GRLPGWPKGS
451 ASFVKLQVKV PLCACALCAT RECLYLSSH DIEQHAPYRH LPASRVVGT
55 501 EPSLGARAPQ DPGGMAQACE EYLSQIHSCQ TLQDRTEKMK EIVGWMLMA
551 AQKDFFW EAL DMLQRAEGGG GVGPPAPET

```

## BLASTP hits

No BLASTP hits available

5

Alert BLASTP hits for DKFZphtes3\_22111, frame 2

TREMBL:AF053356\_11 product: "ORF4"; Homo sapiens chromosome 7q22 sequence, complete sequence., N = 1, Score = 1554, P = 1.6e-159

10

TREMBL:AF130441\_1 gene: "UVR8"; product: "UVB-resistance protein UVR8"; Arabidopsis thaliana UVB-resistance protein UVR8 (UVR8) mRNA, complete

15

cds., N = 1, Score = 109, P = 0.0082

TREMBL:AF044677\_1 gene: "Rpgr"; product: "retinitis pigmentosa GTPase regulator"; Mus musculus retinitis pigmentosa GTPase regulator (Rpgr) mRNA, complete cds., N = 1, Score = 106, P = 0.035

20

>TREMBL:AF053356\_11 product: "ORF4"; Homo sapiens chromosome 7q22 sequence, complete sequence.  
Length = 318

25

HSPs:

30

Score = 1554 (233.2 bits), Expect = 1.6e-159, P = 1.6e-159  
Identities = 303/318 (95%), Positives = 303/318 (95%)

Query: 1  
MGEKAVPLLRRRRVKRSCPCGSELGVEEKRGKGNPISIQLFPPPELVEHIISFLPVRDLV 60

35

MGEKAVPLLRRRRVKRSCPCGSELGVEEKRGKGNPISIQLFPPPELVEHIISFLPVRDLV  
Sbjct: 1  
MGEKAVPLLRRRRVKRSCPCGSELGVEEKRGKGNPISIQLFPPPELVEHIISFLPVRDLV 60

40

Query: 61  
ALGQTCRYFHEVCDGEGVWRRICRRLSPRLQDQSGSVRPWKRAAILNYTKGLYFQAFGGR 120  
ALGQTCRYFHEVCDGEGVWRRICRRLSPRLQDQ

TKGLYFQAFGGR

45

Sbjct: 61 ALGQTCRYFHEVCDGEGVWRRICRRLSPRLQDQD-----  
TKGLYFQAFGGR 106

Query: 121  
RRCLSKSVAPLLAHGYRRFLPTKDHVFILDYVGTLFFLKNALVSTLGQMQRACRYVVL 180

50

RRCLSKSVAPLLAHGYRRFLPTKDHVFILDYVGTLFFLKNALVSTLGQMQRACRYVVL  
Sbjct: 107  
RRCLSKSVAPLLAHGYRRFLPTKDHVFILDYVGTLFFLKNALVSTLGQMQRACRYVVL 166

55

Query: 181  
CRGAKDFASDPRCDTVYRKLYVLATREPQEVVGTSSRACDCVEVYLQSSGQRVFKMTF 240

CRGAKDFASDPRCDTVYRKLYVLATREPQEVVGTSSRACDCVEVYLQSSGQRVFKMTF



```

      SEQ    EIVGWMPMAAQKDDFFWEALDMLQRAEGGGGGVGPPAPET
      SEG    .....xxxxxxxx.....
15 PRD     hhhhcchhhhhhhhhhhhhhhhhhhhhc cccceeecccccc

```

20 (No Pfam data available for DKFZphtes3\_22i11.2)

5 group: testis derived

DKFZphtes3\_22124 encodes a novel 451 amino acid protein with similarity to the F-box protein FBL2 of the rat.

10 No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

15

similarity to p37NB (Homo sapiens)

Sequenced by LMU

20

Locus: /map="7q22-q31.1"

Insert length: 1537 bp

Poly A stretch at pos. 1459, no polyadenylation signal found

25

```

    1 CAACAGGACG ATGCGACTCC TGCCGAGGCA CTTCCACAAC TTACAGAATC
  51 TTAGTTTGGC TTATTGCAGA CGGTTACACG ACAAAGGCTT ACAGTACCTG
101 AACTTGGGGA ATGGATGCCA CAAGCTCATC TATCTGGACC TCTCTGGCTG
 151 CACCCAGATT TCAGTCCAAG GCTTCAGGTA CATTGCAAAC AGCTGCACTG
201 GAATTATGCA TCTTACCATT AATGACATGC CAACTCTGAC GGACAACTGT
 251 GTAAAAGCTT TAGTTGAAAA ATGCTCTCGT ATTACATCGC TGGTTTTTAC
301 TGGTGCACCG CATATCTCCG ATTGTACTTT CAGAGCTCTT TCTGCTTGTA
 351 AACTCAGAAA GATCCGATTT GAAGGAAATA AAAGGGTTAC TGATGCATCC
35 401 TTCAAATTTA TAGACAAGAA TTATCCAAAT CTCAGTCACA TTTATATGGC
 451 TGA CTGCAAG GGAATAACAG ACAGCAGCCT CAGATCCCTT TCACCTTTGA
501 AGCAACTGAC TGTGTTGAAT TTGGCAAATT GTGTAAGAAT TGGTGATATG
 551 GGA CTAAAGC AATTTCTTGA TGGTCCTGCA AGCATGAGGA TAAGAGAGCT
601 AAATTTAAGC AACTGTGTGC GGCTAAGTGA TGCCTTTGTT ATGAAACTAT
40 651 CTGAGCGCTG CCCTAATTTA AACTACTTGA GTTTACGAAA TTGTGAACAT
 701 TTGACTGCCC AAGGAATTGG ATATATTGTA AACATCTTTT CCTTGGTATC
 751 AATAGATCTC TCTGGAACAG ACATCTCTAA TGAGGGTTTG AATGTGCTTT
801 CCAGACATAA AAAATTGAAG GAACCTTCTG TATCTGAATG TTATAGAATC
 851 ACTGATGATG GAATTCAGGC ATTCTGCAAA AGCTCACTGA TCTTGGAACA
45 901 TTTGGATGTC TCTTATTGCT CCCAGCTGTC AGATATGATT ATCAAAGCAC
 951 TGGCCATTTA CTGCATTAAC CTCACATCTC TCAGCATTGC TGGCTGTCCA
1001 AAGATTACTG ACTCAGCAAT GGAGATGTTA TCGGCAAAAT GCCATTACCT
1051 GCACATTTTG GATATCTCTG GTTGTGTCTT GCTTACTGAC CAAATCCTTG
1101 AGGACCTTCA GATAGGCTGC AAACAACCTC GGATCCTTAA GATGCAATAC
50 1151 TGCACAAATA TTTCCAAGAA GGCAGCTCAA AGAATGTCAT CTAAAGTTCA
 1201 GCAGCAGGAA TACAACACTA ATGACCTTCC ACGTTGGTTT GGCTATGATA
 1251 GGGAAAGGAAA CCCTGTTACA GAGCTTGACA ACATAACATC ATCTAAAGGA
1301 GCCTTAGAAT TAACAGTGAA AAAGTCAACA TACAGCAGTG AAGACCAAGC
1351 AGCGTGACCT TCAGCCTCAA GCAGGAAGAA CAAAAAATCA AGAAGTTGGC
55 1401 AAGTTTTCTC CATTTGTTGC AAGTATGTTT ACTAGCTGAA TCTCAATAAC
 1451 AATGTAAACA AGCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
1501 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAG
```

## BLAST Results

-----

5 Entry AC005250 from database EMBL:  
Homo sapiens BAC clone RG318M05 from 7q22-q31.1, complete  
sequence.  
Score = 830, P = 1.8e-124, identities = 180/193

10 Entry HS32907 from database EMBL:  
Human p37NB.mRNA, complete cds.  
Score = 318, P = 4.6e-04, identities = 70/78

15

## Medline entries

-----

97136875:  
20 Kim D, LaQuaglia MP, Yang SY.; A cDNA encoding a putative 37 kDa  
leucine-rich repeat  
(LRR) protein, p37NB, isolated from S-type neuroblastoma  
cell has a differential tissue distribution. Biochim Biophys Acta  
1996  
25 Dec 11;1309(3):183-8

30

## Peptide information for frame 2

-----

ORF from 11 bp to 1354 bp; peptide length: 448  
Category: similarity to known protein  
35 Classification: unclassified

1 MRLLPRLFHN LQNLSLAYCR RFTDKGLQYL NLGNGCHKLI YLDLSGCTQI  
51 SVQGFRYIAN SCTGIMHLTI NDMPTLTDNC VKALVEKCSR ITSLVFTGAP  
101 HISDCTFRAL SACKLRKIRF EGNKRVTAS FKFIDKNYPN LSHIYMADCK  
40 151 GITDSSLRSL SPLKQLTVLN LANCVRIGDM GLKQFLDGPA SMRIEELNLS  
201 NCVRLSDAFV MKLSERCPNL NYLSLRNCEH LTAQGGIGYIV NIFSLVSLDL  
251 SGTDISNEGL NVLSRHKKLK ELSVSECYRI TDDGIQAFCK SSLILEHLDV  
301 SYCSQLSDMI IKALAIYCIN LTSLSIAGCP KITDSAMEML SAKCHYLHIL  
351 DISGCVLLTD QILEDLQIGC KQLRILKMQY CTNISKKAAQ RMSSKVQQQE  
45 401 YNTNDPPRWF GYDREGNPVT ELDNITSSKG ALELTVKKST YSSEDQAA

## BLASTP hits

50

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3\_22124, frame 2

55 No Alert BLASTP hits found

Pedant information for DKFZphtes3\_22124, frame 2

-----



## Report for DKFZphtes3\_22124.2

```

5  [LENGTH]  451
   [MW]      50545.95
   [pI]      8.68
   [HOMOL]    TREMBLNEW:AF186273_1 product: "leucine-rich
10  repeats containing F-box protein FBL3"; Homo sapiens leucine-rich
   repeats containing F-box protein FBL3 mRNA, complete cds. 8e-31
   [FUNCAT]  11.01 stress response    [S. cerevisiae, YJR090c] 8e-20
   [FUNCAT]  03.01 cell growth       [S. cerevisiae, YJR090c] 8e-20
   [FUNCAT]  08.19 cellular import   [S. cerevisiae, YJR090c] 8e-20
   [FUNCAT]  03.22 cell cycle control and mitosis [S. cerevisiae,
15  YJR090c] 8e-20
   [FUNCAT]  03.04 budding, cell polarity and filament formation
           [S. cerevisiae, YJR090c] 8e-20
   [FUNCAT]  01.05.04 regulation of carbohydrate utilization [S.
20  cerevisiae, YJR090c] 8e-20
   [FUNCAT]  11.04 dna repair (direct repair, base excision repair
   and nucleotide excision repair) [S. cerevisiae, YJR052w] 3e-07
   [FUNCAT]  30.10 nuclear organization [S. cerevisiae, YJR052w]
3e-07
   [BLOCKS]  PR00019B
25  [BLOCKS]  PR00364D
   [BLOCKS]  BP01921A
   [BLOCKS]  BP03743B
   [PIRKW]    tandem repeat 2e-18
   [PIRKW]    zinc finger 1e-07
30  [PIRKW]    DNA binding 1e-07
   [SUPFAM]  leucine-rich alpha-2-glycoprotein repeat homology 2e-18

   [SUPFAM]  regulatory protein ESAG8c 1e-07
   [KW]      Alpha_Beta
35

   SEQ  NRTMRLLP RHFHNLQNL SLAYCRRFTDKGLQYLN LGNGCHKLIYLDLSGCTQISVQGFYR
   PRD  cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

40  SEQ  IANSCTGIMHLTINDMPTLT DNCVKALVEKCSRITSLVFTGAPHISDCTFRALSACKLRK
   PRD  cccccccccccccccccccccchhhhhhhhhhhccccccccccccccccccccccccccccccc

   SEQ  IRFEGNKRVT DASFKFIDKNYPNL SHIYMA DCKGITDSSLRSL SPLKQLTVLNL ANCVRI
   PRD  eccccccccccccccccccccccccccccccccccccccccchhhhhhhhhcccccccccccccccccc

45  SEQ  GDMGLKQFLDGPASMRIRELNLSNCVRLSDAFVMKLSERCPNLNYLSLRNCEHLTAQGIG
   PRD  cccccccccccccccccccccccccccccccccccccccccchhhhhhhhhcccccccccccccccccc

   SEQ  YIVNIFSLVSI DLSGTDISNEGLNVLSRHKKL KELS VSECYRITDDGIQAFCKSSLILEH
50  PRD  eccccccccccccccccccccccccchhhhhhhhhccccccccccccccccccccchhhhhhhhhcccccccccc

   SEQ  LDVSYCSQLSDMI IKALAIYCINLTSL SIAGCPKITDSAMEMLSAKCHYLHILDISGCVL
   PRD  cccccccccchhhhhhhhhccccccccccccccccccccchhhhhhhhhhhcccccccccccccccccc

55  SEQ  LTDQILEDLQIGCKQLRILKMQYCTNISKKAAQRMSSKVQQAQ EYNTNDPPRWFGYDREGN
   PRD  chhhhhhhhhhhcchhhhhhhccccccccchhhhhhhhhhhhhhecccccccccccccccccccccc

   SEQ  PVTELD NITSSKGALELTVKKSTYSSDQAA

```

5

(No Pfam data available for DKFZphtes3\_22124.2)

5 group: testis derived

DKFZphtes3\_26g3 encodes a novel 1090 amino acid protein without similarity to known proteins.

10 No informative BLAST results; No predictive prosite, pfam or SCOP motif.

The new protein can find application in studying the expression profile of testis-specific genes.

15

similarity to C.elegans CD9D4.4

20 on genomic level encoded by HSDJ198I9  
perhaps complete cds.

Sequenced by EMBL

Locus: /map="b"

25

Insert length: 4562 bp

Poly A stretch at pos. 4550, polyadenylation signal at pos. 4515

```
30      1 GATTCAGTTA CTGAAGACTT AGATGCACCC TGGATGGGAA TTCAGAATCT
      51 TCAGAGATCA GAGTCCAGTA AAATGGATAA ATATGAGACT GAAGAAAGCT
     101 CTGTAGCAGG ACTTTCTAGC CCAGAGTTGA AAGTCAGACC TGCTGGTGCC
     151 TCCAGTATTT GGTATACAGA AGGTGAAAAG CAGCTAACAA AATCTCTAAA
     201 AGGAAAGAAT GAAGAATCAA ATAAATCCAA AGTTAAGGTT ACTAAGCTTA
     35  251 TGA AAAACAAT GAAATCTGAA AACACAAAAA AATTAATAAA ACAGAACTCT
     301 AAGGATTCTG TGGTTTTGGT AGGCTACAAA TGTTTGAAAA GTACAGCATC
     351 AAATGATCTC ATTAAATGCT TTGAAGGCAA TCCTTCACAT AGTCAGAAGG
     401 AAGGTCTGGA TCCCACAATA TGTGGATATA ATTTTGACCC AAAGACCTAC
     451 ATGAGACAGA CAAGTCAAAA GGAAGCTAGC TGTTTGCCAA CTAATACAGA
     40  501 GAGAACTGAA CAAAAGTCTC CAGATATTGA AAATGTTCAA CCAGACCAGT
     551 TTGATCCTTT GAACTCTGGC AACCTAAATC TTTGTGCAAA TTTGTCCATT
     601 TCAGGTAAAC TTGATATCTC CCAGGACGAT AGTGAAATTA CACAAATGGA
     651 ACACAATCTG GCATCCAGAA GGTCATCAGA CGATTGCCAT GATCATCAAA
     701 CAACCCCATC TTTGGGAGTT AGAACAATTG AAATAAAGCC CAGTAATAAA
     45  751 GATCCTTTCA GTGGAGAGAA TATAACTGTC AAAGTAGGAC CTTGGACAGA
     801 GCTTCGACAA GAGGAAATAC TTGTGGATAA TTTACTACCC AACTTTGAGT
     851 CCTTAGAATC TAATGGTAAA TCTAAATCTA TAGAAATAAC ATTTGAAAAG
     901 GAAGCTTTGC AAGAAGCAAA GTGTCTTTCT ATTGGAGAAT CATTAATAA
     951 ATTACGAAGT AATCTACCTG CCCCTTCTAC AAAAGAATAT CATGTTGTAG
     50 1001 TAAGTGGAGA TACAATTAAG TTACCAGATA TTAGTGCCAC ATATGCCTCA
     1051 TCTAGATTTT CAGATTGAGG TGTTGAAAAGT GAACCGAGTT CTTTTGCGAC
     1101 ACATCCAAAC ACTGATTTAG TCTTTGAAAC TGTGCAAGGG CAAGGTCTTT
     1151 GCAATAGTGA AAGATTATTT CCTCAGCTTT TGATGAAACC TGATTATAAT
     1201 GTAAAATTTT CATTAGGAAA TCATTGTACT GAGAGTACAA GTGCTATAAG
     55 1251 TGAAATACAG TCATCTTTGA CATCCATAAA CTCTCTACCC TCCGATGATG
     1301 AACTGTCACC TGATGAAAAT TCTAAGAAAT CTGTTGTACC TGAATGCCAT
     1351 CTAAATGATA GCAAACTGT ATTAATCTA GGAACGACTG ATTTGCCAAA
     1401 ATGTGATGAT ACTAAAAAGT CAAGTATCAC TTTGCAACAG CAGAGTGTTG
```

	1451	TATTTTTCAGG	GAACCTTGGAC	AATGAAACTG	TAGCAATACA	TTCCTTAAAT
	1501	TCAAGCATT	AAGACCCTTT	ACAATTTGTT	TTTTTCAGATG	AAGAGACTTC
	1551	CAGTGATGTG	AAAAGTAGTT	GCAGCTCCAA	ACCTAACTTG	GATACTATGT
	1601	GTAAGGCTT	CCAGAGTCCT	GATAAATCTA	ATAACTCTAC	AGGGACAGCA
5	1651	ATTACATTAA	ATTCAAAACT	GATTTGTTTA	GGCACTCCTT	GTGTCAATTC
	1701	AGGTTCCATT	TCTAGTAATA	CAGATGTTAG	TGAAGATAGA	ACTATGAAAA
	1751	AAAATAGTGA	TGTATTAAAT	CTCACACAGA	TGTATTTCAGA	AATCCCTACA
	1801	GTTGAAAGTG	AAACTCATCT	GGGTACAAGT	GATCCTTTTT	CAGCCAGTAC
	1851	TGATATAGTA	AAGCAAGGGC	TTGTGGAAAA	TTATTTTGGT	TCTCAAAGCA
10	1901	GTACGGATAT	TTCTGACACA	TGTGCTGTTA	GCTACAGCAA	TGCACTTAGC
	1951	CCTCAGAAGG	AAACTTCTGA	AAAAGAAATT	AGTAATCTTC	AGCAGGAACA
	2001	GGATAAAGAG	GATGAGGAGG	AAGAGCAGGA	TCAACAAATG	GTTCAAAATG
	2051	GGTACTATGA	AGAAACAGAT	TATTCAGCTT	TGGATGGAAC	AATAAATGCT
	2101	CACTATACAA	GCAGAGATGA	ACTAATGGAA	GAAAGACTTA	CAAAATCTGA
15	2151	AAAAATAAAC	AGTGACTATC	TGAGAGATGG	TATAAACATG	CCTACTGTCT
	2201	GTACTTCTGG	TTGTTTGTCC	TTCCCGTCTG	CACCACGAGA	GTCTCCTTGT
	2251	AATGTTAAAT	ATTCTTCCAA	AAGTAAATTT	GATGCCATTA	CAAAGCAGCC
	2301	AAGCAGTACT	TCTTACAAC	TCACTTCTTC	GATTTCTCTG	TATGAAAGTT
	2351	CACCAAAACC	TCAAATACAA	GCCTTCCTTC	AGGCAAAAGA	AGAAGTGAAG
20	2401	CTACTAAAAC	TTCTGGGTT	CATGTACAGT	GAAGTTCCTC	TGCTGGCATC
	2451	CTCAGTACCT	TATTTTAGTG	TAGAAGAAGA	GGGTGGTTCT	GAAGATGGAG
	2501	TACATCTGAT	TGTCTGTGTG	CACGGTTTAG	ATGGAAACAG	TGCAGATCTC
	2551	CGATTAGTAA	AAACTTACAT	TGAAGTTGGA	TTGCCTGGGG	GAAGAATTGA
	2601	TTTTCTTATG	TCTGAGAGAA	ATCAGAATGA	TACTTTTGCT	GATTTTGATA
25	2651	GCATGACTGA	TCGTCTTTTG	GATGAGATAA	TACAGTATAT	TCAGATATAT
	2701	AGTCTAACAG	TCTCAAAAAT	AAGCTTTATT	GGACATTCTG	TGGGCAATTT
	2751	AATAATTCGT	TCAGTGCTTA	CAAGGCCAAG	GTTTAAATAT	TACCTCAACA
	2801	AACTTCATAC	CTTTCTGTCT	CTTTCTGGAC	CTCACCTTGG	TACACTCTAC
	2851	AACAGCAGTG	CTCTTGTTAA	TACAGGTCTC	TGGTTTATGC	AGAAATGGAA
30	2901	AAAATCAGGT	TCGCTTTTGC	AGCTGACATG	TCGAGATCAC	TCAGACCTTC
	2951	GCCAAACTTT	TTTATATAAG	CTTAGTAACA	AAGCAGGGCT	TCATTATTTT
	3001	AAAAATGTTG	TGCTAGTGGG	ATCCCTACAG	GATCGCTATG	TTCTTTATCA
	3051	CTCTGCCCCG	ATTGAAATGT	GTAAAAACAG	TTTAAAGGAC	AAACAGTCAG
	3101	GACAGATCTA	TTCAGAAATG	ATCCACAAC	TGCTTCGACC	CGTTCTGCAA
35	3151	AGCAAGGACT	GTAATTTGGT	TCCGTATAAT	GTCAATCAATG	CATTGCCCAA
	3201	TACAGCTGAT	TCACTCAATG	GGAGAGCTGC	ACATATAGCT	GTCTTTGATT
	3251	CGGAAATATT	TTTAGAGAAA	TTCTTTCTGG	TTGCTGCCCT	CAAATATTTT
	3301	CAATAGTATA	AAAGCATTGT	TAGCGACTGG	ACAATTACCT	CATTCAACAA
	3351	TGTTTCAAAT	AATGTATTAT	ATTAATAATG	AGATGCTGAT	AAGTTCTAAG
40	3401	AAATATTTAT	ACCTTTTTAT	ATGGAAGATA	ATTTATATCA	TCCATGTTTA
	3451	GTGCTTTTAA	AACATCAACT	TTACTTTCTA	GGTAATGTGG	CTGTGCAATA
	3501	TTTTTTTAAAT	TTTATCTTTT	TACTTTTCTA	TTACTTTTTT	ATATATTTTG
	3551	CTACCTAAGT	ATTTTCAGTG	AACTTTAAGC	CCATACCTGT	GTCTGATTGT
	3601	TTATTATTGG	CTTTCCACAA	TTCTTACATC	AGACTACATT	ATATTAGAGA
45	3651	CCATTATTGC	TAGAATAGCA	TGGGATTTAA	AATTTCTAAT	ACTGGGGGTA
	3701	TTATTTAGTT	AATTATAAAT	TTTTCTTTTC	ACATTTTACT	GTGTTTTAAC
	3751	TGGAAATAAA	ATTATGGCTG	CTACAATATA	TTTTTTGAAA	TCAACTTCTG
	3801	TAGTTCTAAA	ATACAACCTT	ATCATACAAT	CAAACCAGGT	AGTTCATATA
	3851	AAACAGTGTA	ATACAAGTTT	TCTATAAAGT	CATTACTGTT	GCTTAAACAT
50	3901	ATTTTCATGCC	TATTAATAAT	TATTTTCTAC	TGGTGATTTT	AACATTATTT
	3951	CTCATACTGA	CTTTTATTAC	TGGAAATGTT	CCTGTACATG	TTGGCAGCAG
	4001	ATAAAGATTT	TTGAATGTTT	GAATGCCCTC	TGCCTTGATT	TGGTTGGATT
	4051	TTGCTAATTG	GTATGTTGCT	TGAAGTTTAT	GAAGTACATT	TCTTTTAACT
	4101	TTTTTTCATGG	ACTTCCTTAT	ATGTACATAA	TAATTAAATG	TTGAAATTTA
55	4151	TGAAATACTT	TTATGAATTT	AGATAATTTT	TAAATATTGT	TAAATTTTAT
	4201	TGAAGTAAAA	AGTAATGTAA	ATAAATAAAT	TCATGTTAAA	GATGGAACAA
	4251	AATAATTAAC	TTTACATGTT	TGGTGATACA	GATGCAAATG	TTTTTGATAT
	4301	ATGGAGATGT	TGAGTCTTTT	GACTTTACTA	AAGGTGCTGA	ATAGCATTA

4351 ATTCACACTATT TTCCTTTTCT GTTTTACTTG TGAAAATAAA AATGCACTAA  
 4401 GGTGTTGGGTAG AAGTTCTGTT TGCACCTCACT AATTGTGACA GACAGAGGTT  
 4451 TTTGTAAGTA TTTATTGTAC AATTGATGCA TGTATTATTT TAGCGTTGTT  
 4501 ATTGCCTCTG GTGTTAATAA ATGAACAAAT GGCTATCTGG AGGAACAGCT  
 5 4551 AAAAAAAAAA AA

## BLAST Results

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10

Entry HSDJ198I9 from database EMBLNEW:  
 Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
 DJ198I9

15

Score = 7221, P = 0.0e+00, identities = 1455/1461

## Medline entries

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20

No Medline entry

25

## Peptide information for frame 1

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ORF from 34 bp to 3303 bp; peptide length: 1090

Category: similarity to unknown protein

30 Classification: no clue

1 MGIQNLQRSE SSKMDKYETE ESSVAGLSSP ELKVRPAGAS SIWYTEGEKQ  
 51 LTKSLKGKNE ESNKSKVKVT KLMKTMKSEN TKKLIKQNSK DSVVLVGYKC  
 101 LKSTASNDLI KCFEGNPSHS QKEGLDPTIC GYNFDPKTYM RQTSQKEASC  
 35 151 LPTNTERTEQ KSPDIENVQP DQFDPLNSGN LNLCANLSIS GKLDISQDDDS  
 201 EITQMEHNLA SRRSSDDCHD HQTTPSLGVR TIEIKPSNKD PFSGENITVK  
 251 LGPWTELREQ EILVDNLLPN FESLESNGKS KSIEITFEKE ALQEAQCLSI  
 301 GESLTKLRSN LPAPSTKEYH VVVSQDITKL PDISATYASS RFSDSGVESE  
 351 PSSFATHPNT DLVFETVQGG GPCNSERLFP QLLMKPDYNV KFSLGHNHCTE  
 40 401 STSAISEIQS SLTSINSLPS DDELSPDENS KKSVPPECHL NDSKTVLNLG  
 451 TTDLPKCDDT KKSSITLQQQ SVVFSGNLDN ETVAIHSLNS SIKDPLQFVF  
 501 SDEETSSDVK SSCSSKPNLD TMCKGFQSPD KSNNSTGTAI TLNSKLICLG  
 551 TPCVISGSIS SNTDVSEDRT MKKNSDVLNL TQMYSEIPTV ESETHLGTSD  
 601 PFSASTDIVK QGLVENYFGS QSSTDISDTC AVSYSNALSP QKETSEKEIS  
 45 651 NLQEQEQDKED EEEEEQDQDMV QNGYYEETDY SALDGTINAH YTSRDELMEE  
 701 RLTKSEKINS DYLRDGINMP TVCTSGCLSF PSAPRESPCN VKYSSKSKFD  
 751 AITKQPSSTS YNFTSSISWY ESSPKPQIQ A FLQAKEELKL LKLPGFMYSE  
 801 VPLLASSVPY FSVEEEGGSE DGVHLIVCVH GLDGNADLR LVKTYIELGL  
 851 PGGRIDFLMS ERNQNDFAD FDSMTDRLLD EIIQYIQIYS LTVSKISFIG  
 50 901 HSLGNLIIRS VLTRPRFKYY LNKLHTFLSL SGPHLGTLYN SSALVNTGLW  
 951 FMQKWKSGS LLQLTCRDHS DPRQTFLYKL SNKAGLHYFK NVVLVGSLQD  
 1001 RYVPYHSARI EMCKTALKDK QSGQIYSEMI HNLLRPVLQS KDCNLVRYNV  
 1051 INALPNTADS LIGRAAHIAV LDSEIFLEKF FLVAALKYFQ

55

## BLASTP hits

Alert BLASTP hits for DKFZphtes3\_26q3, frame 1

Pedant information for DKFZphtes3\_26q3, frame 1

```

[LENGTH] 1101
[MW] 122245.22
[pI] 5.12
[HOMOL] TREMBL:CEAF219b_1 gene: "C09D4.4"; Caenorhabditis
elegans cosmid C09D4. 2e-38
[FUNCAT] 99 unclassified proteins [S. cerevisiae, Y0R059c]
2e-06
[BLOCKS] BL001208
[KW] Alpha_Beta
[KW] LOW COMPLEXITY 6.72 %

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-361-

(No Pfam data available for DKFZphtes3\_26g3.1)

DKFZphtes3\_29f24

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5 group: signal transduction

DKFZphtes3\_29f24 encodes a novel 526 amino acid protein with similarity to murine net1a.

10 The closely related mNET1 activates signalling pathways in addition to those directly controlled by activated RhoA. The novel protein is expressed ubiquitously.

15 The new protein can find application in modulation/blocking signalling pathways.

similarity to net1a (Mus musculus)

20 perhaps complete cds.

Sequenced by BMFZ

Locus: /map="72.40 cR from top of Chr3 linkage group"

25

Insert length: 3559 bp

Poly A stretch at pos. 3534, polyadenylation signal at pos. 3513

```

30      1 CGCCGCCGCC CGGCATCGTG GAGCTGGGGC CCCCTTTTGC CTGGGAGTTT
      51 TGTAGTCGCC TAGGGTCAGC GGTGACATCC CAAAGGGCAG GCCCGGCAGC
     101 CGCCATGGTG GCCAAGGATT ACCCCTTCTA CCTCACGGTC AAGAGAGCGA
     151 ACTGCAGCCT GGAGCTACCC CCGGCCAGCG GTCCGGCCAA GGACGCTGAG
     201 GAGCCTAGTA ATAAACGGGT CAAACCCCTT TCCCGAGTCA CGTCGCTAGC
35     251 AAACCTCATC CCGCCCGTGA AGGCCACGCC ATTAAGCGC TTCAGTCAAA
     301 CCCTGCAGCG CTCCATTAGC TTCCGCAGTG AGAGCCGCCC TGACATCCTC
     351 GCCCCCGGAC CCTGGTCCAG AAATGCCGCG CCCTCGAGCA CGAAACGGAG
     401 AGATAGCAAG CTGTGGAGTG AGACCTTCGA TGTGTGCGTC AATCAGATGC
     451 TTACATCCAA GGAAATCAAA CGTCAGGAGG CGATCTTTGA GCTTTCCTAA
40     501 GGAGAAGAAG ACTTGATAGA AGACTTGAAA TTAGCAAAAA AGGCCTATCA
     551 TGACCCCATG CTGAAACTCT CCATAATGAC AGAACAAGAG TTGAATCAAA
     601 TTTTGGGAAC ACTGGACTCT CTAATTCCTC TACATGAAGA GCTCCTTAGT
     651 CAGCTTCGAG ATGTTAGGAA GCCTGATGGC TCGACTGAAC ATGTTGGTCC
     701 CATCCTCGTG GGCTGGCTCC CTTGCCTCAG CTCCTATGAT AGCTACTGCA
45     751 GCAATCAAGT AGCCGCCAAA GCTCTGCTGG ACCACAAAAA GCAAGATCAC
     801 CGAGTCCAGG ATTTCTTACA GCGATGTTTA GAATCCCCCT TTAGCCGCAA
     851 ACTAGATCTC TGGAATTTCC TCGATATTCC AAGAAGCCGC CTGGTAAAAT
     901 ACCCTCTGCT TCTCCGAGAA ATCTTGAGGC ACACACCAA TGATAATCCA
     951 GATCAGCAGC ACTTGGGAAG AGCTATAAAT ATCATTGAGG GAATTGTGGC
50    1001 AGAAATCAAC ACCAAGACTG GTGAATCTGA ATGCCGCTAT TATAAGAGC
     1051 GGCTTCTTTA CTTGGAAGAA GGCCAGAAAG ACTCCCTGAT CGACAGCTCT
     1101 CGAGTCTTGT GTTGTCTATG TGAAGTGAAG AACAATCGGG GCGTGAAACT
     1151 GCATGTTTTT CTGTTCCAAG AAGTGCTTGT GATCACTCGA GCCGTCACCC
     1201 ACAATGAGCA GCTTTGCTAC CAGCTGTACC GTCAGCCAAT CCCCGTGAAA
55    1251 GACCTCCTGC TGGAAGACCT CCAGGATGGA GAAGTGAGGC TGGGTGGCTC
     1301 CCTGCGAGGG GCATTGAGCA ACAATGAGAG AATTAAAAAC TTCTTCAGAG
     1351 TCAGTTTCAA AAATGGATCC CAAAGTCAGA CCCACTCGCT ACAAGCCAAT
     1401 GACACTTTCA ACAACAGCA GTGGCTTAAC TGTATTGCTC AAGCCAAAGA

```



1451 AACAGTTTTG TGTGCTGCCG GGCAAGCTGG GGTGCTTGAC TCCGAGGGAT  
 1501 CGTTCCTAAA TCCCACCACC GGGAGCAGAG AGCTACAGGG AGAAACAAAA  
 1551 CTTGAGCAGA TGGACCAATC GGACAGTGAG TCAGACTGTA GTATGGACAC  
 1601 GAGTGAGGTC AGCCTCGACT GTGAGCGCAT GGAACAGACA GACTCTTCCT  
 5 1651 GTGGAAACAG CAGGCACGGT GAAAGTAACG TCTGACAGAA GCATGTGCAC  
 1701 TTCGGGAAGC AGGCCTGCAT CTTACCTGTA CAGTATTTGC ATTCCACAGA  
 1751 TGGAACGGTT TGGAGAAGCA CTTTTTCATA CTTTTGTGAA AGTATACATG  
 1801 TTGGCCCAAG CTCTCGTATC TGTACCTTTG TCCCTAGTAC TGTAACTGCC  
 1851 AATCTGTCTG TGTAAGCTGG AATCTGTGGC AACTATTACC CTGTGTTGTA  
 10 1901 TTTCCCAAAG GTCTGGATGG ATGGAGAGGT ACTCAAACAA GTTACTTTCA  
 1951 GTTGTCCTGC TGGATTTTAA AAAAATAGAA AAAGAATCTC AAAACTACTG  
 2001 TTTTACATAG ATTGTTTGAA GAGTCCTTCC TCTTGTGCTT CTGTACCACT  
 2051 TTCCAGCTC TTAGATGTGG TAGCTAAAGG CACGGAATTT AGACGGCCTT  
 2101 GTAAATAGGG CATGAGGAAC TCATCTGTGT ATTGGGATGG TATTAGAGAG  
 15 2151 AGAATCAGGA AAGACCAACT CATGAAGTGA ACTTGGTTTG ATCTTACTCA  
 2201 ACTAGAAAGC TTGAAAACAT CCCTGGGGAT TCTGAAGGCT TAATTTTGCA  
 2251 AAGGAGGATG CATTGTCTGA ACTTTGCAAC TTCATCCAGT GCAAGTTTGA  
 2301 TGCAAGAATG TATTAGGACA TAAATAGAG GCTGACCTTA AAAGGGCCAG  
 2351 GACAGAAGCG GCTGCCAGCT CTGAATCTTT AACTGAAATG CACATGGCAC  
 20 2401 CAGGAGGTGT CTCTCATAGT TGGTTGCTAG CCTAAAACAT CAGAATAGAA  
 2451 CCCAAAGGGC TTAGGAAGGC CTGCCAGGAT AACAAGAAGG CCCTGTATTC  
 2501 ATTGTGTTTC ATCTGCCTAG GCCTACTCAT TATTTTAGAG AATGAATGAA  
 2551 GCAACAAGGA AGAGAGACCA TGACTCTATC GATGACACTG TTTATAGAAA  
 2601 CACAGGAGAG GAAGAATTTG GAATGAAAAG CACTTCGTCA GAACCTTCTG  
 25 2651 TGGGAGCCAT TGAGAGAAAA GCATGGTCCA GTGCCTTCTG AGAAAGGCCA  
 2701 GAGCTTTGGG CTTTCCTGCT CTGCTTTTGG GTCGTCAATT TGCCATCTCT  
 2751 GGTTCCTGTG TATAATCAGA ATTGTAATTA TGTTCTCCAG AGGCCAATTT  
 2801 CATTAACTCT GATTAATTAG AATCAGCTAG CCAGATTAGT AACCTCTTTG  
 2851 TCCAGCCTTG ATTTACAGTG CAGGGTAAAG TGCAGACCTT AAAAACAGCT  
 30 2901 AAGTACCTAG AAGAGCTCCC TGCAAGTGTA AATATTAAGG ATGACCTGTG  
 2951 CAAAATTATA CCCACACCAG CACTAGTGGT AATTATTCTA AATTATTGCC  
 3001 AAAAAGTTTT TTTTAATCTG TCTTTCAAGT TTACAGAAAA GAAAGCAGTA  
 3051 AATGCATTGA TGTCAATTTA TTATGTACAT ATATCATGTG CATTCAAGCT  
 3101 GTGTGACAAG ATATATCAAT ATAAAAACAA GGTATATACT TTATTATTTT  
 35 3151 TTGAAAACAA GGATATTGTG ATCAATTTTA CCCTGTAAAA CATATTTCTG  
 3201 TATTTATAGG TCTTAAACAT GATGAATTTT TTCTATTACA AGTTTATTTA  
 3251 AAAGTGCCTT CTCAAGTCGT TATTGATACA GCAAGTGAAC CTGCTGCAGA  
 3301 CAGAAGCAGA GGAAAGCCAA GAACAGCCTT TATTGGTGAA GAAAAGAATG  
 3351 AATGATTCTT TGTAGGCGCC ATCAGCCACT TTTAGAAGCC ATCAGCCAGT  
 40 3401 GTGTTGGGAA AAGAGGTTTG TCAAGTGTG GCCTATGGGA AGGTGGTCAA  
 3451 TGAATGTTTT GATGAAATGA ATGTTTTTGT ATAATGGCCT TAACTTTTC  
 3501 TGGAAGTATT TCAAATAAAT TACATTATTA AGTCAAAAAA AAAAAAAAAA  
 3551 AAAAAAAAAA

45

## BLAST Results

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No BLAST result

50

## Medline entries

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55

98336196:

Alberts AS, Treisman R.: Activation of RhoA and SAPK/JNK  
 signalling  
 pathways by the

RhoA-specific exchange factor mNET1. EMB0 J 1998 Jul  
15;17(14):4075-85

5

# Peptide information for frame 3

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10 ORF from 105 bp to 1682 bp; peptide length: 526  
Category: strong similarity to known protein  
Classification: Cell signaling/communication

15 1 MVAKDYPFYL TVKRANCSLE LPPASGPAKD AEPSNKRVK PLSRVTS LAN  
51 LIPPVKATPL KRFSQTLQRS ISFRSESRPD ILAPRPWSRN AAPSSTKRRD  
101 SKLWSETFDV CVNQMLTSKE IKRQEAIFEL SQGEEDLIED LKLAKKAYHD  
151 PMLKLSIMTE QELNQIFGTL DSLIPLHEEL LSQLRDVRKP DGSTEHV GPI  
201 LVGWLPCLSS YDSYCSNQVA AKALLDHKKQ DHRVQDFLQR CLESPFSRKL  
251 DLWNFLDIPR SRLVKYPLLL REILRHTPNQ NPQQAHL EEA INIIQGIVAE  
20 301 INTKTGESEC RYYKERLLYL EEGQKDSLID SSRVLCCHGE LKNNRGVKLH  
351 VFLFQEV LVI TRAVTHNEQL CYQLYRQPIP VKDLLLEDLQ DGEVRLGGSL  
401 RGAFSNNERI KNFFRVSFKN GSQSQTHSLQ ANDTFNKQ QW LNCIRQAKET  
451 VLCAAGQAGV LDSEGSFLNP TTGSRELQGE TKLEQMDQSD SESDCSMDTS  
501 EVSLDCERME QTDSSCGNSR HGESNV  
25

## BLASTP hits

30 No BLASTP hits available

Alert BLASTP hits for DKFZphtes3\_29f24, frame 3

No Alert BLASTP hits found

35

Pedant information for DKFZphtes3\_29f24, frame 3

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## Report for DKFZphtes3\_29f24.3

40

45 [LENGTH] 560  
[MW] 63202.85  
[pI] 6.04  
[HOMOL] TREMBL:AF094520\_1 gene: "Net1"; product: "NET1  
homolog"; Mus musculus NET1 homolog (Net1) mRNA, complete cds.  
1e-162  
[FUNCAT] 09.01 biogenesis of cell wall [S. cerevisiae,  
YLR371w] 3e-16  
50 [FUNCAT] 03.07 pheromone response, mating-type determination,  
sex-specific proteins [S. cerevisiae, YLR371w] 3e-16  
[FUNCAT] 10.02.09 regulation of g-protein activity. [S.  
cerevisiae, YLR371w] 3e-16  
[FUNCAT] 09.04 biogenesis of cytoskeleton [S. cerevisiae,  
55 YLR371w] 3e-16  
[FUNCAT] 03.04 budding, cell polarity and filament formation  
[S. cerevisiae, YLR371w] 3e-16

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(No Prosite data available for DKFZphtes3\_29f24.3)

5 (No Pfam data available for DKFZphtes3\_29f24.3)

DKFZphtes3\_30pb

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5 group: testis derived

DKFZphtes3\_30pb encodes a novel 461 amino acid protein without similarity to known proteins.

10 No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

15

similarity to C.elegans F41H10.4

perhaps complete cds.

20

Sequenced by LMU

Locus: unknown

25 Insert length: 1944 bp

Poly A stretch at pos. 1911, no polyadenylation signal found

```

30      1 GGAACAGACC ACTGGGCTGG CAGCTGAGTT GCAGCAGCAG CAGGCTGAGT
      51 ACGAGGACCT TATGGGACAG AAAGATGACC TCAACTCCCA GCTCCAGGAG
     101 TCATTACGGG CCAATAGTCG ACTGCTGGAA CAACTTCAAG AAATAGGGCA
     151 GGAGAAGGAG CAGTTGACCC AGGAATTACA GGAGGCTCGG AAGAGTGCGG
     201 AGAAGCGGAA GGCCATGCTG GATGAGCTAG CAATGGAAAC GCTGCAAGAG
     251 AAGTCCCAGC ACAAGGAAGA GCTGGGAGCA GTTCGTCTAC GGCATGAGAA
35     301 GGAGGTGCTG GGGGTGCGTG CCCGCTATGA GCGTGAGCTC CGAGAGCTGC
     351 ATGAAGACAA GAAGCGTCAG GAGGAGGAGC TCCGTGGGCA GATCCGGGAG
     401 GAGAAGGCCC GGACACGGGA GCTGGAGACT CTCCAGCAGA CAGTGGAAGA
     451 ACTTCAAGCT CAGGTACATT CCATGGATGG AGCCAAGGGC TGGTTTGAAC
     501 GGCCTTGAA GGAAGCCGAG GAATCCCTGC AGCAGCAGCA GCAGGAACAA
40     551 GAGGAAGCCC TCAAGCAGTG TCGGGAGCAG CACGCTGCCG AGCTGAAGGG
     601 CAAGGAGGAG GAGCTACAGG ATGTACGGGA TCAGCTCGAG CAGGCCCAGG
     651 AGGAGCGGGA CTGCCACCTG AAGACCATTA GCAGCCTGAA GCAGGAGGTG
     701 AAGGACACAG TGGATGGGCA GAGGATCCTG GAGAAGAAGG GCAGTGCTGC
     751 GCTCAAGGAC CTCAAGCGGC AGCTGCATTT GGAGCGGAAA CGGGCAGATA
45     801 AGCTGCAGGA GCGACTGCAG GACATCCTCA CTAACAGCAA GAGCCGCTCA
     851 GGCCTTGAGG AGCTGGTTCT CTCAGAGATG AACTCACCAA GCCGGACCCA
     901 GACAGGGGAC AGCAGTAGCA TCTCCTCCTT CAGCTACCGG GAGATCTTGC
     951 GGGAAAAGGA GAGCTCGGCT GTTCCAGCCA GGTCTTATC CAGCAGCCCT
50    1001 CAAGCCCAGC CCCCTCGGCC AGCAGAGCTG TCAGATGAGG AAGTGGCTGA
     1051 GCTCTTTTCA GGGCTGGCAG AGACACAGCA GGAGAAATGG ATGCTGGAGG
     1101 AGAAGGTGAA GCACCTGGAA GTGAGCAGTG CTTCCATGGC AGAGGACCTC
     1151 TGCCGGAAGA GCGCCATCAT TGAGACCTAC GTCATGGACA GCCGGATCGA
     1201 TGTGTCTGTG GCAGCAGGCC ACACAGACCG CAGCGGGCTG GGCAGCGTCC
     1251 TGAGAGACCT AGTGAAGCCA GGCAGCAGGA ACCTTCGGGA GATGAACAAG
55    1301 AAGCTGCAGA ACATGCTGGA GGAGCAGCTC ACCAAGAATA TGCACTTGCA
     1351 CAAGGATATG GAAGTTCTGT CCCAGGAAAT TGTGCGGCTC AGCAAGGAGT
     1401 GCGTGGGGCC TCCTGACCCA GACCTAGAGC CAGGAGAAAC CAGCTAAAGA
     1451 CCTGCAGGCT GCACCCACCT CCTCCCCTTC CTACCCCTTA GGATGCTATT

```

1501 CCCTTGGGCT GTGGTGGAAA AATGAGGGCT GGAGCCAAAA TCAAATAGCT  
 1551 TGGGAGACTG GACATTAAAG GGGCTAGAGG CCTGATGGTT AGTGTTAATG  
 1601 ATCCTGTCTT AGGGCAGAGG CCACCAGGGA GTGGGGATCC TGAGGGAAGG  
 1651 GGCAGGGATT TCTCCTTCTT CTTGGTCCTG GCTCCCAAGG GCTTCTGTCT  
 5 1701 TCATCTCTGC ATGAGCTCTC CTTCCCAGAG ACCAACTCTT TTTTATTTTA  
 1751 TTTTATTTT TAATTTATGT CTGGAGCCTG GCTACTCTGC ATTTGGGATT  
 1801 GGGGATGCTG GGTGGGTGTG TGGTCCATGT TCAGCGTTCT AGCAACACGT  
 1851 GTGTGTGTGT GTGTGTAAAG GCTATGCAGC CAAAATACCA TCTGGCCAGA  
 1901 CGGGCCCACC CACAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAG

10

## BLAST Results

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15 No BLAST result

## Medline entries

-----

20  
 No Medline entry

## Peptide information for frame 2

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ORF from 62 bp to 1444 bp; peptide length: 461

Category: similarity to unknown protein

30 Classification: no clue

1 MGQKDDLNSQ LQESLRANSR LLEQLQEIGQ EKEQLTQELQ EARKSAEKRK  
 51 AMLDELAMET LQEKSQHKEE LGAVRLRHEK EVLGVRARYE RELRELHEDK  
 101 KRQEEELRGQ IREEKARTRE LETLQQTVEE LQAQVHSM DG AKGWFERRLK  
 35 151 EAEESLQQQQ QEQEEALKQC REQHAAELKG KEEELQDVRD QLEQAQEERD  
 201 CHLKTISLKL QEVKDTVDGQ RILEKKGSAA LKDLKRQLHL ERKRADKLQE  
 251 RLQDILTNSK SRSGLEELVL SEMNSPSRTQ TGDSSSISSF SYREILREKE  
 301 SSAVPARSL SSSQAQPPRP AELSDEEVAE LFQRLAETQK EKWMLEEKVK  
 351 HLEVSSASMA EDLCRKSAII ETYVMDSRID VSVAAGHTDR SGLGSVLRDL  
 40 401 VKPGDENLRE MNKKLQNMLE EQLTKNMHLH KDMEVLSQEI VRLSKECVGP  
 451 PDPDLEPGET S

45 BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3\_30pb, frame 2

50  
 No Alert BLASTP hits found

Pedant information for DKFZphtes3\_30pb, frame 2

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55  
 Report for DKFZphtes3\_30pb.2

[[LENGTH]] 481  
[[MW]] 55398.10  
[[pI]] 5.07  
[[HOMOL]] TREMBL:CEF41H10\_4 gene: "F41H10.4"; Caenorhabditis  
5 elegans cosmid F41H10. 2e-12  
[[FUNCAT]] 30.03 organization of cytoplasm [[S. cerevisiae,  
YDL058w]] 5e-04  
[[FUNCAT]] 08.07 vesicular transport (golgi network, etc.) [[S.  
cerevisiae, YDL058w]] 5e-04  
10 [[BLOCKS]] BLO11000 NNMT/PNMT/TEMT family of methyltransferases  
proteins  
[[KW]] All\_Alpha  
[[KW]] LOW\_COMPLEXITY 19.13 %  
[[KW]] COILED\_COIL 40.96 %  
15

SEQ EQTTGLAAELQQQQAEEYEDLMGQKDDLNSQLQESLRANSRLLEQLQEIGQEKEQLTQELQ  
SEG .....xx  
20 PRD ccchhh  
COILS  
...CC

SEQ EARKSAEKRKAMLDLAME TLQEK SQHKEELGAVRLRHEKEVLGVRARYERELRELHEDK  
SEG x.....  
25 PRD hhh  
COILS  
CCCCCCCC.....

SEQ KRQEEELRGQIREEKARTRELETLQQTVEELQAQVHSM DGAKGWFERRLKEAEESLQQQQ  
SEG .....xx  
30 PRD hhh  
COILS  
.....CC

35 SEQ QEQEEALKQCREQHAAELKGKEEELQDV RDQLQEQEERDCHLKTIS SLKQEVKDTV DGGQ  
SEG xxxxxxxxxxxx.....  
PRD hhh  
COILS  
CCCCCCCCCCCCCCCC.....CC.....

40 SEQ RILEKKGSAALKDLKRQLHLERKRADKLQERLQDILTNSKSRSGLEELVLSEMNSPRTQ  
SEG .....  
PRD cccccccchhh  
COILS  
45 ....CC.....

SEQ TGDSSSISSFSYREILREKESSAVPARSLSSSPQAQPPRPAELSDEEVAELFQRLAETQQ  
SEG ...xxxxxxxxx.....xx  
50 PRD cccccccchhh  
COILS  
.....

SEQ EKWMLEEKVKHLEVSSASMAEDLCRKSAIIETVMDSRIDVSVAAGHTDRSGLGSVLRDL  
SEG .....  
55 PRD hhh  
COILS  
.....

**PCT/IB01/02050**

5 . . . . CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC. . . . .

10 COILS

15 (No Pfam data available for DKFZphtes3\_30pb.2)



DKFZphtes3\_31a10

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5 group: nucleic acid management

DKFZphtes3\_31a10 encodes a novel 542 amino acid protein with similarity to histone H1 of *Drosophila hydei*.

10 Histone H1 variants are known to act as specific regulators of genes via the differential condensation of DNA.

The new protein can find application in modulating/blocking the transcriptional activity and in expression profiling.

15

weak similarity to *Drosophila* histone H1

perhaps complete cds.

20

Sequenced by LMU

Locus: /map="13"

25 Insert length: 2887 bp

Poly A stretch at pos. 2855, polyadenylation signal at pos. 2839

30 1 AGATGATCCC CAAAGTCAAC ATATGACATT AAGCCAGGCA TTTCACCTTA  
51 AAAACAATAG TAAAAAGAAA CAAATGACTA CAGAAAAACA AAAGCAAGAT  
101 GCTAACATGC CCAAGAAACC TGTGCTTGA TCTTATCGTG GCCAGATTGT  
151 TCAGTCTAAG ATTAATTTCAT TTAGAAAACC TCTACAAGTC AAAGATGAGA  
201 GTTCTGCAGC AACAAAGAAA CTTTCAGCCA CTATACCTAA AGCCACAAAA  
251 CCTCAGCCTG TAAACACCAG CAGTGTAACA GTGAAAAGTA ATAGATCCTC  
35 301 CAATATGACT GCCACTACTA AATTTGTGAG CACTACATCT CAGAACACAC  
351 AACTTGTGCG ACCTCCTATT AGAAGTCATC ACAGTAATAC CCGGGACACT  
401 GTGAAACAAG GCATCAGTAG AACCTCTGCC AATGTTACAA TCCGGAAAGG  
451 GCCTCATGAA AAAGAACTAT TACAATCAAA AACAGCTTTA TCTAGTGTCA  
501 AAACCAGTTC TTCTCAAGGT ATAATAAGAA ATAAGACTCT ATCAAGATCC  
40 551 ATAGCATCTG AAGTTGTAGC CAGGCCTGCT TCATTGTCTA ATGATAAACT  
601 GATGGAAAAAG TCAGAGCCCG TTGACCAGCG AAGACATACT GCAGGAAAAAG  
651 CAATTGTTGA TAGTAGATCA GCTCAGCCCA AAGAAACCTC GGAAGAGAGA  
701 AAAGCTCGTC TGAGTGAGTG GAAAGCTGGC AAAGGAAGAG TGCTAAAAAG  
751 GCCCCCTAAT TCAGTAGTTA CTCAGCATGA GCCTGCAGGA CAAAATGAAA  
45 801 AACTAGTTGG GTCTTTTTGG ACTACCATGG CAGAAGAAGA TGAACAAAGA  
851 TTATTTACTG AAAAAAGTAA CAACACATTT TCTGAATGCC TGAAGTTGAT  
901 TAATGAGGGA TGTCCAAAAG AAGATATACT GGTCACTACT AATGACCTGA  
951 TTAATAATAT TCCAGATGCC AAAAAGCTTG TTAAGTATTG GATATGTCTT  
1001 GCACTTATTG AACCAATCAC AAGTCCTATT GAAAATATTA TTGCAATCTA  
50 1051 TGAGAAAGCC ATTCTGGCAG GGGCTCAGCC TATTGAAGAG ATGCGACACA  
1101 CGATTGTAGA TATTCTAACA ATGAAGAGTC AAGAAAAAGC TAATTTAGGA  
1151 GAAAATATGG AGAAGTCTTG TGCAAGCAAG GAAGAAGTCA AAGAAGTCAG  
1201 TATTGAAGAT ACAGGTGTTG ATGTAGATCC AGAAAACTG GAAATGGAGA  
1251 GTAAACTTCA TAGAAATTTG CTATTTCAAG ATTGTGAAAA AGAGCAAGAC  
55 1301 AACAAAACAA AAGATCCAAC CCATGATGTT AAAACCCCA ATACAGAAAC  
1351 GAGGACAAGT TGCTTAATTA AATATAATGT GTCTACTACG CCATACTTGC  
1401 AAAGTGTGAA AAAAAAGGTG CAGTTTGTAT GAACAAATTC CGCATTTAAA  
1451 GAGCTGAAGT TTTTAACACC AGTGAGACGT TCTCGACGTC TTCAAGAGAA

```

1501 AACTTCTAAA TTGCCAGATA TGTAAAAAGA TCATTATCCT TGTGTGTCTT
1551 CATTGGAACA GCTAACGGAG TTGGGAAGAG AAACGTATGC TTTTGTATGC
1601 CGCCCTAATG CAGCACTGTG CCGGGTGTAC TATGAGGCTG ATACAACATA
1651 AGAGAAATAA AGCTCTGTTA GGGAAATGGGG TTTTATTAT TGTGGGGTG
5 1701 TTTTGTTTTG AGTAGCTTTA TATTGCTCTT AGGTCTGGAG TTGGCCATGT
1751 ACCTATGTAT CCTAAGCATT CACGGCAGTG AGCTCCTTTA CTAACATTCA
1801 TGTATGGCA AGAGTTGTCC TCTACATTGG AAAGCTAATC CTACCTTGTC
1851 AGTTTCAACC AACTGAGTTT TTTCTTTAAG AAAGGTAAAT TTTGTCAGCT
1901 AGTTTACTAT GTTCCTTGAA TATAAACAGG TTATAATACT ACCCTGTTCA
10 1951 CTTTACTAAA TATAAGTACA GTAATGATGC ATAATTAGAA AATGAGGTAT
2001 TCTAGGTAAA ATGTATGTTT GCCTTGACAT GTTTTTAAAA GTTATGATGT
2051 ACCTCCCTGC CTTTAAACAG AATACTTTTT TCTTTTTTTT GGCCTTTCTC
2101 AGATTAGTCA AAAATTCTAT AGAATGACTC ACTTCGAATA CTAAGACACA
2151 GGAGGTTTAG CCTGCTTTCT TACCAAATTC ATGTTACCCA GACTTGTGTT
15 2201 CTCTTGCGTC CCTTGGACTG CCTGTTGATT GATGGAAAGT GTCTGCACTG
2251 ACACTTTTCG TCAGTAGTCT GTAGTTTCGT GGCCTCTTTT GATTATAACT
2301 GGGGTCACCA AGAAGGTTTA CTTAATTAAA TACCGCATTT CTAAGAGAAG
2351 ATACTTTGTG TAAGAAAAGA TGCCACATTT AGTGGTTTAA CTTTTGTAAC
2401 TTCACTTGAT AGTTTTTAAG CAATTAGAAT GGAGTTAGGG AAAGAACATA
20 2451 TCATACTGAA CAAATGTCAT TCTAGTTTAG ATAGCATTTT TAAGATAACT
2501 GATACTAATA CTTGTTTTCT TCCCTATAAC ATAAAAAACT TCACTGTAA
2551 GTCATGTCCC TTGAAACATG ATAGTTACAT ACACAGTTTT CTCTCCACAC
2601 ATAAATAACA CCACTAAAGT TGTTTTGTAA GGTTCCAAAC TAATATGGCA
2651 TATATCAACT CTACAGTTTC AAATAAATGA CTTTTTAATT GTAAAAGATT
25 2701 AGTTGAAAAA CTGTATGAAT GTGAAGATCA CATGCTTAGT CATTTTTATG
2751 TTCATTCCAC TTTGTATATC TTTTCTATTT ATTGACTTCT CATGTTCTAG
2801 AGAGTAGGAC TTTTATTCCG TGTACCTGAT ATATATACAA TTAATATATC
2851 TGTATAATTA AAAAAAAAAA AAAAAAAAAA AAAAAAG

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30

## BLAST Results

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No BLAST result

35

## Medline entries

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40 No Medline entry

## Peptide information for frame 2

45

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ORF from 23 bp to 1648 bp; peptide length: 542

Category: similarity to known protein

Classification: unclassified

50

55

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1  MTLNQAFHLK NNSKKKQMTT EKQKQDANMP KKPVLGSYRG QIVQSKINSF
51 RKPLQVKDES SAATKKLSAT IPKATKPQPV NTSSVTVKSN RSSNMTATTK
101 FVSTTSQNTQ LVRPPIRSHH SNTRDTVKQG ISRTSANVTI RKGPKHEKELL
151 QSKTALSSVK TSSSQGIIRN KTLRSIASE VVARPASLSN DKLMEKSEPV
201 DQRRHTAGKA IVDSRSAQPK ETSEERKARL SEWKAGKGRV LKRPPNSVVT
251 QHEPAGQNEK LVGSFWTTMA EEDEQRLFTE KVNNTFSECL NLINEGCPKE
301 DILVTLNDLI KNIPDAKKLV KYWICLALIE PITSPIENII AIYEKAILAG
351 AQPIEEMRHT IVDILTMKSQ EKANLGENME KSCASKEEVK EVSIEDTGVD

```

401 VDPEKLEMES KLHRNLLFQD CEKEQDNKTK DPTHQVKTPTN TETRISCLIK  
451 YNVSTTPYLQ SVKKKVQFDG TNSAFKELKF LTPVRRSRRL QEKTSKLPDM  
501 LKDHYPVCVSS LEQLTELGRE TDAFVCRPNA ALCRVYYEAD TT

5

## BLASTP hits

No BLASTP hits available

10

Alert BLASTP hits for DKFZphtes3\_31a10, frame 2

No Alert BLASTP hits found

15

Pedant information for DKFZphtes3\_31a10, frame 2

## Report for DKFZphtes3\_31a10.2

20

[[LENGTH]] 549  
[[MW]] 61677.36  
[[pI]] 9.33  
[[KW]] Alpha\_Beta  
25 [[KW]] LOW\_COMPLEXITY 2.19 %

30

SEQ DDPQSQHMTLSQAFHLKNNSSKKKQMTTEKQKQDANMPKKPVLGSYRGQIVQSKINSFRKP  
SEG .....xxxxxxxxxxxxx.....  
PRD cccccchhhheeeccccccccchhhhhhhhhcccccccccccccccccccccccccccc

35

SEQ LQVKDESSAATKKLSATIPKATKPQPVNTSSVTVKSNRSSNMTATTKFVSTTSQNTQLVR  
SEG .....  
PRD cccccchhhhhhhhhhhcc

40

SEQ PPIRSHHSNTRDTVKGISRTSANVTIRKGPHEKELLQSKTALSSVKTSSSQGIIRNKTL  
SEG .....  
PRD ccc

45

SEQ KAGKGRVLKRPPNSVVTQHEPAGQNEKLVGSFWTTMAEEDQRLFTEKVNNTFSECLNLI  
SEG .....  
PRD hcc

50

SEQ NEGCPKEDILVTLNDLIKNIPIQDAKKLVKYWICLALIEPITSPIENIIAIYEKAILAGAQP  
SEG .....  
PRD ccc

55

SEQ IEEMRHTIVDILTMKSQEKANLGENMEKSCASKEEVKEVSIEDTGVDVDPEKLEMESKLH  
SEG .....  
PRD hhh

SEQ RNLLFQDCEKEQDNKTKDPTHQVKTPTNTETRISCLIKYNVSTTPYLQSVKKKVQFDGTNS  
SEG .....  
PRD ccc

SEQ AFKELKFLTPVRRSRRLQEKTSKLPDMLKDHYPVCVSSLEQLTELGRETD AFVCRPNAALC  
SEG .....  
PRD hhhhhhchhhhhhhhhhhhhhhccccccccccccchhhhhhhhhcccccccccccccc

5

SEQ RYYEADTT  
SEG .....  
PRD eeecccccc

10

(No Prosite data available for DKFZphtes3\_31a10.2)

(No Pfam data available for DKFZphtes3\_31a10.2)

DKFZphtes3\_31j20

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5 group: signal transduction

DKFZphtes3\_31j20 encodes a novel 392 amino acid protein that contains a Protein phosphatase 2C motif.

10 The novel protein shares 95% identity with the rat protein phosphatase 2C and is expressed ubiquitously. PP2C is a structurally diversified protein phosphatase family with a wide range of functions in cellular signal transduction. The transcription of the PP2Cdelta gene was activated in response to  
15 stress, like alcohol or UV irradiation. PP2C plays a role in cell cycle control.

The new protein can find application in and the diagnosis/therapy of stress related diseases and cancer, as well as a for  
20 modulation of cell cycle and signal transduction.

strong similarity to protein phosphatase 2C (*Rattus norvegicus*)

25 Sequenced by LMU

Locus: unknown

Insert length: 1436 bp

30 Poly A stretch at pos. 1367, polyadenylation signal at pos. 1341

```

      1 CGCTGCTCGC GGGCTGAGTG TCTGTGCTG CTGCCGCCTC CACCCAGCCT
      51 CCGCCATGGA CCTCTTCGGG GACCTGCCGG AGCCCGAGCG CTCGCCGCGC
35 101 CCGGCTGCCG GGAAAGAAGC TCAGAAAGGA CCCCTGCTCT TTGATGACCT
    151 CCCTCCGGCC AGCAGTACTG ACTCAGGATC AGGGGGACCT TTGCTTTTGG
    201 ATGATCTCCC ACCCGCTAGC AGTGGCGATT CAGGTTCTCT TGCCACATCA
    251 ATATCCCAGA TGGTAAAGAC TGAAGGGAAA GGAGCAAAGA GAAAAACCTC
    301 CGAGGAAGAG AAGAATGGCA GTGAAGAGCT TGTGGAAAAG AAAGTTTGTA
40 351 AAGCCTCTTC GGTGATCTTT GGTCTGAAGG GCTATGTGGC TGAGCGGAAG
    401 GGTGAGAGGG AGGAGATGCA GGATGCCAC GTCATCCTGA ACGACATCAC
    451 CGAGGAGTGT AGGCCCCCAT CGTCCCTCAT TACTCGGGTT TCATATTTTG
    501 CTGTTTTTGA TGGACATGGA GGAATTCGAG CCTCAAAATT TGCTGCACAG
    551 AATTTGCATC AAAACTTAAT CAGAAAATTT CCTAAAGGAG ATGTAATCAG
45 601 TGTAGAGAAA ACCGTGAAGA GATGCCTTTT GGACACTTTC AAGCATACTG
    651 ATGAAGAGTT CCTTAAACAA GCTTCCAGCC AGAAGCCTGC CTGGAAAGAT
    701 GGGTCCACTG CCACGTGTGT TCTGGCTGTA GACAACATTC TTTATATTGC
    751 CAACCTCGGA GATAGTCGGG CAATCTTGTG TCGTTATAAT GAGGAGAGTC
    801 AAAAACATGC AGCCTTAAGC CTCAGCAAAG AGCATAATCC AACTCAGTAT
50 851 GAAGAGCGGA TGAGGATACA GAAGGCTGGA GGAAACGTCA GGGATGGGCG
    901 TGTTTTGGGC GTGCTAGAGG TGTACGCTC CATTGGGGAC GGGCAGTACA
    951 AGCGCTGCGG TGTACCTCT GTGCCGACA TCAGACGCTG CCAGCTGACC
1001 CCCAATGACA GGTTCAATTT GTTGGCCTGT GATGGGCTCT TCAAGGTCTT
1051 TACCCAGAA GAAGCCGTGA ACTTCATCTT GTCCTGTCTC GAGGATGAAA
55 1101 AGATCCAGAC CCGGGAAGGG AAGTCCGCAG CCGACGCCCG CTACGAAGCA
    1151 GCCTGCAACA GGCTGGCCAA CAAGGCGGTG CAGCGGGGCT CGGCCGACAA
    1201 CGTCACTGTG ATGGTGGTGC GGATAGGGCA CTGAGGGGTG GCGCGCGGCC
    1251 AGGAGCACGC ATGGTATTGA CTAAAAGGT TCATTTTGTG TGTGTGACA

```

1301 TTGTGTGTTT TGTGTACTCC TGTGGGACTC CCATGGTTGT AAATAAAGGT  
1351 TTCTCTTTTT TTTTCCTAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA  
1401 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAG

5

## BLAST Results

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No BLAST result

10

## Medline entries

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15

99074314:

Tong Y, Quirion R, Shen SH.; Cloning and characterization of a novel

mammalian PP2C

isozyme. J Biol Chem 1998 Dec 25;273(52):35282-90

20

## Peptide information for frame 2

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25

ORF from 56 bp to 1231 bp; peptide length: 392

Category: strong similarity to known protein

Classification: Protein management

30

Prosites motifs: PP2C (147-155)

35

1 MDLFGDLPEP ERSRPAAGK EAQKGPLLFD DLPPASSTDS GSGGPLLFDD  
51 LPPASSGDSG SLATSISQMV KTEGKGAKRK TSEEEKNGSE ELVEKKVCKA  
101 SSVIFGLKGY VAERKGEREE MQDAHVILND ITEECRPPSS LITRVSYFAV  
151 FDGHGGIRAS KFAAQNLHQN LIRKFPKGDV ISVEKTVKRC LLDTFKHTDE  
201 EFLKQASSQK PAWKDGSTAT CVLAVDNILY IANLGDRAI LCRYNEESQK  
251 HAALSLSKEH NPTQYEERM IRQKAGGNVRD GRVLGVLEVS RSIGDGQYKR  
301 CGVTSVPDIR RCQLTPNDRF ILLACDGLFK VFTPEEAVNF ILSCLEDEKI  
40 351 QTREGKSAAD ARYEAAACNRL ANKAVQRGSA DNVTVMVVRI GH

## BLASTP hits

45

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3\_31j20, frame 2

50

No Alert BLASTP hits found

Pedant information for DKFZphtes3\_31j20, frame 2

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55

Report for DKFZphtes3\_31j20.2

[LENGTH] 410

[MW] 44759.85  
 [pI] 7.95  
 [HOMOL] TREMBL:AF095927\_1 product: "protein phosphatase 2C"; Rattus norvegicus protein phosphatase 2C mRNA, complete cds.  
 5 0.0  
 [FUNCAT] 03.01 cell growth [S. cerevisiae, YDL006w] 6e-25  
 [FUNCAT] 10.03.13 key phosphatases [S. cerevisiae, YDL006w] 6e-25  
 [FUNCAT] 09.16 mitochondrial biogenesis [S. cerevisiae, YDL006w] 6e-25  
 10 [FUNCAT] 11.01 stress response [S. cerevisiae, YDL006w] 6e-25  
 [FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YDL006w] 6e-25  
 [FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YDL006w] 6e-25  
 15 [FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YER089c] 1e-23  
 [FUNCAT] 99 unclassified proteins [S. cerevisiae, YOR090c] 1e-12  
 20 [FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YJL005w] 3e-10  
 [FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YJL005w] 3e-10  
 [FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YJL005w] 3e-10  
 25 [FUNCAT] 01.03.10 metabolism of cyclic and unusual nucleotides [S. cerevisiae, YJL005w] 3e-10  
 [FUNCAT] 10.04.03 second messenger formation [S. cerevisiae, YJL005w] 3e-10  
 30 [BLOCKS] PRO1023F  
 [BLOCKS] PRO0677D  
 [BLOCKS] BL01032I  
 [BLOCKS] BL01032H  
 [BLOCKS] BL01032G  
 35 [BLOCKS] BL01032C Protein phosphatase 2C proteins  
 [BLOCKS] BL01032B Protein phosphatase 2C proteins  
 [SCOP] d1abq\_ 4.98.1.1.1 Protein serine/threonine phosphatase 2C [Huma] 1e-107  
 [EC] 3.1.3.43 [Pyruvate dehydrogenase (lipoamide)]-phosphatase 3e-09  
 40 [EC] 3.1.3.16 Phosphoprotein phosphatase 7e-35  
 [EC] 4.6.1.1 Adenylate cyclase 2e-11  
 [PIRKW] duplication 5e-11  
 [PIRKW] tandem repeat 8e-09  
 45 [PIRKW] serine/threonine-specific phosphatase 2e-27  
 [PIRKW] magnesium 6e-26  
 [PIRKW] cAMP biosynthesis 5e-11  
 [PIRKW] liver 2e-27  
 [PIRKW] leucine zipper 1e-08  
 50 [PIRKW] mitochondrion 3e-09  
 [PIRKW] phosphoric monoester hydrolase 7e-35  
 [PIRKW] phosphorus-oxygen lyase 2e-11  
 [SUPFAM] leucine-rich alpha-2-glycoprotein repeat homology 2e-11  
 55 [SUPFAM] yeast adenylate cyclase catalytic domain homology 2e-11  
 [SUPFAM] kinase interaction domain homology 3e-11  
 [SUPFAM] yeast adenylate cyclase 5e-11

[illegible]

30 PS01032 165->174 PP2C PD0C00792

```

35                                     Pfam for DKFZphtes3_31j20-2

HMM_NAME    Protein phosphatase 2C

40  HMM
    *G1CcMqGPRWRMsMEDaHiaylNF.....pcn1DWWhiMFFGVFDGHg
                                     +++ +G    R++M+DAH+ + ++      P++L ++
    +++F+VFDGHG
    Query           128  YVAERKG--EREEMQDAHVILNDITEECRPPSSLITR-
45  VSYFAVFDGHG     173

HMM
                                GDQCSQWCgeHWHdII*
                                G+++S++  +++H+ +
    Query           174  GIRASKFAAQNLHQNL      189

```



5. group: signal transduction

DKFZphtes3\_5k22 encodes a novel 455 amino acid protein with similarity to human paraneoplastic neuronal antigen MA1.

10 Antibodies against MA1 were found in patients with paraneoplastic neurological disorders. The protein is predominantly expressed in testis and brain, but ESTs are also found in liver, lung uterus and kidney.

15 The new protein can find application in studying/therapy of paraneoplastic neurological disorders.

strong similarity to paraneoplastic neuronal antigen MA1

20 Sequenced by Qiagen

Locus: unknown

25 Insert length: 3534 bp  
Poly A stretch at pos. 3514, polyadenylation signal at pos. 3494

```

    1 GAACGTCCGC GCTGGGAGCC AGGGGTGCCC GACCCCGTC CGCCGCCGCC
30   51 GCCGCCGCC CGCATAGCCC CCGGAGAGCC CTCTGGGGAC CCCGACCAGA
   101 AGGGACCTTG CCCTGGGAGA AGGCTGTGGA GACCTGGGCC TTCTGCGATC
   151 ACCCTAGGAG TTGATCCAGA TATGTGCCTC ACGCCCTGAT CACTCCCCCC
   201 AAATTAGTAT CCGCAGAGAT TCGAGGACAT GCCGTTGACC TTGTTACAGG
   251 ACTGGTGTCT GGGGGAACAC CTGAACACCC GGAGGTGCAT GCTCATCCTG
35   301 GGGATCCCCG AGGACTGTGG CGAGGATGAG TTTGAGGAGA CACTCCAGGA
   351 GGCTTGCAGG CACCTGGGCA GATACAGGGT GATTGGCAGG ATGTTTAGGA
   401 GGGAGGAGAA CGCCCAGGCG ATTCTACTGG AGCTGGCACA AGATATCGAC
   451 TATGCTTTGC TCCCAAGGGA AATACCAGGA AAGGGGGGGC CCTGGGAAGT
   501 GATTGTAAAA CCCCCTAACT CAGATGGGGA ATTTCTCAAC AGACTGAACC
40   551 GCTTCTTAGA GGAGGAGAGG CGGACCGTGT CAGATATGAA CCGAGTCCTC
   601 GGGTCGGACA CCAATTGTTC GGCTCCAAGA GTGACTATAT CACCAGAGTT
   651 CTGGACCTGG GCCCAGACTC TGGGGGCAGC AGTGCAGCCT CTGCTAGAAC
   701 AAATGTTGTA CCGAGAACTA AGAGTGTTTT CTGGGAACAC CATATCCATC
   751 CCAGGTGCAC TGGCCTTTGA TGCCTGGCTT GAGCACACCA CTGAGATGCT
45   801 ACAGATGTGG CAGGTGCCCC AGGGGGAAAA GAGGCGGAGG CTGATGGAAT
   851 GCTTACGGGG CCCTGCTCTC CAGGTGGTCA GTGGGCTCCG GGCCAGCAAT
   901 GCTTCCATAA CTGTGGAGGA GTGCCTGGCT GCCTTGCAAG AGGTGTTCTG
   951 ACCTGTGGAG AGCCATAAAA TTGCCCAGGT GAAGTTGTGT AAAGCCTATC
50  1001 AGGAGGCAGG AGAGAAAGTA TCTAGCTTTG TGTTACGTTT GGAACCCCTG
  1051 CTCCAAAGAG CTGTAGAAAA CAATGTGGTA TCACGTAGAA ACGTGAATCA
  1101 GACTCGCCTG AAACGAGTCT TAAGTGGGGC CACCCTTCCT GACAAACTCC
  1151 GAGATAAGCT TAAGCTGATG AAACAGCGAA GGAAGCCTCC TGGTTTCTCT
  1201 GCCCTGGTGA AGCTCCTGCG TGAGGAGGAG GAATGGGAGG CCACTTTAGG
  1251 TCCAGATAGG GAGAGTCTGG AGGGGCTGGA AGTAGCCCCA AGGCCACCTG
55  1301 CCAGGATCAC TGGGGTTGGG GCAGTACCTC TCCCTGCCTC TGGCAACAGT
  1351 TTTGATGCGA GGCCTTCCCA GGGCTACCGG CGCCGGAGGG GCAGAGGCCA
  1401 ACACCGAAGG GGTGGTGTGG CAAGGGCTGG CTCTCGAGGC TCAAGAAAAC
  1451 GGAAACGCCA CACATTCTGC TATAGCTGTG GGAAGACGG CCACATCAGG
```

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1501 GTACAGTGCA TCAACCCCTC CAACCTGCTC TTGGCCAAGG AGACAAAAGA
1551 GATATTGGAA GGAGGGGAAA GAGAAGCCCA GACAAACAGC AGATGAGTTG
1601 AGTGGGGCAG AGGGACAGGG CAGCCAGACC AAGGCCAAGC CTTCTCACCC
1651 TTGGCCAGCT GGAAGGGACT TCAGCAACCA AGACCACCTG GCAACAGGCT
5 1701 CAGTGGGGGT CAGGTCCAGG TCCCCGAAGA GGTGCTGGAG AGGAAAGCAG
1751 GGAGCCACTG CATCCAGCAC ATGGGGTGCC TGGGCCTCAG ATGGGGACCC
1801 CAAAGAAGCA GAAGCTGAAG AAGGTACGGC TGGGGGTTCT GTCTGCTCA
1851 TCCAACCACC CCTAAATACC CACCTGTGG ACTTTGAGCT GAACATGCCC
1901 ACTGGCCCCC AGGCCACATG GGACCTGGAG GAGCCTACCT GGGGCCTGCC
10 1951 CCTGCCAGCA GGTGCCAGGG CTGGTGAGGA AGAGCTGGGG GGCAGAGGTA
2001 AAGCCCTGCA GGGGAGGCCA CAGGGTCCAT CCCGTCTTCA GGATCATCTA
2051 CACTGCACTA GGGGAGCCCC AGGAAGGCAG CACCCTGGAG GCCCTGTGCC
2101 AGTGAGGACA GGAGACCCTA AGGCCCCGGG AGCCCACTGC CAGCCAGAGG
2151 TTGTGCAGGC AAGGAGACCA AAGATTGATG AGAAGACCCC CAGCAGGGGT
15 2201 ACTGGGTACC CGGCAGGCCA GTGCCCTCAC AGTTGACTTG GACCAGGGTG
2251 GCTGTGAAGG GAAGTCTTTG TTGCAAAGGA GGAGGAGGAA AAGGGAGGAC
2301 TTGGTAGGGT TTTGTTTCTT CTGCTTGTTT CTGTACAGGG CCACCAGACT
2351 CCTGGAGAGA TCAAGCAAGG AGAACCTGGG GCTGCCATGG CCAAAGCAAC
2401 TCAACAGATG CCAATGCCAA TTCCAAGGCC AGCCACAACC CTGCCACCTT
20 2451 GGGGAATCCA GCCTGGAGGC ATCCCCTAAG CAGCCAGCCA TGGCCTGGGT
2501 GGAGGCACCT GAAGACGTCT GTCCCAAACCT CCCCAGCCC TGAGCTGGGA
2551 GATGACAGGG GGAAAGAGGC CCTCTCAAGG GTGCCAGATG CCTGGGTCTC
2601 CCAAGAGGGG TCCCCCAACT CACCGTTCCC GGGACAGGCT GCCCCCTGTT
2651 CCAGGAAGCT CATCCTCACC TGTGTAGGCC CCTGTAGTGA CCCACGCGTC
25 2701 CAGCAGACGC CCACCCACCG CTAGCCGTTG TTCCTGTGCA AAGTAGTGTG
2751 CTATGCACCC ACCCAGGTGG CCGCCTCTGG GCCCAAGGCA CATGCTGTGA
2801 GCTTCCTGTG AGCCCAGGCT CTGCTCACTG CTGTCCCGCG TCATGAGCAC
2851 CACCTCTGCT TTCCCTGTGT AGATCTAGGC CAGTGGCTGC TTGTTCTTGT
2901 GGAGCTGTGT GTGTTCTTCT CTGAGCAGCT CCTCCCCGGA GTCCCCCAGC
30 2951 ACAGTCCCAG GAGATGACAG GAAGGAAGCA CCAGGGCAAG GCGGACGCTC
3001 ACCCTGTGAC CACGATGGTG ACCGTGGCTG TGGGAGGAAG AACTGGACCC
3051 AGGACGGAGC GGGGCTGCCC TGCTGAGGC TCCCGAGGAG CTTTGTGCTT
3101 TGGTGTTCCTA CCCCTGTTGT TACTCATGAC TCAGTTTCCT TGACCTGGTA
3151 GGGTGTTCCT TGCTGTGTTT TCCAGTGTCC TGTGACTGTC CTGTGCGGGC
35 3201 CATAGGGCAG GGCCCTGCCC CAGCAGATGG GCTTGGGAGG GGGCTCCCTA
3251 AAGCCAGTGG ACACTGCCAG AGTCTACCTT CCTGGCAAGA GGCAGACCCC
3301 GGGGCCCTCA GGAAGGAGGG AGTTGGCAGC GGGGGCTGCA GCAGGAGTAG
3351 GAGCAGATGA GCGGTCTTGC CAGGAACCTC AGGAGGAGGG GGGCCGGGAC
3401 CTGTGTGGGA CCTGTGTCTT GTGGTGGCCG TTTGCAGTTT CTCTCTGTG
40 3451 TGTGATTCCC TTCTCTTCAA TGGTTTCAGT ACGTGTTCCT CTTCAATAAA
3501 CTTCAATTCAG TGTAAAAAAA AAAAAAAAAA AAAA

```

## BLAST Results

-----

No BLAST result

## Medline entries

-----

99158179:

Mal, a novel neuron- and testis-specific protein, is recognized by the serum of patients with paraneoplastic neurological disorders.

## Peptide information for frame 1

5

ORF from 229 bp to 1593 bp; peptide length: 455  
 Category: strong similarity to known protein  
 Classification: unclassified

```

10  1  MPLTLLQDWCR RGEHLNTRRC MLILGIPEDC GEDEFEEETLQ EACRHLGRYR
    51  VIGRMFRREE NAQAILLELA QDIDYALLPR EIPGKGGPWE VIVKPRNSDG
    101 EFLNRLNRFL EEERRTVSDM NRVLGSDTNC SAPRVTISPE FWTWAQTLGA
    151 AVQPLLEQML YRELRVFSGN TISIPGALAF DAWLEHTTEM LQMWQVPEGE
    201 KRRRLMECLR GPALQVVSGL RASNASITVE ECLAALQQVF GPVESHKIAQ
15  251 VKLCKAYQEA GEKVSSFVLR LEPLLQRAVE NNVVSRRNVN QTRLKRVLSG
    301 ATLPDKLRDK LKLMKQRRKP PGFLALVKLL REEEEWEATL GPDRSLEGL
    351 EVAPRPPARI TGVGAVPLPA SGNSFDARPS QGYRRRRGRG QHRRGGVARA
    401 GSRGSRKRKR HTFCYSCGED GHIRVQCINP SNLLAKETK EILEGGGERA
    451 QTNRSR
  
```

20

## BLASTP hits

25 No BLASTP hits available

## Alert BLASTP hits for DKFZphtes3\_5k22, frame 1

```

30  TREMBLNEW:AB020690_1 gene: "KIAA0883"; product: "KIAA0883
    protein";
    Homo sapiens mRNA for KIAA0883 protein, complete cds., N = 1,
    Score =
    722, P = 2.4e-71
35  TREMBL:AF037364_1 gene: "MAL"; product: "paraneoplastic neuronal
    antigen MAL"; Homo sapiens paraneoplastic neuronal antigen MAL
    (MAL)
    mRNA, complete cds., N = 1, Score = 665, P = 2.6e-65
40  >TREMBLNEW:AB020690_1 gene: "KIAA0883"; product: "KIAA0883
    protein"; Homo
        sapiens mRNA for KIAA0883 protein, complete cds.
        Length = 364
  
```

45

## HSPs:

Score = 722 (108.3 bits), Expect = 2.4e-71, P = 2.4e-71  
 Identities = 156/348 (44%), Positives = 215/348 (61%)

50

```

Query:      1
MPLTLLQDWCRGEHLNTRRCMLILGIPEDCGEDEFEEETLQ EACRHLGRYRVIGRMFRREE 60
              M L LL+DWCR  ++ ++ +++ GIP D  E E +E LQE  +
LGRYR++G++FR++E
55  Sbjct:      1
MALALLEDWCRIMSVDEQKSLMVTGIPADFEEAEIQEVLQETLKSLGRYRLLGKIFRKQE 60
  
```

Query: 61  
 NAQAILLELAQDIDYALLPREIPGKGGPWVIVKPRNSDXXXXXXXXXXXXXXXXXTVSDM 120  
 NA A+LLEL +D D + +P E+ GKGG W+VI K N D

TVS M

5 Sbjct: 61  
 NANAVLLELLEDTDVSAIPSEVQGKGGVWVKVIFKTPNQDTEFLERLNLFEKEGQTVSGM 120

Query: 121 NRVLGSDTNC SAPRVTISPEFWTW--

10 AQTGAAVQPLLEQMLYREL RVFSGNTISIPGAL 178  
 R LG + A ISPE Q + A QPLL M YR+LRVFSG+  
 + P

Sbjct: 121 FRALGQEGVSPATVPCISPELLAHLGQAMAHAPQPLLP-  
 MRYRKLRVFSGSAVPAPEEE 179

15 Query: 179  
 AFDWLEHTTEMLQMWQVPEGEKRRRLMECLRG PALQVVSGLRASNASITVEECLAALQ 238  
 +F+ WLE TE+++ W V E EK+R L E LRGPAL ++ ++A N

SI+VEECL A +Q

20 Sbjct: 180  
 SFEVWLEQATEIVKEWPVTEAEKKRWLAESLRGPALDLMHIVQADNPSISVEECLEAFK 239

Query: 239  
 VFGPVESHKIAQVKLCKAYQAGEKVS SFVLRLEPLLQXXXXXXXXXXXXXXXXX LKRVL 298  
 VFG +ES + AQV+ K YQE GEKVS++VLRLE LL+

25 L++V+  
 Sbjct: 240  
 VFGSLESRRTAQVRYLKTYQEEGEKVSAYVLRLETLLRRAVEKRAIPRRIADQVRLEQVM 299

30 Query: 299 SGATLPDKLRDKLKLKMKQRRKPPGFLALVKLLREEEEWEATLGPDRSLE  
 348

+GATL L +L+ +K + PP FL L+K++REEEE EA+ + ES+E  
 Sbjct: 300 AGATLNQMLWCRLRELKDQGPSPFLELMKVIREEEEEASF--ENESIE  
 347

35 Pedant information for DKFZphtes3\_5k22, frame 1  
 -----

40 Report for DKFZphtes3\_5k22.1

45 [LENGTH] 455  
 [MW] 51514.34  
 [pI] 9.27  
 [HOMOL] TREMBLNEW:AB020690\_1 gene: "KIAA0883"; product:  
 "KIAA0883 protein"; Homo sapiens mRNA for KIAA0883 protein,  
 complete cds. 3e-75  
 [BLOCKS] BLO08768 Indoleamine 2,3-dioxygenase proteins  
 [PFAM] Zinc finger, CCHC class  
 50 [KW] Alpha\_Beta  
 [KW] LOW\_COMPLEXITY 13.41 %

55 SEQ MPLTLLQDWCRGEHLNTRRCMLILGIPEDCGEDEFEE TLQEACRHLGRYRVIGRMFRREE  
 SEG .....  
 PRD ccchhhhhccccccccccccccccccccccccchhhhhhhhhhhhhhhccceehhhhhhhhh

SEQ NAQAILLELAQDIDYALLPREIPGKGGPWVIVKPRNSDGEFLNRLNRFLEEERTVSDM

(No Prosite data available for DKFZphtes3\_5k22.1)

Pfam for DKFZphtes3\_5k22.1

```

35  HMM_NAME   Zinc finger, CCHC class
      HMM              *QkCWNCGKPGHMMRD CPE*
                        C++CG+ GH+  +C +
Query              412  TFCYSCGEDGHIRVQGIN
40

```

DKFZphtes3\_7n12

-----

5 group: transmembrane protein

DKFZphtes3\_7n12 encodes a novel 703 amino acid protein without similarity to known proteins.

10 The novel protein contains 1 transmembrane domain  
No informative BLAST results; No predictive prosite, pfam or SCOP  
motife.

15 The new protein can find application in studying the expression  
profile of testis-specific genes and as a new marker for  
testicular cells.

putative protein

20 contains transmembrane domain  
perhaps complete cds.

Sequenced by BMFZ

25 Locus: unknown

Insert length: 2347 bp

30 Poly A stretch at pos. 2271, polyadenylation signal at pos. 2253

```

      1 CGGCTGCAGT CTGGGCCCGGG GCCCTGTGCC GCTGAAGACA TGGAGTTTGT
    51 GTCTGGATAC CGGGATGAGT TCCTTGATTT CACTGCCCTT CTCTTCGGCT
   101 GGTTCGAAAG GTTTGTGGCA GAGCGTGGAG CTGTAGGGAC TAGCCTTGAG
   151 GGCCGCTGCC GGCAGCTGGA GGCCCAAGATC AGAAGGCTAC CCCAGGACCC
   201 TGCCCTTTGG GTGCTCCATG TCCTGCCCAA CCATAGTGTG GGCATCAGCC
   251 TGGGGCAAGG GGCAGAACCA GGTCTGGAC CAGGCCTGGG GACTGCCTGG
   301 CTCCTGGGAG ACAACCCTCC ACTCCACCTG CGAGACCTGA GCCCCTACAT
   351 CAGCTTTGTC AGCCTAGAGG ATGGGGAGGA AGGGGAGGAG GAAGAGGAGG
   401 AAGATGAAGA AGAAGAGAAG AGAGAGGACG GGGGTGCAGG CAGCACAGAG
   451 AAGGTGGAAC CAGAGGAGGA CCGGGAGCTA GCCCCTACCA GCAGGGAGTC
   501 CCCCCAGGAA ACAAAACCTC CAGGAGAGTC AGAGGAGGCT GCCCGGGAGG
   551 CAGGAGGTGG CAAGGATGGC TGCCGAGAGG ACAGGGTGGA GAACGAAACA
   601 AGACCCGAGA AGAGGAAGGG ACAGAGGAGT GAGGCTGCCC CCCTGCACGT
   651 TTCCTGTCTC TTACTTGTGA CGGATGAGCA TGGCACCATC TTGGGCATTG
   701 ATCTGCTAGT GGATGGAGCC CAGGGAACCG CAAGCTGGGG CTCAGGGACC
   751 AAGGACCTGG CTCCTTGGGC CTATGCTCTC CTCTGTCACA GCATGGCCTG
   801 TCCCATGGGC TCTGGGGATC CCCGAAAGCC CCGACAGCTT ACTGTGGGAG
   851 ATGCCCGGCT GCATCGAGAG CTGGAGAGCT TGGTCCCAAG GCTAGGTGTG
   901 AAGTTAGCCA AAACCCCAAT GCGGACATGG GGTCCCCGGC CAGGCTTCAC
   951 CTTTGCTTCC CTTCTGTGCTC GAACCTGCCA TGTGTGTAC AGGCACAGCT
  1001 TTGAAGCGAA GCTGACACCT TGCCCCCAGT GTAGTGCTGT CTTGTATTGT
  1051 GGAGAGGCTT GTCTCCGGGC TGACTGGCAG CGGTGCCCAG ATGATGTGAG
  1101 TCACCGATTT TGGTGCCCAA GGCTTGCAAG CTTTATGGAG CGGGCAGGAG
  1151 AACTGGCAAC CCTACCTTTT ACCTACACCG CAGAGGTGAC CAGTGAAACC
  1201 TTCAACAAAG AGGCCTTCCT GGCCTCTCGG GGCCTCACTC GTGGCTATTG
  1251 GACCCAGCTC AGCATGCTGA TTCCAGGCCG GGGCTTCTCC AGACACCCCC
  1301 GAGGCAACAC GCCATCCCTC AGCCTTCTTC GCGGTGGAGA CCCCTACCAG

```

```

1351 CTTCTCCAGG GAGACGGGAC TGCCCTGATG CCTCCTGTGC CCCCACATCC
1401 ACCCCGGGGT GTTTTGTCC CTGAGCTCAA CATCCAAAAC AAACAGTCAC
1451 TGAAGATCCA CGTGGTGGAG GCCGGGAAGG AGTTTGACCT TGTTCATGGTG
1501 TTTTGGGAGC TTTTGGTCCT GCTCCCCCAT GTGGCCCTGG AGTCAGCTT
5 1551 TGTAGGTGAT GGCCTGCCCC CCGAAAAGCGA CGAGCAGCAT TTTACCTGTC
1601 AGAGGGACAG CCTGGAGGTG TCTGTCCGGC CTGGTTCCGG CATATCAGCA
1651 CGGCCAGCT CTGGCACTAA GGAGAAAGGG GGCCGCAGGG ACCTGCAGAT
1701 CAAGGTGTCA GCAAGGCCCT ACCACCTGTT CCAGGGGCCC AAGCCTGACC
1751 TGGTTATTGG ATTTAACTCC GGGTTTGCTC TCAAGGATAC GTGGCTGAGG
10 1801 TCTCTGCCCC GTTACAGTC CCTCCGAGTG CCAGCCTTCT TCACCGAGAG
1851 CAGCGAGTAC AGCTGTGTGA TGGACGGCCA GACCATGGCG GTGGCCACTG
1901 GAGGGGGGAC CAGCCCTCCC CAGCCCAACC CCTTCCGCTC CCCCTTTCGC
1951 CTCAGAGCGG CCGACAACCTG CATGTCCTGG TACTGCAATG CCTTCATCTT
2001 CCACCTGGTT TACAAGCCTG CTCAAGGGAG CGGGGCCCGC CCGGCGCCCG
15 2051 GGGCCCCACC CCCATCCCCA ACTCCCTCTG CTCCTCCTGC CCCCACCCGA
2101 AGGCGCCGAG GAGAAAAGAA ACCTGGGCGG GGGGCCCGCC GGCGGAAATG
2151 AATGCTGATA CCCTAGTAGT CCCCAGCTCC CAAACACTGA AAGGAAAACG
2201 TGAAAACACT CAAGGCCTAG GGGGAGGACA GGTGTTGTTAA ACATGAAAAG
2251 GTAAATAAAA TTACTTGTTT GAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
20 2301 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA

```

## BLAST Results

-----

25

No BLAST result

## Medline entries

-----

30

No Medline entry

35

## Peptide information for frame 1

-----

```

40 ORF from 40 bp to 2148 bp; peptide length: 703
Category: putative protein
Classification: Transmembrane proteins unclassified

```

```

1 MEFVSGYRDE FLDFTALLFG WFRKFVAERG AVGTSLEGRC RQLEAQIRRL
51 PQDPALWVLH VLPNHSVGIS LGQGAEPGPG PGLGTAWLLG DNPPLHLRDL
45 101 SPYISFVSLE DGEEGEEEE EDEEEKRED GGAGSTEKVE PEEDRELAPT
151 SRESPQETNP PGESEEAARE AGGGKDGCRE DRVENETRPQ KRKGQRSEAA
201 PLHVSCLLLV TDEHGTILGI DLLVDGAQGT ASWGSGBKDL APWAYALLCH
251 SMACPMGSGD PRKPRQLTVG DARLHRELES LVPRLGVKLA KTPMRTWGPR
301 PGFTFASLRA RTCHVCHRHS FEAKLTPCPQ CSAVLYCGEA CLRADWQRCF
50 351 DDVSHRFWCP RLAAFMERAG ELATLPFTYT AEVTSETFNK EAFLASRLT
401 RGYWTQLSML IPGPGFSRHP RGNTPSLSLL RGGDPYQLLQ GDGTALMPPV
451 PPHPPRGV FV PELNIQNKQS LKIHVVEAGK EFDLVMVFE LLVLLPHVAL
501 ELQFVGDGLP PESDEQHFTL QRDLSLEVSVR PGSGISARPS SGTKEKGGRR
55 551 DLQIKVSARP YHLFQGP KPD LVIGFNSGFA LKDTWLRLSLP RLQSLRVP AF
601 FTESSEYSCV MDGQTM AVAT GGGTSP PQPN PFRSPFRLRA ADN CMSWYCN
651 AFIFHLVYKP AQGSGARPAP GPPPPSPTPS APPAPTRRRR GEKKPGRGAR
701 RRK

```

5 No BLASTP hits available

No Alert BLASTP hits found

Report for DKFZphtes3\_7n12.1

```
SEQ    MEFVSGYRDEFLDFTALLFGWFRKFVAERGAVGTSLEGRCRQLAQIRRLPQDPALWVLH
SEG      .....
PRD     cccceecchhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhccccccccccc
MEM
```

```
SEQ      VLPNHSVGISLGQGAEPGPGPLGTAWLLGDNPPHLRLDSPYISFVSLEDGEEGEEEEEE
SEG      .....xxxxxxxxxxxx
PRD      cccccccccccccccccccccceeeeeccccccccccccccccceeeeecccccchhhhhhhh
MEM      .....
```

```
SEQ EDEEEKREDGGAGSTEKVEPEEDRELAPTSRESPQETNPPGESEEAAREAGGKGDCRE  
SEG xxxxxxxxxxxxxxxx.....-xxxxxxxxxxxxxxxxxx.....  
PRD hhhhhhccccccccccccccccccccccccccchhhhhhcccccccce  
MEM .....-
```

```
SEQ  DRVENETRPQKRKGQRSEAAPLHVSCLLLVTDEHGTILGIDLLVDGAQGTASWGSGTKDL
SEG  .....
PRD  eeeeeeeeeeeeeeeeeeechhhhhhheeeeeeeeeeechhhhhhcccccccccccccccc
MEM  .....
```

```
SEQ  APWAYALLCHSMACPMGSGDPRKPRQLTVGDARLHRELESLVPRLGVKLAKTPMRTWGPR
SEG  .....
PRD  hhhhhhhhhhhhhhhccccccccccccccbeeeecchhhhhhhhhhhhhcccccccccccccccccc
MEM  .....
```

SEQ	PGFTFASLRARTCHVCHRHSFEAKLTPCPQCSAVLYCGEACLRADWQRCPPDVSHRFWCP
SEG	.....
PRD	ccccchhhhhhhhhcc
MEM	.....

```
SEQ  RLAAFMERAGELATLPFTYTAEVTSETFNKEAFLASRGLTRGYWTQLSMLIPGPGFSRHP
SEG  .....
PRD  hhhhhhhhhhhhhhhccccccccchhhhhhhhhhhhhhhhhccccchhhhhcccccccccccc
MEM  .....
```



5

10

15

20

25

30

0000 0000 0000 0000 0000 0000 0000 0000 0000 0000 0000 0000 0000

**Locus:** unknown

Insert length: 2011 bp

Poly A stretch at pos. 1986, no polyadenylation signal found

```

5      1 CATGGCAACA TGAGCAGTGC TGAGATAATT GGTCTACAA ATCTTATAAT
      51 TCTGCTAGAG GATGAAGTCT TTGCCGATTT TTTCAACACA TTTCTTTCCC
     101 TCCCCGTTTT TGGTCAGACA CCATTTTATA CTGTTGAAAA TTCACAGTGG
     151 AGCTTGTGGC CAGAAATACC TTGTAACCTG ATTGCCAAAT ACAAAGGGTT
     201 ATTGACCTGG TTGGAAAAAT GCCGATTACC TTTCTTCTGT AAAACAAACT
10     251 TGTGTTTCCA TTACATTCTC TGTCAGGAGT TCATCAGTTT CATTAAGTCC
     301 CCAGAAGGAG CCAAGATGAT GAGATGGAAA AAGGCAGACC AGTGGCTACT
     351 CCAGAAATGC ATTGGCGGGG TCAGAGGGAT GTGGCGCTTC TATTCCTACC
     401 TCACAGGCAG TGCAGGTGAA GAATTGGTGG ATTTCTGGAT CCTTGCTGAG
     451 AACATCCTGA GCATAGATGA GATGGACCTG GAAGTGAGAG ACTACTACCT
15     501 GTCCCTCCTC CTCATGCTGA GGGCCACTCA TCTGCAGGAG GGCTCCAGGG
     551 TGGTAACCTT CTGTAACATG AACATCAAGT CCCTCCTGAA CCTCTCCATC
     601 TGGCATCCCA ACCAATCAAC CACTAGGAGG GAGATCCTGA GCCACATGCA
     651 GAAAGTGGCT CTGTTCAAAC TCCAGAGCTA TTGGCTTCCC AACTTTTACA
     701 CCCACACCAA GATGACCATG GCCAAGGAGG AAGCATGCCA TGGTCTGATG
20     751 CAAGAGTACG AGACTCGCTT ATACAGCGTT TGCTACACCC ACATAGGAGG
     801 GCTCCCTCTG AACATGAGCA TCAAGAAGTG CCACCACTTT CAGAAACGGT
     851 ACTCAAGCAG GAAAGCCAAG AGGAAGATGT GGCAATTGGT AGATCCTGAC
     901 TCTTGGTCTC TGGAAATGGA TCTCAAGCCA GATGCTATTG GTATGCCCCCT
     951 ACAGGAGACA TGTCTCAAG AGAAGGTGGT TATACAAATG CCTTCCCTGA
25    1001 AAATGGCTTC TTCAAAGGAA ACAAGAATCA GTTCCCTGGA AAAGGATATG
     1051 CATTATGCAA AAATATCCAG CATGGAGAAT AAAGCCAAGA GCCACCTCCA
     1101 CATGGAAGCC CCCTTTGAGA CAAAGGTCTC TACCCACCTG AGGACTGTCA
     1151 TCCCCATTGT CAATCACTCC TCCAAGATGA CAATTCAGAA GGCCATCAAG
     1201 CAAAGCTTCT CCTTAGGATA CATCCACTTG GCCTTGTGTG CTGATGCCTG
30    1251 TGCAGGGAAC CCTTTCGGG ACCACCTGAA GAAGCTGAAT TTGAAAGTGG
     1301 AGATCCAAC TCTTGACCTC TGGCAGGACT TGCAGCATTT CCTCAGTGTC
     1351 CTTCTGAATA ACAAAAAGAA TGGGAATGCA ATCTTTCGTC ACTTGCTGGG
     1401 TGACAGAATC TGCGAGCTCT ACCTGAATGA GCAGATTGGT CCGTGCTTAC
     1451 CACTCAAATC CCAAACCATT CAGGGCCTGA AGGAACTATT GCCCTCTGGG
35    1501 GATGTGATCC CCTGGATTCC CAAAGCCCAG AAGGAGATTG GCAAGATGCT
     1551 CAGTCCCTGG TATGATGAGT TTCTAGATGA AGAGGACTAC TGGTTTCTCC
     1601 TTTTTACGGT AGGAAGGACT TTGGGTTAGG AAGGAATCAT GAGGATGAGG
     1651 GAAGAAGAAA GAGTAATTAC TGTTTTAAAA GGGTTATGTG TTAAGTAAA
     1701 TGAAATTGTT ATTTTTCCTA GAGTCAACCA AAGATCAGCA TGGTCCCTGT
40    1751 TGTCTATAAG CTAAACCTCT CAAGGAAAAG GACTCAGTGC ATAAGATGAC
     1801 TTTGGTGAAA CCGGTCTCT ACTAAAAATA CAAAAAATTA GCCGGGCGTA
     1851 GTGGCGGGCG CCTGTAGTCC CAGCTACTTG GGAGGCTGAG GCAGGAGAAT
     1901 GGTGTGAACC CGGGAGGCGG AGCTTGCAGT GAGCCGAGAT CCCGCCACTG
     1951 CACGCCAGCC TGGGCGACAG AGCGAGACTC CGTCTCAAAA AAAAAAAAAA
45    2001 AAAAAAAAAA G

```

## BLAST Results

-----

50

No BLAST result

## Medline entries

-----

55

No Medline entry

## Peptide information for frame 1

5

ORF from 10 bp to 1626 bp; peptide length: 539  
 Category: putative protein  
 Classification: no clue

```

10      1 MSSAEIIGST NLIILLEDEV FADFFNTFLS LPVFGQTPFY TVENSQWSLW
      51 PEIPCNLIAK YKGLLTWLEK CRLPFFCKTN LCFHYILCQE FISFIKSPEG
     101 AKMMRWKKAD QWLLQKCIGG VRGMWRFYSY LTGSAGEELV DFWILAENIL
     151 SIDEMDLEVR DYYLSLLML RATHLQEGSR VVTLCNMNIK SLLNLSIWHP
     201 NQSTTRREIL SHMQKVALFK LQSYWLPNFY THTKMTMAKE EACHGLMQEY
15      251 ETRLYSVCYT HIGGLPLNMS IKKCHHFQKR YSSRKAKRKM WQLVDPDSWS
     301 LEMDLKPDAI GMPLQETCPQ EKVVIQMPSL KMASSKETRI SSLEKDMHYA
     351 KISSMENKAK SHLHMEAPFE TKVSTHLRTV IPIVNHSSKM TIQKAIKQSF
     401 SLGYIHLALC ADACAGNPFR DHLKKLNLKV EIQLLDLWQD LQHFSLVLLN
     451 NKKNGNAIFR HLLGDRICEL YLNEQIGPCL PLKSQTIQGL KELLPSGDVI
20      501 PWIPKAQKEI CKMLSPWYDE FLDEEDYWFL LFTVGRTLGL
  
```

## BLASTP hits

25

No BLASTP hits available

Alert BLASTP hits for DKFZphtes3\_9e1b, frame 1

30 No Alert BLASTP hits found

Pedant information for DKFZphtes3\_9e1b, frame 1

35

Report for DKFZphtes3\_9e1b.1

```

      [LENGTH] 542
      [MW]      62906.06
40      [pI]      8.35
      [KW]      Alpha_Beta

      SEQ HGNMSSAEIIGSTNLIILLEDEVFADFFNTFLSLPVFGQTPFYTVENSQWSLWPEIPCNL
45      PRD cccccceeeccccceehhhhhhhhhccccccccccccccccccccccccccccccccchh

      SEQ IAKYKGLLTWLEKCRLPFFCKTNLCFHYILCQEFISFIKSPEGAKMMRWKKADQWLLQKC
      PRD hhhccceeeccccccccccccccccceehhhhhhhhhhhccccchhhhhhhhhcchhhhhhhh

50      SEQ IGGVRGMWRFYSYLTGSAGEELVDFWILAENILSIDEMDLEVRDYYLSLLMLRATHLQE
      PRD cccccceeeccccccccchhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhccc

      SEQ GSRVVTLCNMNIKSLNLSIWHPNQSTTRREILSHMQKVALFKLQSYWLPNFYTHTKMTM
      PRD cceeeeccccchhhhhhhhhccccccchhhhhhhhhhhhhhhhhhhhhccccchhhhhhh

55      SEQ AKEEACHGLMQEYETRLYSVCYTHIGGLPLNMSIKKCHHFQKRYSSRKAKRKMWQLVDPD
      PRD hhhhhhhhhhhhhhhhhheeeeeeccccccccccccccccchhhhhhhhhhhhhheeeccc
  
```



- 5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55
- CONSENSUS: C-x-[DN]-x(4)-[FY]-x-C-x-C.  
 NAME: Vitamin K-dependent carboxylation domain.  
 CONSENSUS: x(12)-E-x(3)-E-x-C-x(6)-[DEN]-x-[LIVMFY]-x(9)-[FYW].  
 NAME: Phosphopantetheine attachment site.  
 CONSENSUS: [DEQGSTALMKRH]-[LIVMFYSTAC]-[GNQ]-[LIVMFYAG]-[DNEKHS]-S-[LIVMST]-  
 CONSENSUS: {PCFY}-[STAGCPQLIVMF]-[LIVMATN]-[DENQGTAKRHLM]-[LIVMWSTAJ]-[LIVGSTACR]-  
 CONSENSUS: x(2)-[LIVMFA].  
 NAME: Acyl carrier protein phosphopantetheine domain profile.  
 NAME: Prokaryotic membrane lipoprotein lipid attachment site.  
 CONSENSUS: {DERK}(6)-[LIVMFYSTAG](2)-[LIVMFYSTAGQ]-[AGS]-C.  
 NAME: Prokaryotic N-terminal methylation site.  
 CONSENSUS: [KRHEQSTAG]-G-[FYLIVM]-[ST]-[LT]-[LIVP]-E-[LIVMFYSTAG](14).  
 NAME: Prenyl group binding site (CAAX box).  
 CONSENSUS: C-{DENQ}-[LIVM]-x>.  
 NAME: Protein splicing signature.  
 CONSENSUS: [DNEG]-x-[LIVFA]-[LIVMY]-[LVAST]-H-N-[STC].  
 NAME: Endoplasmic reticulum targeting sequence.  
 CONSENSUS: [KRHQSA]-[DENQ]-E-L>.  
 NAME: Microbodies C-terminal targeting signal.  
 CONSENSUS: [STAGCN]-[RKH]-[LIVMAFY]>.  
 NAME: Gram-positive cocci surface proteins 'anchoring' hexapeptide.  
 CONSENSUS: L-P-x-T-G-[STGAVDE].  
 NAME: Bipartite nuclear targeting sequence.  
 NAME: Cell attachment sequence.  
 CONSENSUS: R-G-D.  
 NAME: ATP/GTP-binding site motif A (P-loop).  
 CONSENSUS: [AG]-x(4)-G-K-[ST].  
 NAME: Cyclic nucleotide-binding domain signature 1.  
 CONSENSUS: [LIVM]-[VIC]-x(2)-G-[DENQTA]-x-[GAC]-x(2)-[LIVMFY](4)-x(2)-G.  
 NAME: Cyclic nucleotide-binding domain signature 2.  
 CONSENSUS: [LIVMF]-G-E-x-[GAS]-[LIVM]-x(5,11)-R-[STAQ]-A-x-[LIVMA]-x-[STACV].  
 NAME: cAMP/cGMP binding motif.

- NAME: EF-hand calcium-binding domain.  
 CONSSENSUS: D-x-[DNS]-[ILVFW]-[DENSTG]-[DNQHRK]-[GP]-  
 [LIVMC]-[DENQSTAGC]-x(2)-  
 5 CONSSENSUS: [DE]-[LIVMFYW].
- NAME: Actinin-type actin-binding domain signature 1.  
 CONSSENSUS: [EQ]-x(2)-[ATV]-[FY]-x(2)-W-x-N.
- 10 NAME: Actinin-type actin-binding domain signature 2.  
 CONSSENSUS: [LIVM]-x-[SGN]-[LIVM]-[DAGHE]-[SAG]-x-[DNEAG]-  
 [LIVM]-x-[DEAG]-x(4)-  
 CONSSENSUS: [LIVM]-x-[LM]-[SAG]-[LIVM]-[LIVMT]-W-x-[LIVM](2).
- 15 NAME: Anaphylatoxin domain signature.  
 CONSSENSUS: [CSH]-C-x(2)-[GAP]-x(7,8)-[GASTDEQR]-C-[GASTDEQL]-  
 x(3,9)-[GASTDEQN]-x(2)-  
 CONSSENSUS: [CE]-x(6,7)-C-C.
- 20 NAME: Anaphylatoxin domain profile.
- NAME: Apple domain.  
 CONSSENSUS: C-x(3)-[LIVMFY]-x(5)-[LIVMFY]-x(3)-[DENQ]-  
 [LIVMFY]-x(10)-C-x(3)-C-T-  
 CONSSENSUS: x(4)-C-x-[LIVMFY]-F-x-[FY]-x(13,14)-C-x-[LIVMFY]-  
 25 [RK]-x-[ST]-x(14,15)-  
 CONSSENSUS: S-G-x-[ST]-[LIVMFY]-x(2)-C.
- NAME: Band 4.1 family domain signature 1.  
 CONSSENSUS: W-[LIV]-x(3)-[KRQ]-x-[LIVM]-x(2)-[QH]-x(0,2)-  
 30 [LIVMF]-x(6,8)-[LIVMF]-  
 CONSSENSUS: x(3,5)-F-[FY]-x(2)-[DENS].
- NAME: Band 4.1 family domain signature 2.  
 CONSSENSUS: [HYW]-x(9)-[DENQSTV]-[SA]-x(3)-[FY]-[LIVM]-x(2)-  
 35 [ACV]-x(2)-[LM]-x(2)-  
 CONSSENSUS: [FY]-G-x-[DENQST]-[LIVMFYS].
- NAME: Band 4.1 family domain profile.
- 40 NAME: Clq domain signature.  
 CONSSENSUS: F-x(5)-[ND]-x(4)-[FYWL]-x(6)-F-x(5)-G-x-Y-x-F-x-  
 [FY].
- NAME: C-terminal cystine knot signature.  
 45 CONSSENSUS: C-C-x(13)-C-x(2)-[GN]-x(12)-C-x-C-x(2,4)-C.
- NAME: C-terminal cystine knot profile.
- NAME: CUB domain profile.
- 50 NAME: Death domain profile.
- NAME: EGF-like domain signature 1.  
 CONSSENSUS: C-x-C-x(5)-G-x(2)-C.
- 55 NAME: EGF-like domain signature 2.  
 CONSSENSUS: C-x-C-x(2)-[GP]-[FYW]-x(4,8)-C.

- NAME: Calcium-binding EGF-like domain pattern signature.  
 CONSENSUS: [DEQN]-x-[DEQN](2)-C-x(3,14)-C-x(3,7)-C-x-[DN]-x(4)-[FY]-x-C.
- 5 NAME: Laminin-type EGF-like (LE) domain signature.  
 CONSENSUS: C-x(1,2)-C-x(5)-G-x(2)-C-x(2)-C-x(3,4)-[FYW]-x(3,15)-C.
- 10 NAME: Coagulation factors 5/8 type C domain (FA58C) signature 1.  
 CONSENSUS: [GAS]-W-x(7,15)-[FYW]-[LIV]-x-[LIVFA]-[GSTDEN]-x(6)-[LIVF]-x(2)-[IV]-x-  
 CONSENSUS: [LIVT]-[QKM]-G.
- 15 NAME: Coagulation factors 5/8 type C domain (FA58C) signature 2.  
 CONSENSUS: P-x(8,10)-[LM]-R-x-[GE]-[LIVP]-x-G-C.
- 20 NAME: Forkhead-associated (FHA) domain profile.  
 NAME: Fibrinogen beta and gamma chains C-terminal domain signature.  
 CONSENSUS: W-W-[LIVMFYW]-x(2)-C-x(2)-[GSA]-x(2)-N-G.
- 25 NAME: Type I fibronectin domain.  
 CONSENSUS: C-x(6,8)-[LFY]-x(5)-[FYW]-x-[RK]-x(8,10)-C-x-C-x(6,9)-C.
- 30 NAME: Type II fibronectin collagen-binding domain.  
 CONSENSUS: C-x(2)-P-F-x-[FYWI]-x(7)-C-x(8,10)-W-C-x(4)-[DNSR]-[FYW]-x(3,5)-[FYW]-x-  
 CONSENSUS: [FYWI]-C.
- 35 NAME: Hemopexin domain signature.  
 CONSENSUS: [LIFAT]-x(3)-W-x(2,3)-[PE]-x(2)-[LIVMFY]-[DENQS]-[STA]-[AV]-[LIVMFY].
- 40 NAME: Kringle domain signature.  
 CONSENSUS: [FY]-C-R-N-P-[DNR].
- NAME: Kringle domain profile.
- NAME: LDL-receptor class A (LDLRA) domain signature.  
 CONSENSUS: C-[VILMA]-x(5)-C-[DNH]-x(3)-[DENQHT]-C-x(3,4)-[STADE]-[DEH]-[DE]-x(1,5)-  
 45 CONSENSUS: C.
- NAME: LDL-receptor class A (LDLRA) domain profile.
- 50 NAME: C-type lectin domain signature.  
 CONSENSUS: C-[LIVMFYATG]-x(5,12)-[WL]-x-[DNSR]-x(2)-C-x(5,6)-[FYWLIVSTA]-[LIVMSTA]-  
 CONSENSUS: C.
- 55 NAME: C-type lectin domain profile.
- NAME: Link domain signature.  
 CONSENSUS: C-x(15)-A-x(3,4)-G-x(3)-C-x(2)-G-x(8,9)-P-x(7)-C.

- NAME: Osteonectin domain signature 1.  
 5 CONSENSUS: C-x-[DN]-x(2)-C-x(2)-G-[KRH]-x-C-x(6,7)-P-x-C-x-C-x(3,5)-C-P.
- NAME: Osteonectin domain signature 2.  
 CONSENSUS: F-P-x-R-[IM]-x-D-W-L-x-[NQ].
- NAME: Somatomedin B domain signature.  
 10 CONSENSUS: C-x-C-x(3)-C-x(5)-C-C-x-[DN]-[FY]-x(3)-C.
- NAME: Thyroglobulin type-1 repeat signature.  
 CONSENSUS: [FYWHP]-x-P-x-C-x(3,4)-G-x-[FYW]-x(3)-Q-C-x(4,10)-C-[FYW]-C-V-x(3,4)-  
 15 CONSENSUS: [SG].
- NAME: P-type 'Trefoil' domain signature.  
 CONSENSUS: R-x(2)-C-x-[FYPT]-x(3,4)-[ST]-x(3)-C-x(4)-C-C-[FYWH].  
 20
- NAME: Cellulose-binding domain, bacterial type.  
 CONSENSUS: W-N-[STAGR]-[STDN]-[LIVM]-x(2)-[GST]-x-[GST]-x(2)-[LIVMFT]-[GA].
- NAME: Cellulose-binding domain, fungal type.  
 25 CONSENSUS: C-G-G-x(4,7)-G-x(3)-C-x(5)-C-x(3,5)-[NHG]-x-[FYWM]-x(2)-Q-C.
- NAME: Chitin recognition or binding domain signature.  
 30 CONSENSUS: C-x(4,5)-C-C-S-x(2)-G-x-C-G-x(4)-[FYW]-C.
- NAME: Barwin domain signature 1.  
 CONSENSUS: C-G-[KR]-C-L-x-V-x-N.
- NAME: Barwin domain signature 2.  
 35 CONSENSUS: V-[DN]-Y-[EQ]-F-V-[DN]-C.
- NAME: BIR repeat.  
 CONSENSUS: [HKEPILVY]-x(2)-R-x(3,7)-[FYW]-x(11,14)-[STAN]-G-[LMF]-X-[FYHDA]-X(4)-  
 40 CONSENSUS: [DESL]-X(2,3)-C-X(2)-C-X(6)-[WA]-X(9)-H-X(4)-[PRSD]-X-C-X(2)-[LIVMA].
- NAME: WAP-type 'four-disulfide core' domain signature.  
 45 CONSENSUS: C-x-[C]-[DN]-x(2)-C-x(5)-C-C.
- NAME: Phorbol esters / diacylglycerol binding domain.  
 CONSENSUS: H-x-[LIVMFYW]-x(8,11)-C-x(2)-C-x(3)-[LIVMFC]-x(5,10)-C-x(2)-C-x(4)-[HD]-  
 50 CONSENSUS: x(2)-C-x(5,9)-C.
- NAME: C2 domain signature.  
 CONSENSUS: [ACG]-x(2)-L-x(2,3)-D-x(1,2)-[NGSTLIF]-[GTMR]-x-[ESTAP]-D-[PA]-[FY].  
 55
- NAME: C2-domain profile.
- NAME: CAP-Gly domain signature.



CONSENSUS: G-x(8,10)-[FYW]-x-G-[LIVM]-x-[LIVMFY]-x(4)-G-K-  
 [NH]-x-G-[STAR]-x(2)-G-  
 CONSENSUS: x(2)-[LY]-F.

5 NAME: Ly-b / u-PAR domain signature.  
 CONSENSUS: [EQR]-C-[LIVMFYAH]-x-C-x(5,8)-C-x(3,8)-[EDNQSTV]-  
 C-[C]-x(5)-C-  
 CONSENSUS: x(12,24)-C.

10 NAME: MAM domain signature.  
 CONSENSUS: G-x-[LIVMFY](2)-x(3)-[STA]-x(10,11)-[LV]-x(4)-  
 [LIVMF]-x(6,7)-C-[LIVM]-x-  
 CONSENSUS: F-x-[LIVMFY]-x(3)-[GSC].

15 NAME: MAM domain profile.

NAME: PH domain profile.

NAME: Phosphotyrosine interaction domain (PID) profile.

20

NAME: Src homology 2 (SH2) domain profile.

NAME: Src homology 3 (SH3) domain profile.

25 NAME: VWFC domain signature.  
 CONSENSUS: C-x(2,3)-C-x-C-x(6,14)-C-x(3,4)-C-x(2,10)-C-  
 x(9,16)-C-C-x(2,4)-C.

NAME: WW/rsp5/WWP domain signature.  
 30 CONSENSUS: W-x(9,11)-[VFY]-[FYW]-x(6,7)-[GSTNE]-[GSTQCR]-  
 [FYW]-x(2)-P.

NAME: WW/rsp5/WWP domain profile.

35 NAME: ZP domain signature.  
 CONSENSUS: [LIVMFYW]-x(7)-[STAPDNL]-x(3)-[LIVMFYW]-x-  
 [LIVMFYW]-x-[LIVMFYW]-x(2)-C-  
 CONSENSUS: [LIVMFYW]-x-[ST]-[PSL]-x(2,4)-[DENS]-x-[STADNQLF]-  
 x(6)-[LIVM](2)-x(3,4)-  
 40 CONSENSUS: C.

NAME: S-layer homology domain signature.  
 CONSENSUS: [LVFYT]-x-[DA]-x(2,5)-[DNGSATPHY]-[WYFPDA]-x(4)-  
 [LIV]-x(2)-[GTALV]-

45 CONSENSUS: x(4,6)-[LIVFYC]-x(2)-G-x-[PGSTA]-x(2,3)-[MFYA]-x-  
 [PGAV]-x(3,10)-[LIVMA]-  
 CONSENSUS: [STKR]-[RY]-x-[EQ]-x-[STALIVM].

NAME: 'Homeobox' domain signature.  
 50 CONSENSUS: [LIVMFYG]-[ASLVR]-x(2)-[LIVMSTACN]-x-[LIVM]-x(4)-  
 [LIV]-[RKNESTAIY]-  
 CONSENSUS: [LIVFSTNKH]-W-[FYVC]-x-[ENDQTAH]-x(5)-[RKNAIMW].

NAME: 'Homeobox' domain profile.

55

NAME: 'Homeobox' antennapedia-type protein signature.  
 CONSENSUS: [LIVMFE]-[FY]-P-W-M-[KRQTA].

- NAME: 'Homeobox' engrailed-type protein signature.  
 CONSENSUS: L-M-A-Q-G-L-Y-N.
- 5 NAME: 'Paired box' domain signature.  
 CONSENSUS: R-P-C-x(11)-C-V-S.
- NAME: 'POU' domain signature 1.  
 CONSENSUS: [RKQ]-R-[LIM]-x-[LF]-G-[LIVMFY]-x-Q-x-[DNQ]-V-G.
- 10 NAME: 'POU' domain signature 2.  
 CONSENSUS: S-Q-[ST]-[TA]-I-[SC]-R-F-E-x-[LSQ]-x-[LI]-[ST].
- NAME: Zinc finger, C2H2 type, domain.  
 CONSENSUS: C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H.
- 15 NAME: Zinc finger, C3HC4 type (RING finger), signature.  
 CONSENSUS: C-x-H-x-[LIVMFY]-C-x(2)-C-[LIVMYA].
- NAME: Nuclear hormones receptors DNA-binding region  
 signature.  
 CONSENSUS: C-x(2)-C-x-[DE]-x(5)-[HN]-[FY]-x(4)-C-x(2)-C-x(2)-  
 F-F-x-R.
- 20 NAME: GATA-type zinc finger domain.  
 CONSENSUS: C-x-[DN]-C-x(4,5)-[ST]-x(2)-W-[HR]-[RK]-x(3)-[GN]-  
 x(3,4)-C-N-[AS]-C.
- NAME: Poly(ADP-ribose) polymerase zinc finger domain  
 signature.  
 CONSENSUS: C-[KR]-x-C-x(3)-I-x-K-x(3)-[RG]-x(16,18)-W-[FYH]-  
 H-x(2)-C.
- 30 NAME: Poly(ADP-ribose) polymerase zinc finger domain  
 profile.
- 35 NAME: Fungal Zn(2)-Cys(6) binuclear cluster domain  
 signature.  
 CONSENSUS: [GASTPV]-C-x(2)-C-[RKHSTACW]-x(2)-[RKHQ]-x(2)-C-  
 x(5,12)-C-x(2)-C-x(6,8)-
- 40 CONSENSUS: C.
- NAME: Fungal Zn(2)-Cys(6) binuclear cluster domain profile.
- NAME: Prokaryotic dksA/traR C4-type zinc finger.  
 CONSENSUS: C-[DES]-x-C-x(3)-I-x(3)-R-x(4)-P-x(4)-C-x(2)-C.
- 45 NAME: Copper-fist domain signature.  
 CONSENSUS: M-[LIVMF](3)-x(3)-K-[MY]-A-C-x(2)-C-I-[KR]-x-H-  
 [KR]-x(3)-C-x-H-x(8)-
- 50 CONSENSUS: [KR]-x-[KR]-G-R-P.
- NAME: Copper fist DNA binding domain profile.
- NAME: Leucine zipper pattern.  
 CONSENSUS: L-x(6)-L-x(6)-L-x(6)-L.
- 55 NAME: bZIP transcription factors basic domain signature.

- CONSENSUS: [KR]-x(1,3)-[RKSAQ]-N-x(2)-[SAQ](2)-x-[RKTAENQ]-x-R-x-[RK].
- 5 NAME: Myb DNA-binding domain repeat signature 1.  
CONSENSUS: W-[ST]-x(2)-E-[DE]-x(2)-[LIV].
- NAME: Myb DNA-binding domain repeat signature 2.  
CONSENSUS: W-x(2)-[LI]-[SAG]-x(4,5)-R-x(8)-[YW]-x(3)-[LIVM].
- 10 NAME: Myc-type, 'helix-loop-helix' dimerization domain signature.  
CONSENSUS: [DENSTAP]-K-[LIVMWAGSN]-{FYWCPHKR}-[LIVT]-[LIV]-x(2)-[STAV]-[LIVMSTAC]-x-  
CONSENSUS: [VMFYH]-[LIVMTA]-{P}-{P}-[LIVMSR].
- 15 NAME: p53 tumor antigen signature.  
CONSENSUS: M-C-N-S-S-C-M-G-G-M-N-R-R.
- 20 NAME: CBF-A/NF-YB subunit signature.  
CONSENSUS: C-V-S-E-x-I-S-F-[LIVM]-T-[SG]-E-A-[SC]-[DE]-[KRQ]-C.
- NAME: CBF-B/NF-YA subunit signature.  
CONSENSUS: Y-V-N-A-K-Q-Y-x-R-I-L-K-R-R-x-A-R-A-K-L-E.
- 25 NAME: 'Cold-shock' DNA-binding domain signature.  
CONSENSUS: [FY]-G-F-I-x(6,7)-[DER]-[LIVM]-F-x-H-x-[STKR]-x-[LIVMFY].
- 30 NAME: CTF/NF-I signature.  
CONSENSUS: R-K-R-K-Y-F-K-K-H-E-K-R.
- NAME: Ets-domain signature 1.  
CONSENSUS: L-[FYW]-[QEDH]-F-[LI]-[LVQK]-x-[LI]-L.
- 35 NAME: Ets-domain signature 2.  
CONSENSUS: [RKH]-x(2)-M-x-Y-[DENQ]-x-[LIVM]-[STAG]-R-[STAG]-[LI]-R-x-Y.
- 40 NAME: Ets-domain profile.
- NAME: Fork head domain signature 1.  
CONSENSUS: [KR]-P-[PTQ]-[FYLVQH]-S-[FY]-x(2)-[LIVM]-x(3,4)-[AC]-[LIM].
- 45 NAME: Fork head domain signature 2.  
CONSENSUS: W-[QKR]-[NS]-S-[LIV]-R-H.
- NAME: Fork head domain profile.
- 50 NAME: HSF-type DNA-binding domain signature.  
CONSENSUS: L-x(3)-[FY]-K-H-x-N-x-[STAN]-S-F-[LIVM]-R-Q-L-[NH]-x-Y-x-[FYW]-[RKH]-K-  
CONSENSUS: [LIVM].
- 55 NAME: Tryptophan pentad repeat (IRF family) signature.  
CONSENSUS: W-x-[DNH]-x(5)-[LIVF]-x-[IV]-P-W-x-H-x(9,10)-[DE]-x(2)-[LIVF]-F-[KRQ]-x-

CONSENSUS: [WR]-A.

NAME: LIM domain signature.

5 CONSENSUS: C-x(2)-C-x(15,21)-[FYWH]-H-x(2)-[CH]-x(2)-C-x(2)-  
C-x(3)-[LIVMF].

NAME: LIM domain profile.

NAME: NF-kappa-B/Rel/dorsal domain signature.

10 CONSENSUS: F-R-Y-x-C-E-G.

NAME: MADS-box domain signature.

CONSENSUS: R-x-[RK]-x(5)-I-x-[DN]-x(3)-[KR]-x(2)-T-[FY]-x-  
[RK](3)-x(2)-[LIVM]-x-

15 CONSENSUS: K(2)-A-x-E-[LIVM]-[ST]-x-L-x(4)-[LIVM]-x-  
[LIVM](3)-x(6)-[LIVMF]-x(2)-  
CONSENSUS: [FY].

NAME: MADS-box domain profile.

20

NAME: T-box domain signature 1.

CONSENSUS: L-W-x(2)-[FC]-x(3,4)-[NT]-E-M-[LIV](2)-T-x(2)-G-  
[RG]-[KRQ].

NAME: T-box domain signature 2.

25

CONSENSUS: [LIVMYW]-H-[PADH]-[DEN]-[GS]-x(3)-G-x(2)-W-M-x(3)-  
[IVA]-x-F.

NAME: TEA domain signature.

30

CONSENSUS: G-R-N-E-L-I-x(2)-Y-I-x(3)-[TC]-x(3)-R-T-[RK](2)-Q-  
[LIVM]-S-S-H-[LIVM]-  
CONSENSUS: Q-V.

NAME: Transcription factor TFIIB repeat signature.

35

CONSENSUS: G-[KR]-x(3)-[STAGN]-x-[LIVMYA]-[GSTA](2)-[CSAV]-  
[LIVM]-[LIVMFY]-[LIVMA]-  
CONSENSUS: [GSA]-[STAC].

NAME: Transcription factor TFIID repeat signature.

40

CONSENSUS: Y-x-P-x(2)-[IF]-x(2)-[LIVM](2)-x-[KRH]-x(3)-P-  
[RKQ]-x(3)-L-[LIVM]-F-x-  
CONSENSUS: [STN]-G-[KR]-[LIVM]-x(3)-G-[TAGL]-[KR]-x(7)-[AGC]-  
x(7)-[LIVM].

NAME: TFIIS zinc ribbon domain signature.

45

CONSENSUS: C-x(2)-C-x(9)-[LIVMQSAR]-[QH]-[STQL]-[RA]-[SACR]-  
x-[DE]-[DET]-[PGSEA]-  
CONSENSUS: x(6)-C-x(2,5)-C-x(3)-[FW].

NAME: TSC-22 / dip / bun family signature.

50

CONSENSUS: M-D-L-V-K-x-H-L-x(2)-A-V-R-E-E-V-E.

NAME: Prokaryotic transcription elongation factors signature 1.

55

CONSENSUS: [ST]-x(2)-[GS]-x(3)-[LI]-x(2)-E-L-x(2)-L-x(3,4)-R-  
x(2)-[IV]-x(3)-[LIV]-  
CONSENSUS: x(6)-G-D-x(2)-E-N-[GSA]-x-Y.

- NAME: Prokaryotic transcription elongation factors signature 2.  
 5 CONSENSUS: S-x(2)-S-P-[LIVM]-[AG]-x-[SAG]-[LIVM]-[LIVMY]-x(4)-[DG]-[DE].
- NAME: DEAD-box subfamily ATP-dependent helicases signature.  
 CONSENSUS: [LIVMF](2)-D-E-A-D-[RKEN]-x-[LIVMFYGSTN].
- NAME: DEAH-box subfamily ATP-dependent helicases signature.  
 10 CONSENSUS: [GSAH]-x-[LIVMF](3)-D-E-[ALIV]-H-[NECR].
- NAME: Eukaryotic putative RNA-binding region RNP-1 signature.  
 CONSENSUS: [RK]-G-[EDRKHPCG]-[AGSCI]-[FY]-[LIVA]-x-[FYLM].  
 15
- NAME: Fibrillarin signature.  
 CONSENSUS: [GST]-[LIVMAP]-V-Y-A-[IV]-E-[FY]-[SA]-x-R-x(2)-R-[DE].
- NAME: MCM family signature.  
 20 CONSENSUS: G-[IVT]-[LVAC](2)-[IVT]-D-[DE]-[FL]-[DNST].
- NAME: MCM family domain.
- NAME: XPA protein signature 1.  
 25 CONSENSUS: C-x-[DE]-C-x(3)-[LIVMF]-x(1,2)-D-x(2)-L-x(3)-F-x(4)-C-x(2)-C.
- NAME: XPA protein signature 2.  
 30 CONSENSUS: [LIVM](2)-T-[KR]-T-E-x-K-x-[DE]-Y-[LIVMF](2)-x-D-x-[DE].
- NAME: XPG protein signature 1.  
 CONSENSUS: [VI]-[KRE]-P-x-[FYIL]-V-F-D-G-x(2)-[PIL]-x-[LVC]-K.  
 35
- NAME: XPG protein signature 2.  
 CONSENSUS: [GS]-[LIVM]-[PER]-[FYS]-[LIVM]-x-A-P-x-E-A-[DE]-[PAS]-[QS]-[CLM].  
 40
- NAME: Bacterial regulatory proteins, araC family signature.  
 CONSENSUS: [KRQ]-[LIVMA]-x(2)-[GSTALIV]-[FYWPGDN]-x(2)-[LIVMSA]-x(4,9)-[LIVMF]-  
 CONSENSUS: x(2)-[LIVMSTA]-[GSTACIL]-x(3)-[GANQRF]-[LIVMFY]-  
 45 x(4,5)-[LFY]-x(3)-  
 CONSENSUS: [FYIVA]-[FYWHCM]-x(3)-[GSADENQKR]-x-[NSTAPKL]-[PARL].
- NAME: Bacterial regulatory proteins, araC family DNA-binding domain profile.  
 50
- NAME: Bacterial regulatory proteins, arsR family signature.  
 CONSENSUS: C-x(2)-D-[LIVM]-x(6)-[EST]-x(4)-S-[HYR]-[HQ].
- NAME: Bacterial regulatory proteins, asnC family signature.  
 55 CONSENSUS: [GSTAP]-x(2)-[DNEA]-[LIVM]-[GSA]-x(2)-[LIVMFY]-[GN]-[LIVMST]-[EST]-x(6)-R-  
 CONSENSUS: [LVT]-x(2)-[LIVM]-x(3)-G.

- NAME: Bacterial regulatory proteins, crp family signature.  
 CONSENSUS: [LIVM]-[STAG]-[RHNW]-x(2)-[LIM]-[GA]-x-[LIVMFYA]-  
 [LIVSC]-[GA]-x-[STACN]-  
 5 CONSENSUS: x(2)-[MST]-x-[GSTN]-R-x-[LIVMF]-x(2)-[LIVMF].
- NAME: Bacterial regulatory proteins, deoR family signature.  
 CONSENSUS: R-x(3)-[LIVM]-x(3)-[LIVM]-x(16,17)-[STA]-x(2)-T-  
 [LIVMA]-[RH]-[KRNA]-D-  
 10 CONSENSUS: [LIVMF].
- NAME: Bacterial regulatory proteins, gntR family signature.  
 CONSENSUS: [LIVAPKR]-[PILV]-x-[EQTIVMR]-x(2)-[LIVM]-x(3)-  
 [LIVMFYK]-x-[LIVFT]-  
 15 CONSENSUS: [DNGSTK]-[RGTLV]-x-[STAIVP]-[LIVA]-x(2)-[STAGV]-  
 [LIVMFYH]-x(2)-[LMA].
- NAME: Bacterial regulatory proteins, iclR family signature.  
 CONSENSUS: [GA]-x(3)-[DS]-x(2)-E-x(6)-[CSA]-[LIVM]-[GSA]-  
 20 x(2)-[LIVM]-[FYH]-[DN].
- NAME: Bacterial regulatory proteins, lacI family signature.  
 CONSENSUS: [LIVM]-x-[DE]-[LIVM]-A-x(2)-[STAGV]-x-V-[GSTP]-  
 x(2)-[STAG]-[LIVMA]-x(2)-  
 25 CONSENSUS: [LIVMFYAN]-[LIVMC].
- NAME: Bacterial regulatory proteins, luxR family signature.  
 CONSENSUS: [GDC]-x(2)-[NSTAVY]-x(2)-[IV]-[GSTA]-x(2)-  
 [LIVMFYWCT]-x-[LIVMFYWCR]-x(3)-  
 30 CONSENSUS: [NST]-[LIVM]-x(5)-[NRHSA]-[LIVMSTA]-x(2)-[KR].
- NAME: Bacterial regulatory proteins, lysR family signature.  
 CONSENSUS: [NQKRHSTAG]-[LIVMFYTA]-x(2)-[STAGLV]-[STAG]-x(4)-  
 [LIVMYCTQR]-[PSTANLVER]-  
 35 CONSENSUS: x-[PSTAGQV]-[PSTAGNVMF]-[LIVMFA]-[STAGH]-x(2)-  
 [LIVMF]-x(2)-[LIVMFW]-  
 CONSENSUS: [RKEAV]-x(2)-[LIVMFYNTAE]-x(3)-[LIMVT].
- NAME: Bacterial regulatory proteins, marR family signature.  
 40 CONSENSUS: [STNA]-[LIA]-x-[RNGS]-x(4)-[LM]-[EIV]-x(2)-[GES]-  
 [LFYW]-[LIVC]-x(7)-  
 CONSENSUS: [DN]-[RKQG]-[RK]-x(6)-T-x(2)-[GA].
- NAME: Bacterial regulatory proteins, merR family signature.  
 45 CONSENSUS: [GSA]-x-[LIVMFA]-[ASM]-x(2)-[STACLIV]-[GSDENQR]-  
 [LIVC]-[STANHK]-x(3)-  
 CONSENSUS: [LIVM]-[RHF]-x-[YW]-[DEQ]-x(2,3)-[GHDNQ]-  
 [LIVMF](2).
- NAME: Bacterial regulatory proteins, tetR family signature.  
 50 CONSENSUS: G-[LIVMFYS]-x(2,3)-[TS]-[LIVMT]-x(2)-[LIVM]-x(5)-  
 [LIVQS]-[STAGENQH]-x-  
 CONSENSUS: [GPAR]-x-[LIVMF]-[FYST]-x-[HFY]-[FV]-x-[DNST]-K-  
 x(2)-[LIVM].  
 55
- NAME: Transcriptional antiterminators bglG family signature.  
 CONSENSUS: [ST]-x-H-x(2)-[FA](2)-[LIVM]-[EQK]-R-x(2)-[QNK].

- NAME: Sigma-54 factors family signature 1.  
 CONSENSUS: P-[LIVM]-x-[LIVM]-x(2)-[LIVM]-A-x(2)-[LIVMF]-x(2)-[HS]-x-S-T-[LIVM]-S-R.
- 5 NAME: Sigma-54 factors family signature 2.  
 CONSENSUS: R-R-T-[IV]-[AT]-K-Y-R.
- NAME: Sigma-54 factors family profile.
- 10 NAME: Sigma-70 factors family signature 1.  
 CONSENSUS: [DE]-[LIVMF](2)-[HEQS]-x-G-x-[LIVMFA]-G-L-[LIVMFYE]-x-[GSAM]-[LIVMAP].
- NAME: Sigma-70 factors family signature 2.  
 15 CONSENSUS: [STN]-x(2)-[DEQ]-[LIVM]-[GAS]-x(4)-[LIVMF]-[PSTG]-x(3)-[LIVMA]-x-[NQR]-  
 CONSENSUS: [LIVMA]-[EQH]-x(3)-[LIVFW]-x(2)-[LIVM].
- NAME: Sigma-70 factors ECF subfamily signature.  
 20 CONSENSUS: [STAIV]-[PQDEL]-[DE]-[LIV]-[LIVTA]-Q-x-[STAV]-[LIVMFYC]-[LIVMAK]-x-  
 CONSENSUS: [GSTAIV]-[LIMFYWQ]-x(12,14)-[STAP]-[FYW]-[LIF]-x(2)-[IV].
- 25 NAME: Sigma-54 interaction domain ATP-binding region A signature.  
 CONSENSUS: [LIVMFY](3)-x-G-[DEQ]-[STE]-G-[STAV]-G-K-x(2)-[LIVMFY].
- 30 NAME: Sigma-54 interaction domain ATP-binding region B signature.  
 CONSENSUS: [GS]-x-[LIVMF]-x(2)-A-[DNEQASH]-[GNEK]-G-[STIM]-[LIVMFY](3)-[DE]-[EK]-  
 CONSENSUS: [LIVM].
- 35 NAME: Sigma-54 interaction domain C-terminal part signature.  
 CONSENSUS: [FYW]-P-[GS]-N-[LIVM]-R-[EQ]-L-x-[NHAT].
- NAME: Sigma-54 interaction domain profile.
- 40 NAME: Single-strand binding protein family signature 1.  
 CONSENSUS: [LIVMF]-[NST]-[KRT]-[LIVM]-x-[LIVMF](2)-G-[NHRK]-[LIVM]-[GST]-x-[DET].
- NAME: Single-strand binding protein family signature 2.  
 45 CONSENSUS: T-x-W-[HY]-[RNS]-[LIVM]-x-[LIVMF]-[FY]-[NGKR].
- NAME: Bacterial histone-like DNA-binding proteins signature.  
 CONSENSUS: [GSK]-F-x(2)-[LIVMF]-x(4)-[RKEQA]-x(2)-[RST]-x-[GA]-x-[KN]-P-x-T.
- 50 NAME: Dps protein family signature 1.  
 CONSENSUS: H-[FW]-x-[LIVM]-x-G-x(5)-[LV]-H-x(3)-[DE].
- NAME: Dps protein family signature 2.  
 55 CONSENSUS: [LIVMFY]-[DH]-x-[LIVM]-[GA]-E-R-x(3)-[LIF]-[GDN]-x(2)-[PA].

NAME: DNA repair protein radC family signature.  
 CONSENSUS: H-N-H-P-S-G.

5 NAME: recA signature.  
 CONSENSUS: A-L-[KR]-[IF]-[FY]-[STA]-[STAD]-[LIVM]-R.

NAME: RecF protein signature 1.  
 CONSENSUS: P-[ED]-x(3)-[LIVM](2)-x-G-[GSAD]-P-x(2)-R-R-x-[FY]-[LIVM]-D.

10 NAME: RecF protein signature 2.  
 CONSENSUS: [LIVMFY](2)-x-D-x(2,3)-[SA]-[EH]-L-D-x(2)-[KRH]-x(3)-L.

15 NAME: RecR protein signature.  
 CONSENSUS: C-x(2)-C-x(3)-[ST]-x(4)-C-x-I-C-x(4)-R.

NAME: Histone H2A signature.  
 CONSENSUS: [AC]-G-L-x-F-P-V.

20 NAME: Histone H2B signature.  
 CONSENSUS: [KR]-E-[LIVM]-[EQ]-T-x(2)-[KR]-x-[LIVM](2)-x-[PAG]-[DE]-L-x-[KR]-H-A-  
 CONSENSUS: [LIVM]-[STA]-E-G.

25 NAME: Histone H3 signature 1.  
 CONSENSUS: K-A-P-R-K-Q-L.

NAME: Histone H3 signature 2.  
 30 CONSENSUS: P-F-x-[RA]-L-[VA]-[KRQ]-[DEG]-[IV].

NAME: Histone H4 signature.  
 CONSENSUS: G-A-K-R-H.

35 NAME: HMG1/2 signature.  
 CONSENSUS: [FI]-S-[KR]-K-C-S-[EK]-R-W-K-T-M.

NAME: HMG-I and HMG-Y DNA-binding domain (A+T-hook).  
 40 CONSENSUS: [AT]-x(1,2)-[RK](2)-[GP]-R-G-R-P-[RK]-x.

NAME: HMG14 and HMG17 signature.  
 CONSENSUS: R-R-S-A-R-L-S-A-[RK]-P.

NAME: Bromodomain signature.  
 45 CONSENSUS: [STANVF]-x(2)-F-x(4)-[DNS]-x(5,7)-[DENQTF]-Y-[HFY]-x(2)-[LIVMFY]-x(3)-  
 CONSENSUS: [LIVM]-x(4)-[LIVM]-x(6,8)-Y-x(12,13)-[LIVM]-x(2)-N-[SACF]-x(2)-[FY].

50 NAME: Bromodomain profile.

NAME: Chromo domain signature.  
 CONSENSUS: [FYL]-x-[LIVMC]-[KR]-W-x-[GDNR]-[FYWLE]-x(5,6)-[ST]-W-[ES]-[PSTDN]-x(3)-  
 55 CONSENSUS: [LIVMC].

NAME: Chromo and chromo shadow domain profile.



- NAME: Regulator of chromosome condensation (RCC1) signature 1.  
 1. CONSENSUS: G-x-N-D-x(2)-[AV]-L-G-R-x-T.
- 5 NAME: Regulator of chromosome condensation (RCC1) signature 2.  
 CONSENSUS: [LIVMFA]-[STAGC](2)-G-x(2)-H-[STAGLI]-[LIVMFA]-x-[LIVM].
- 10 NAME: Protamine P1 signature.  
 CONSENSUS: [AV]-R-[NFY]-R-x(2,3)-[ST]-x-S-x-S.
- NAME: Nuclear transition protein 1 signature.  
 CONSENSUS: S-K-R-K-Y-R-K.
- 15 NAME: Nuclear transition protein 2 signature 1.  
 CONSENSUS: H-x(3)-H-S-[NS]-S-x-P-Q-S.
- NAME: Nuclear transition protein 2 signature 2.  
 20 CONSENSUS: K-x-R-K-x(2)-E-G-K-x(2)-K-[KR]-K.
- NAME: Ribosomal protein L1 signature.  
 CONSENSUS: [IM]-x(2)-[LIVA]-x(2,3)-[LIVM]-G-x(2)-[LMS]-[GSNH]-[PTKR]-[KRAV]-G-x-  
 25 CONSENSUS: [LMF]-P-[DENSTK].
- NAME: Ribosomal protein L2 signature.  
 CONSENSUS: P-x(2)-R-G-[STAIV](2)-x-N-[APK]-x-[DE].
- 30 NAME: Ribosomal protein L3 signature.  
 CONSENSUS: [FL]-x(6)-[DN]-x(2)-[AGS]-x-[ST]-x-G-[KRH]-G-x(2)-G-x(3)-R.
- NAME: Ribosomal protein L5 signature.  
 35 CONSENSUS: [LIVM]-x(2)-[LIVM]-[STAC]-[GGE]-[QV]-x(2)-[LIVMA]-x-[STC]-x-[STAG]-[KR]-  
 CONSENSUS: x-[STA].
- NAME: Ribosomal protein L6 signature 1.  
 40 CONSENSUS: [PS]-[DENS]-x-Y-K-[GA]-K-G-[LIVM].
- NAME: Ribosomal protein L6 signature 2.  
 CONSENSUS: Q-x(3)-[LIVM]-x(2)-[KR]-x(2)-R-x-F-x-D-G-[LIVM]-Y-[LIVM]-x(2)-[KR].
- 45 NAME: Ribosomal protein L9 signature.  
 CONSENSUS: G-x(2)-[GN]-x(4)-V-x(2)-G-[FY]-x(2)-N-[FY]-L-x(5)-[GA]-x(3)-[STN].
- 50 NAME: Ribosomal protein L10 signature.  
 CONSENSUS: [DEH]-x(2)-[GS]-[LIVMF]-[STN]-[VA]-x-[DEQK]-[LIVMA]-x(2)-[LIM]-R.
- NAME: Ribosomal protein L11 signature.  
 55 CONSENSUS: [RKN]-x-[LIVM]-x-G-[ST]-x(2)-[SNQ]-[LIVM]-G-x(2)-[LIVM]-x(0,1)-[DENG].
- NAME: Ribosomal protein L13 signature.

CONSENSUS: [LIVM]-[KRV]-[GK]-M-[LIV]-[PS]-x(4,5)-[GS]-  
[NQEKRA]-x(5)-[LIVM]-x-[AIV]-  
CONSENSUS: [LFY]-x-[GDN].

5 NAME: Ribosomal protein L14 signature.  
CONSENSUS: [GA]-[LIV](3)-x(9,10)-[DNS]-G-x(4)-[FY]-x(2)-[NT]-  
x(2)-V-[LIV].

10 NAME: Ribosomal protein L15 signature.  
CONSENSUS: K-[LIVM](2)-[GAL]-x-[GT]-x-[LIVMA]-x(2,5)-[LIVM]-  
x-[LIVMF]-x(3,4)-  
CONSENSUS: [LIVMF]-[ST]-x(2)-A-x(3)-[LIVM]-x(3)-G.

15 NAME: Ribosomal protein L16 signature 1.  
CONSENSUS: [KR]-R-x-[GSAC]-[KQVA]-[LIVM]-W-[LIVM]-[KR]-  
[LIVM]-[LFY]-[AP].

20 NAME: Ribosomal protein L16 signature 2.  
CONSENSUS: R-M-G-x-[GR]-K-G-x(4)-[FWKR].

NAME: Ribosomal protein L17 signature.  
CONSENSUS: I-x-[ST]-[GT]-x(2)-[KR]-x-K-x(6)-[DE]-x-[LIMV]-  
[LIVMT]-T-x-[STAG]-[KR].

25 NAME: Ribosomal protein L19 signature.  
CONSENSUS: [RT]-[KRSVY]-[GSA]-x-V-[RS]-[KR]-[SA]-K-L-Y-Y-L-R.

30 NAME: Ribosomal protein L20 signature.  
CONSENSUS: K-x(3)-[KRC]-x-[LIVM]-W-[IV]-[STNALV]-R-[LIVM]-N-  
x(3)-[RKH].

35 NAME: Ribosomal protein L21 signature.  
CONSENSUS: [IVT]-x(3)-[KR]-x(3)-[KRQ]-K-x(6)-G-[HF]-R-[RQ]-  
x(2)-T.

NAME: Ribosomal protein L22 signature.  
CONSENSUS: [RKQN]-x(4)-[RH]-[GAS]-x-G-[KRQS]-x(9)-[HDN]-  
[LIVM]-x-[LIVMS]-x-[LIVM].

40 NAME: Ribosomal protein L23 signature.  
CONSENSUS: [RK](2)-[AM]-[IVFYT]-[IV]-[RKT]-L-[STANQK]-x(7)-  
[LIVMFT].

45 NAME: Ribosomal protein L24 signature.  
CONSENSUS: [GDEN]-D-x-V-x-[IV]-[LIVMA]-x-G-x(2)-[KA]-[GN]-  
x(2,3)-[GA]-x-[IV].

50 NAME: Ribosomal protein L27 signature.  
CONSENSUS: G-x-[LIVM](2)-x-R-Q-R-G-x(5)-G.

NAME: Ribosomal protein L29 signature.  
CONSENSUS: [KNQS]-[PSTL]-x(2)-[LIMFA]-[KRGSA]-x-[LIVYSTA]-  
[KR]-[KRH]-[DESTANRL]-  
CONSENSUS: [LIV]-A-[KRCQVT]-[LIVMA].

55 NAME: Ribosomal protein L30 signature.  
CONSENSUS: [IVT]-[LIVM]-x(2)-[LF]-x-[LI]-x-[KRHQEG]-x(2)-  
[STNQH]-x-[IVT].

- CONSENSUS: x(10)-[LMS]-[LIV]-x(2)-[LIVA]-x(2)-[LMFY]-[IVT].
- NAME: Ribosomal protein L31 signature.  
 5 CONSENSUS: H-P-F-[FY]-[TI]-x(9)-G-R-[AV]-x-[KR].
- NAME: Ribosomal protein L33 signature.  
 CONSENSUS: Y-x-[ST]-x-[KR]-[NS]-x(4)-[PAT]-x(1,2)-[LIVM]-[EA]-x(2)-K-[FY]-[CS].
- 10 NAME: Ribosomal protein L34 signature.  
 CONSENSUS: K-[RG]-T-[FYWL]-[EQS]-x(5)-[KRHS]-x(4,5)-G-F-x(2)-R.
- NAME: Ribosomal protein L35 signature.  
 15 CONSENSUS: [LIVM]-K-[TV]-x(2)-[GSA]-[SAIL]-x-K-R-[LIVMFY]-[KRL].
- NAME: Ribosomal protein L36 signature.  
 CONSENSUS: C-x(2)-C-x(2)-[LIVM]-x-R-x(3)-[LIVMN]-x-[LIVM]-x-  
 20 C-x(3,4)-[KR]-H-x-Q-x-Q.
- NAME: Ribosomal protein L1e signature.  
 CONSENSUS: N-x(3)-[KR]-x(2)-A-[LIVT]-x-S-A-[LIV]-x-A-[ST]-[SGA]-x(7)-[RK]-G-H.
- 25 NAME: Ribosomal protein L6e signature.  
 CONSENSUS: N-x(2)-P-L-R-R-x(4)-[FY]-V-I-A-T-S-x-K.
- NAME: Ribosomal protein L7Ae signature.  
 30 CONSENSUS: [CA]-x(4)-[IV]-P-[FY]-x(2)-[LIVM]-x-[GSQ]-[KRQ]-x(2)-L-G.
- NAME: Ribosomal protein L10e signature.  
 CONSENSUS: R-x-A-[FYW]-G-K-[PA]-x-G-x(2)-A-R-V.
- 35 NAME: Ribosomal protein L13e signature.  
 CONSENSUS: [KR]-Y-x(2)-K-[LIVM]-R-[STA]-G-[KR]-G-F-[ST]-L-x-E.
- NAME: Ribosomal protein L15e signature.  
 40 CONSENSUS: [DE]-[KR]-A-R-x-L-G-[FY]-x-[SAP]-x(2)-G-[LIVMFY](4)-R-x-R-V-x-R-G.
- NAME: Ribosomal protein L18e signature.  
 45 CONSENSUS: [KRE]-x-L-x(2)-[PS]-[KR]-x(2)-[RH]-[PSA]-x-[LIVM]-[NS]-[LIVM]-x-[RK]-  
 CONSENSUS: [LIVM].
- NAME: Ribosomal protein L19e signature.  
 50 CONSENSUS: R-x-[KR]-x(5)-[KR]-x(3)-[KRH]-x(2)-G-x-G-x-R-x-G-x(3)-A-R-x(3)-[KQ]-  
 CONSENSUS: x(2)-W-x(7)-R-x(2)-L-x(3)-R.
- NAME: Ribosomal protein L21e signature.  
 55 CONSENSUS: G-[DE]-x-V-x(10)-[GV]-x(2)-[FYH]-x(2)-[FY]-x-G-x-T-G.
- NAME: Ribosomal protein L24e signature.

CONSENSUS: [FY]-x-[GS]-x(2)-[IV]-x-P-G-x-G-x(2)-[FYV]-x-[KRHE]-x-D.

5 NAME: Ribosomal protein L27e signature.  
 CONSENSUS: G-K-N-x-W-F-F-x-K-L-R-F>.

10 NAME: Ribosomal protein L30e signature 1.  
 CONSENSUS: [STA]-x(5)-G-x-[QKR]-x(2)-[LIVM]-[KQT]-x(2)-[KR]-x-G-x(2)-K-x-[LIVM](3).

NAME: Ribosomal protein L30e signature 2.  
 CONSENSUS: [DE]-L-G-[STA]-x(2)-G-[KR]-x(6)-[LIVM]-x-[LIVM]-x-[DEN]-x-G.

15 NAME: Ribosomal protein L31e signature.  
 CONSENSUS: V-[KR]-[LIVM]-x(3)-[LIVM]-N-x-[AK]-x-W-x-[KR]-G.

20 NAME: Ribosomal protein L32e signature.  
 CONSENSUS: F-x-R-x(4)-[KR]-x(2)-[KR]-[LIVM]-x(3)-W-R-[KR]-x(2)-G.

NAME: Ribosomal protein L34e signature.  
 CONSENSUS: Y-x-[ST]-x-S-[NY]-x(5)-[KR]-T-P-G.

25 NAME: Ribosomal protein L35Ae signature.  
 CONSENSUS: G-K-[LIVM]-x-R-x-H-G-x(2)-G-x-V-x-A-x-F-x(3)-[LI]-P.

30 NAME: Ribosomal protein L36e signature.  
 CONSENSUS: P-Y-E-[KR]-R-x-[LIVM]-[DE]-[LIVM](2)-[KR].

NAME: Ribosomal protein L37e signature.  
 CONSENSUS: G-T-x-[SA]-x-G-x-[KR]-x(3)-[ST]-x(0,1)-H-x(2)-C-x-R-C-G.

35 NAME: Ribosomal protein L39e signature.  
 CONSENSUS: [KRA]-T-x(3)-[LIVM]-[KRQF]-x-[NHS]-x(3)-R-[NHY]-W-R-R.

40 NAME: Ribosomal protein L44e signature.  
 CONSENSUS: K-x-[TV]-K-K-x(2)-L-[KR]-x(2)-C.

45 NAME: Ribosomal protein S2 signature 1.  
 CONSENSUS: [LIVMFA]-x(2)-[LIVMFYC](2)-x-[STAC]-[GSTANQEK]-[STALV]-[HY]-[LIVMF]-G.

50 NAME: Ribosomal protein S2 signature 2.  
 CONSENSUS: P-x(2)-[LIVMF](2)-[LIVMS]-x-[GDN]-x(3)-[DENL]-x(3)-[LIVM]-x-E-x(4)-  
 CONSENSUS: [GNQKRH]-[LIVM]-[AP].

55 NAME: Ribosomal protein S3 signature.  
 CONSENSUS: [GSTA]-[KR]-x(6)-G-x-[LIVMT]-x(2)-[NQSCH]-x(1,3)-[LIVFCA]-x(3)-[LIV]-  
 CONSENSUS: [DENQ]-x(7)-[LMT]-x(2)-G-x(2)-G.

NAME: Ribosomal protein S4 signature.

CONSENSUS: [LIVM]-[DE]-x-R-L-x(3)-[LIVMC]-[VMFYHQ]-[KRT]-  
 x(3)-[STAGCF]-x-[ST]-x(3)-  
 CONSENSUS: [SAI]-[KR]-x-[LIVMF](2).

5 NAME: Ribosomal protein S5 signature.  
 CONSENSUS: G-[KRQ]-x(3)-[FY]-x-[ACV]-x(2)-[LIVMA]-[LIVM]-  
 [AG]-[DN]-x(2)-G-x-  
 CONSENSUS: [LIVM]-G-x-[SAG]-x(5,6)-[DEQ]-[LIVM]-x(2)-A-  
 [LIVMF].

10 NAME: Ribosomal protein S6 signature.  
 CONSENSUS: G-x-[KRC]-[DENQRH]-L-[SA]-Y-x-I-[KRNSA].

NAME: Ribosomal protein S7 signature.  
 15 CONSENSUS: [DENSK]-x-[LIVMET]-x(3)-[LIVMFT](2)-x(6)-G-K-[KR]-  
 x(5)-[LIVMF]-[LIVMFC]-  
 CONSENSUS: x(2)-[STA].

NAME: Ribosomal protein S8 signature.  
 20 CONSENSUS: [GE]-x(2)-[LIV](2)-[STY]-T-x(2)-G-[LIVM](2)-x(4)-  
 [AG]-[KRHAYI].

NAME: Ribosomal protein S9 signature.  
 CONSENSUS: G-G-G-x(2)-[GSA]-Q-x(2)-[SA]-x(3)-[GSA]-x-[GSTAV]-  
 25 [KR]-[GSAL]-[LIF].

NAME: Ribosomal protein S10 signature.  
 CONSENSUS: [AV]-x(3)-[GDNSR]-[LIVMSTA]-x(3)-G-P-[LIVM]-x-  
 [LIVM]-P-T.

30 NAME: Ribosomal protein S11 signature.  
 CONSENSUS: [LIVMF]-x-[GSTAC]-[LIVMF]-x(2)-[GSTAL]-x(0,1)-  
 [GSN]-[LIVMF]-x-[LIVM]-  
 CONSENSUS: x(4)-[DEN]-x-T-P-x-[PA]-[STCH]-[DN].

35 NAME: Ribosomal protein S12 signature.  
 CONSENSUS: [RK]-x-P-N-S-[AR]-x-R.

NAME: Ribosomal protein S13 signature.  
 40 CONSENSUS: [KRQS]-G-x-R-H-x(2)-[GSNH]-x(2)-[LIVMC]-R-G-Q.

NAME: Ribosomal protein S14 signature.  
 CONSENSUS: [RP]-x(0,1)-C-x(11,12)-[LIVMF]-x-[LIVMF]-[SC]-  
 [RG]-x(3)-[RN].

45 NAME: Ribosomal protein S15 signature.  
 CONSENSUS: [LIVM]-x(2)-H-[LIVMFY]-x(5)-D-x(2)-[SAGN]-x(3)-  
 [LF]-x(9)-[LIVM]-x(2)-  
 CONSENSUS: [FY].

50 NAME: Ribosomal protein S16 signature.  
 CONSENSUS: [LIVMT]-x-[LIVM]-[KR]-L-[STAK]-R-x-G-[AKR].

NAME: Ribosomal protein S17 signature.  
 55 CONSENSUS: G-D-x-[LIV]-x-[LIVA]-x-[QEK]-x-[RK]-P-[LIV]-S.

NAME: Ribosomal protein S18 signature.

- CONSENSUS: [IV]-[DY]-Y-x(2)-[LIVMT]-x(2)-[LIVM]-x(2)-[FYT]-  
 [LIVM]-[ST]-[DERP]-x-  
 CONSENSUS: [GY]-K-[LIVM]-x(3)-R-[LIVMAS].
- 5 NAME: Ribosomal protein S19 signature.  
 CONSENSUS: [STDNQ]-G-[KRQM]-x(6)-[LIVM]-x(4)-[LIVM]-[GSD]-  
 x(2)-[LF]-[GAS]-[DE]-F-  
 CONSENSUS: x(2)-[ST].
- 10 NAME: Ribosomal protein S21 signature.  
 CONSENSUS: [DE]-x-A-[LY]-[KR]-R-F-K-[KR]-x(3)-[KR].
- NAME: Ribosomal protein S3Ae signature.  
 CONSENSUS: [LIV]-x-[GH]-R-[IV]-x-E-x-[SC]-L-x-D-L.
- 15 NAME: Ribosomal protein S4e signature.  
 CONSENSUS: H-x-K-R-[LIVM]-[SAN]-x-P-x(2)-W-x-[LIVM]-x-[KR].
- NAME: Ribosomal protein S6e signature.  
 20 CONSENSUS: [LIVM]-[STAMR]-G-G-x-D-x(2)-G-x-P-M.
- NAME: Ribosomal protein S7e signature.  
 CONSENSUS: [KR]-L-x-R-E-L-E-K-K-F-[SAP]-x-[KR]-H.
- 25 NAME: Ribosomal protein S8e signature.  
 CONSENSUS: R-x(2)-T-G-[GA]-x(5)-[HR]-K-[KR]-x-K-x-E-[LM]-G.
- NAME: Ribosomal protein S12e signature.  
 CONSENSUS: A-L-[KRQP]-x-V-L-x(2)-[SA]-x(3)-[DN]-G-L.
- 30 NAME: Ribosomal protein S17e signature.  
 CONSENSUS: A-x-I-x-[ST]-K-x-L-R-N-[KR]-I-A-G-[FY]-x-T-H.
- NAME: Ribosomal protein S19e signature.  
 35 CONSENSUS: P-x(6)-[SAN]-x(2)-[LIVMA]-x-R-x-[ALIV]-[LV]-Q-x-L-  
 [EQ].
- NAME: Ribosomal protein S21e signature.  
 CONSENSUS: L-Y-V-P-R-K-C-S-[SA].
- 40 NAME: Ribosomal protein S24e signature.  
 CONSENSUS: [FA]-G-x(2)-[KR]-[STA]-x-G-[FY]-[GA]-x-[LIVM]-Y-  
 [DN]-[SN].
- 45 NAME: Ribosomal protein S26e signature.  
 CONSENSUS: [YH]-C-V-S-C-A-I-H.
- NAME: Ribosomal protein S27e signature.  
 CONSENSUS: [QK]-C-x(2)-C-x(6)-F-[GS]-x-[PSA]-x(5)-C-x(2)-C-  
 50 [GS]-x(2)-L-x(2)-P-x-G.
- NAME: Ribosomal protein S28e signature.  
 CONSENSUS: E-[ST]-E-R-E-A-R-x-L.
- 55 NAME: DNA mismatch repair proteins mutL / hexB / PMS1  
 signature.  
 CONSENSUS: G-F-R-G-E-A-L.

- NAME: DNA mismatch repair proteins mutS family signature.  
 CONSENSUS: [EST]-[LIVM]-x-[LIVM]-x-D-E-[LIVMY]-[GCD]-[RKH]-G-[GST]-x(4)-G.
- 5 NAME: mutT domain signature.  
 CONSENSUS: G-x(5)-E-x(4)-[STAGC]-[LIVMAC]-x-R-E-[LIVMFT]-x-E-E.
- 10 NAME: DnaA protein signature.  
 CONSENSUS: I-[GA]-x(2)-[LIVMF]-[SGDNK]-x(0,1)-[KR]-x-H-[STP]-[STV]-[LIVM](2)-x-[SA]-x(2)-[KRE]-[LIVM].
- 15 NAME: Small, acid-soluble spore proteins, alpha/beta type, signature 1.  
 CONSENSUS: K-x-E-[LIV]-A-x-[DE]-[LIVMF]-G-[LIVMF].
- NAME: Small, acid-soluble spore proteins, alpha/beta type, signature 2.  
 20 CONSENSUS: [KR]-[SAQ]-x-G-x-V-G-G-x-[LIVM]-x-[KR](2)-[LIVM](2).
- NAME: Zinc-containing alcohol dehydrogenases signature.  
 25 CONSENSUS: G-H-E-x(2)-G-x(5)-[GA]-x(2)-[IVSAC].
- NAME: Quinone oxidoreductase / zeta-crystallin signature.  
 CONSENSUS: [GSD]-[DEQH]-x(2)-L-x(3)-[SA](2)-G-G-x-G-x(4)-Q-x(2)-[KR].
- 30 NAME: Iron-containing alcohol dehydrogenases signature 1.  
 CONSENSUS: [STALIV]-[LIVF]-x-[DE]-x(6,7)-P-x(4)-[ALIV]-x-[GST]-x(2)-D-[TAIVM]-[LIVMF]-x(4)-E.
- 35 NAME: Iron-containing alcohol dehydrogenases signature 2.  
 CONSENSUS: [GSW]-x-[LIVTSACD]-[GH]-x(2)-[GSAE]-[GSHYQ]-x-[LIVTP]-[GAST]-[GAS]-x(3)-[LIVMT]-x-[HNS]-[GA]-x-[GTAC].
- 40 NAME: Short-chain dehydrogenases/reductases family signature.  
 CONSENSUS: [LIVSPADNK]-x(12)-Y-[PSTAGNCV]-[STAGNQCIVM]-[STAGC]-K-[PC]-[SAGFR]-[LIVMSTAGD]-x(2)-[LIVMFYW]-x(3)-[LIVMFYWGAPTHQ]-[GSACQRHM].
- 45 NAME: Aldo/keto reductase family signature 1.  
 CONSENSUS: G-[FY]-R-[HSAL]-[LIVMF]-D-[STAGC]-[AS]-x(5)-E-x(2)-[LIVM]-G.
- 50 NAME: Aldo/keto reductase family signature 2.  
 CONSENSUS: [LIVMFY]-x(9)-[KREQ]-x-[LIVM]-G-[LIVM]-[SC]-N-[FY].
- 55 NAME: Aldo/keto reductase family putative active site signature.  
 CONSENSUS: [LIVM]-[PAIV]-[KR]-[ST]-x(4)-R-x(2)-[GSTAEQK]-[NSL]-x(2)-[LIVMFA].

- NAME: Homoserine dehydrogenase signature.  
 5 CONSENSUS: A-x(3)-G-[[LIVMFY]]-[[STAG]]-x(2,3)-[[DNS]]-P-x(2)-D-  
 [[LIVM]]-x-G-x-D-x(3)-K.
- NAME: NAD-dependent glycerol-3-phosphate dehydrogenase  
 signature.  
 CONSENSUS: G-[[AT]]-[[LIVM]]-K-[[DN]]-[[LIVM]](2)-A-x-[[GA]]-x-G-  
 10 [[LIVMF]]-x-[[DE]]-G-[[LIVM]]-x-  
 CONSENSUS: [[LIVMFYW]]-G-x-N.
- NAME: FAD-dependent glycerol-3-phosphate dehydrogenase  
 signature 1.  
 15 CONSENSUS: [[IV]]-G-G-G-x(2)-G-[[STACV]]-G-x-A-x-D-x(3)-R-G.
- NAME: FAD-dependent glycerol-3-phosphate dehydrogenase  
 signature 2.  
 CONSENSUS: G-G-K-x(2)-[[GSTE]]-Y-R-x(2)-A.
- 20 NAME: Mannitol dehydrogenases signature.  
 CONSENSUS: [[LIVMY]]-x-[[FS]]-x(2)-[[STAGCV]]-x-V-D-R-[[IV]]-x-[[PS]].
- NAME: Histidinol dehydrogenase signature.  
 25 CONSENSUS: I-D-x(2)-A-G-P-[[ST]]-E-[[LIVS]]-[[LIVMA]](3)-[[AC]]-x(3)-  
 A-x(4)-[[LIVM]]-[[AV]]-  
 CONSENSUS: [[SACL]]-[[DE]]-[[LIVMFC]]-[[LIVM]]-[[SA]]-x(2)-E-H.
- NAME: L-lactate dehydrogenase active site.  
 30 CONSENSUS: [[LIVMA]]-G-[[EQ]]-H-G-[[DN]]-[[ST]].
- NAME: D-isomer specific 2-hydroxyacid dehydrogenases NAD-  
 binding signature.  
 CONSENSUS: [[LIVMA]]-[[AG]]-[[IVT]]-[[LIVMFY]]-[[AG]]-x-G-[[NHKRQGSAC]]-  
 35 [[LIV]]-G-x(13,14)-  
 CONSENSUS: [[LIVfMT]]-x(2)-[[FYwCTH]]-[[DNSTK]].
- NAME: D-isomer specific 2-hydroxyacid dehydrogenases  
 signature 2.  
 40 CONSENSUS: [[LIVMFYWAA]]-[[LIVFYWC]]-x(2)-[[SAC]]-[[DNQHR]]-[[IVFA]]-  
 [[LIVF]]-x-[[LIVF]]-[[HNI]]-x-  
 CONSENSUS: P-x(4)-[[STN]]-x(2)-[[LIVMF]]-x-[[GSDN]].
- NAME: D-isomer specific 2-hydroxyacid dehydrogenases  
 signature 3.  
 45 CONSENSUS: [[LMFATC]]-[[KPQ]]-x-[[GSTDN]]-x-[[LIVMFYWR]]-  
 [[LIVMFYW]](2)-N-x-[[STAGC]]-R-[[GP]]-x-  
 CONSENSUS: [[LIVH]]-[[LIVMC]]-[[DNV]].
- NAME: 3-hydroxyisobutyrate dehydrogenase signature.  
 50 CONSENSUS: [[LIVMFY]](2)-G-L-G-x-[[MQ]]-G-x-[[PGS]]-[[MA]]-[[SA]].
- NAME: Hydroxymethylglutaryl-coenzyme A reductases signature  
 1.  
 CONSENSUS: [[RKH]]-x(6)-D-x-M-G-x-N-x-[[LIVMA]].
- 55 NAME: Hydroxymethylglutaryl-coenzyme A reductases signature  
 2.  
 CONSENSUS: [[LIVM]]-G-x-[[LIVM]]-G-G-[[AG]]-T.



- NAME: Hydroxymethylglutaryl-coenzyme A reductases signature 3.  
 5 CONSENSUS: A-[LIVM]-x-[STAN]-x(2)-[LI]-x-[KRNQ]-[GSA]-H-[LM]-x-[FYLH].
- NAME: Hydroxymethylglutaryl-coenzyme A reductases profile.
- NAME: 3-hydroxyacyl-CoA dehydrogenase signature.  
 10 CONSENSUS: [DNE]-x(2)-[GA]-F-[LIVMFY]-x-[NT]-R-x(3)-[PA]-[LIVMFY](2)-x(5)-  
 CONSENSUS: [LIVMFYCT]-[LIVMFY]-x(2)-[GV].
- NAME: Malate dehydrogenase active site signature.  
 15 CONSENSUS: [LIVM]-T-[TRKMN]-L-D-x(2)-R-[STA]-x(3)-[LIVMFY].
- NAME: Malic enzymes signature.  
 20 CONSENSUS: F-x-[DV]-D-x(2)-G-T-[GSA]-x-[IV]-x-[LIVMA]-[GAST](2)-[LIVMF](2).
- NAME: Isocitrate and isopropylmalate dehydrogenases signature.  
 25 CONSENSUS: [NS]-[LIMYT]-[FYDN]-G-[DNT]-[IMVY]-x-[STGDN]-[DN]-x(2)-[SGAP]-x(3,4)-G-  
 CONSENSUS: [STG]-[LIVMPA]-G-[LIVMF].
- NAME: 6-phosphogluconate dehydrogenase signature.  
 CONSENSUS: [LIVM]-x-D-x(2)-[GA]-[NQS]-K-G-T-G-x-W.
- 30 NAME: Glucose-6-phosphate dehydrogenase active site.  
 CONSENSUS: D-H-Y-L-G-K-[EQK].
- NAME: IMP dehydrogenase / GMP reductase signature.  
 35 CONSENSUS: [LIVM]-[RK]-[LIVM]-G-[LIVM]-G-x-G-S-[LIVM]-C-x-T.
- NAME: Bacterial quinoprotein dehydrogenases signature 1.  
 CONSENSUS: [DEN]-W-x(3)-G-[RK]-x(6)-[FYW]-S-x(4)-[LIVM]-N-x(2)-N-V-x(2)-L-[RK].
- 40 NAME: Bacterial quinoprotein dehydrogenases signature 2.  
 CONSENSUS: W-x(4)-Y-D-x(3)-[DN]-[LIVMFY](4)-x(2)-G-x(2)-[STA]-P.
- NAME: FMN-dependent alpha-hydroxy acid dehydrogenases active site.  
 45 CONSENSUS: S-N-H-G-[AG]-R-Q.
- NAME: GMC oxidoreductases signature 1.  
 50 CONSENSUS: [GA]-[RKN]-x-[LIV]-G(2)-[GST](2)-x-[LIVM]-N-x(3)-[FYWA]-x(2)-[PAG]-x(5)-  
 CONSENSUS: [DNESH].
- NAME: GMC oxidoreductases signature 2.  
 55 CONSENSUS: [GS]-[PSTA]-x(2)-[ST]-P-x-[LIVM](2)-x(2)-S-G-[LIVM]-G.
- NAME: Eukaryotic molybdopterin oxidoreductases signature.

CONSENSUS: [GA]-x(3)-[KRNQHT]-x(11,14)-[LIVMFYWS]-x(8)-  
[LIVMF]-x-C-x(2)-[DEN]-R-  
CONSENSUS: x(2)-[DE].

5 NAME: Prokaryotic molybdopterin oxidoreductases signature 1.  
CONSENSUS: [STAN]-x-[CH]-x(2,3)-C-[STAG]-[GSTVMF]-x-C-x-  
[LIVMFYW]-x-[LIVMA]-x(3,4)-  
CONSENSUS: [DENQKHT].

10 NAME: Prokaryotic molybdopterin oxidoreductases signature 2.  
CONSENSUS: [STA]-x-[STAC](2)-x(2)-[STA]-D-[LIVMY](2)-L-P-x-  
[STAC](2)-x(2)-E.

15 NAME: Prokaryotic molybdopterin oxidoreductases signature 3.  
CONSENSUS: A-x(3)-[GDT]-I-x-[DNQTK]-x-[DEA]-x-[LIVM]-x-  
[LIVMC]-x-[NS]-x(2)-[GS]-  
CONSENSUS: x(5)-A-x-[LIVM]-[ST].

20 NAME: Aldehyde dehydrogenases glutamic acid active site.  
CONSENSUS: [LIVMFGA]-E-[LIMSTAC]-[GS]-G-[KNLM]-[SADN]-  
[TAPFV].

25 NAME: Aldehyde dehydrogenases cysteine active site.  
CONSENSUS: [FYLVA]-x(3)-G-[QE]-x-C-[LIVMGSTANC]-[AGCN]-x-  
[GSTADNEKR].

30 NAME: Aspartate-semialdehyde dehydrogenase signature.  
CONSENSUS: [LIVM]-[SADN]-x(2)-C-x-R-[LIVM]-x(4)-[GSC]-H-  
[STA].

NAME: Glyceraldehyde 3-phosphate dehydrogenase active site.  
CONSENSUS: [ASV]-S-C-[NT]-T-x(2)-[LIM].

35 NAME: N-acetyl-gamma-glutamyl-phosphate reductase active  
site.  
CONSENSUS: [LIVM]-[GSA]-x-P-G-C-[FY]-[AVP]-T-[GA]-x(3)-  
[GTAC]-[LIVM]-x-P.

40 NAME: Gamma-glutamyl phosphate reductase signature.  
CONSENSUS: V-x(5)-A-[LIV]-x-H-I-x(2)-[HY]-[GS]-[ST]-x-H-[ST]-  
[DE]-x-I.

45 NAME: Dihydrodipicolinate reductase signature.  
CONSENSUS: E-[IV]-x-E-x-H-x(3)-K-x-D-x-P-S-G-T-A.

NAME: Dihydroorotate dehydrogenase signature 1.  
CONSENSUS: [GS]-x(4)-[GK]-[STA]-[IVSTA]-[GT]-x(3)-[NQR]-x-G-  
[NH]-x(2)-P-[RT].

50 NAME: Dihydroorotate dehydrogenase signature 2.  
CONSENSUS: [LIV](2)-[GSA]-x-G-G-[IV]-x-[STGN]-x(3)-[ACV]-  
x(6)-G-A.

55 NAME: Coproporphyrinogen III oxidase signature.  
CONSENSUS: K-x-W-C-x(2)-[FYH](3)-[LIVM]-x-H-R-x-E-x-R-G-  
[LIVM]-G-G-[LIVM]-F-F-D.

NAME: Fumarate reductase / succinate dehydrogenase FAD-binding site.

CONSENSUS: R-[ST]-H-[ST]-x(2)-A-x-G-G.

5 NAME: Acyl-CoA dehydrogenases signature 1.

CONSENSUS: [GAC]-[LIVM]-[ST]-E-x(2)-[GSAN]-G-[ST]-D-x(2)-[GSA].

NAME: Acyl-CoA dehydrogenases signature 2.

10 CONSENSUS: [QDE]-x(2)-G-[GS]-x-G-[LIVMFY]-x(2)-[DEN]-x(4)-[KR]-x(3)-[DEN].

NAME: Alanine dehydrogenase & pyridine nucleotide transhydrogenase signature 1.

15 CONSENSUS: G-[LIVM]-P-x-E-x(3)-N-E-x(1,3)-R-V-A-x-[ST]-P-x-[GST]-V-x(2)-L-x-[KRH]-

CONSENSUS: x-G.

NAME: Alanine dehydrogenase & pyridine nucleotide transhydrogenase signature 2.

20 CONSENSUS: [LIVM](2)-G-[GA]-G-x-A-G-x(2)-[SA]-x(3)-[GA]-x-[SG]-[LIVM]-G-A-x-V-

CONSENSUS: x(3)-D.

25 NAME: Glu / Leu / Phe / Val dehydrogenases active site.

CONSENSUS: [LIV]-x(2)-G-G-[SAG]-K-x-[GV]-x(3)-[DNST]-[PL].

NAME: D-amino acid oxidases signature.

30 CONSENSUS: [LIVM](2)-H-[NHA]-Y-G-x-[GSA](2)-x-G-x(5)-G-x-A.

NAME: Pyridoxamine 5'-phosphate oxidase signature.

CONSENSUS: [LIVF]-E-F-W-[QHG]-x(4)-R-[LIVM]-H-[DNE]-R.

NAME: Copper amine oxidase topaquinone signature.

35 CONSENSUS: [LIVM]-[LIVMA]-[LIVM]-x(4)-T-x(2)-N-Y-[DE]-[YN].

NAME: Copper amine oxidase copper-binding site signature.

CONSENSUS: T-x-G-x(2)-H-[LIVMF]-x(3)-E-[DE]-x-P.

40 NAME: Lysyl oxidase putative copper-binding region signature.

CONSENSUS: W-E-W-H-S-C-H-Q-H-Y-H.

NAME: Delta 1-pyrroline-5-carboxylate reductase signature.

45 CONSENSUS: [PALF]-x(2,3)-[LIV]-x(3)-[LIVM]-[STAC]-[STV]-x-[GAN]-G-x-T-x(2)-[AG]-

CONSENSUS: [LIV]-x(2)-[LMF]-[DENQK].

NAME: Dihydrofolate reductase signature.

50 CONSENSUS: [LVAGC]-[LIF]-G-x(4)-[LIVMF]-P-W-x(4,5)-[DE]-x(3)-[FYIV]-x(3)-[STIQ].

NAME: Tetrahydrofolate dehydrogenase/cyclohydrolase signature 1.

55 CONSENSUS: [EQ]-x-[EQK]-[LIVM](2)-x(2)-[LIVM]-x(2)-[LIVMY]-N-x-[DN]-x(5)-[LIVMF](3)-

CONSENSUS: Q-L-P-[LV].

- NAME: Tetrahydrofolate dehydrogenase/cyclohydrolase  
signature 2.  
CONSENSUS: P-G-G-V-G-P-[MF]-T-[IV].
- 5 NAME: Oxygen oxidoreductases covalent FAD-binding site.  
CONSENSUS: P-x(10)-[DE]-[LIVM]-x(3)-[LIVM]-x(9)-[LIVM]-x(3)-[GSA]-[GST]-G-H.
- 10 NAME: Pyridine nucleotide-disulphide oxidoreductases class-I active site.  
CONSENSUS: G-G-x-C-[LIVA]-x(2)-G-C-[LIVM]-P.
- NAME: Pyridine nucleotide-disulphide oxidoreductases class-II active site.  
15 CONSENSUS: C-x(2)-C-D-[GA]-x(2,4)-[FY]-x(4)-[LIVM]-x-[LIVM](2)-G(3)-[DN].
- NAME: Respiratory-chain NADH dehydrogenase subunit 1  
signature 1.  
20 CONSENSUS: G-[LIVMFYKRS]-[LIVMAGP]-Q-x-[LIVMFY]-x-D-[AGIM]-[LIVMFTA]-K-[LVMYST]-  
CONSENSUS: [LIVMFYG]-x-[KR]-[EQG].
- NAME: Respiratory-chain NADH dehydrogenase subunit 1  
signature 2.  
25 CONSENSUS: P-F-D-[LIVMFYQ]-[STAGPVM]-E-[GAC]-E-x-[EQ]-[LIVMS]-x(2)-G.
- NAME: Respiratory-chain NADH dehydrogenase 20 Kd subunit  
signature.  
30 CONSENSUS: [GN]-x-D-[KRST]-[LIVMF](2)-P-[IV]-D-[LIVMFYW](2)-x-P-x-C-P-[PT].
- NAME: Respiratory-chain NADH dehydrogenase 24 Kd subunit  
signature.  
35 CONSENSUS: D-x(2)-F-[ST]-x(5)-C-L-G-x-C-x(2)-[GA]-P.
- NAME: Respiratory chain NADH dehydrogenase 30 Kd subunit  
signature.  
40 CONSENSUS: E-R-E-x(2)-[DE]-[LIVMF](2)-x(6)-[HK]-x(3)-[KRP]-x-[LIVM]-[LIVMS].
- NAME: Respiratory chain NADH dehydrogenase 49 Kd subunit  
signature.  
45 CONSENSUS: [LIVMH]-H-[RT]-[GA]-x-E-K-[LIVMT]-x-E-x-[KRQ].
- NAME: Respiratory-chain NADH dehydrogenase 51 Kd subunit  
signature 1.  
50 CONSENSUS: G-[AM]-G-[AR]-Y-[LIVM]-C-G-[DE](2)-[STA](2)-[LIM](2)-[EN]-S.
- NAME: Respiratory-chain NADH dehydrogenase 51 Kd subunit  
signature 2.  
CONSENSUS: E-S-C-G-x-C-x-P-C-R-x-G.
- 55 NAME: Respiratory-chain NADH dehydrogenase 75 Kd subunit  
signature 1.  
CONSENSUS: P-x(2)-C-[YWS]-x(7)-G-x-C-R-x-C.

- NAME: Respiratory-chain NADH dehydrogenase 75 Kd subunit signature 2.  
 5 CONSENSUS: C-P-x-C-[DE]-x-[GS](2)-x-C-x-L-Q.
- NAME: Respiratory-chain NADH dehydrogenase 75 Kd subunit signature 3.  
 CONSENSUS: R-C-[LIVM]-x-C-x-R-C-[LIVM]-x-[FY].
- 10 NAME: Nitrite and sulfite reductases iron-sulfur/siroheme-binding site.  
 CONSENSUS: [STV]-G-C-x(3)-C-x(6)-[DE]-[LIVMF]-[GAT]-[LIVMF].
- NAME: Uricase signature.  
 15 CONSENSUS: L-x-[LV]-L-K-[ST]-T-x-S-x-F-x(2)-[FY]-x(4)-[FY].
- NAME: Heme-copper oxidase catalytic subunit, copper B binding region signature.  
 20 CONSENSUS: [YWG]-[LIVFYWTA](2)-[VGS]-H-[LNP]-x-V-x(44,47)-H-H.
- NAME: CO II and nitrous oxide reductase dinuclear copper centers signature.  
 25 CONSENSUS: V-x-H-x(33,40)-C-x(3)-C-x(3)-H-x(2)-M.
- NAME: Cytochrome c oxidase subunit Vb, zinc binding region signature.  
 CONSENSUS: [LIVM](2)-[FYW]-x(10)-C-x(2)-C-G-x(2)-[FY]-K-L.
- 30 NAME: Multicopper oxidases signature 1.  
 CONSENSUS: G-x-[FYW]-x-[LIVMFYW]-x-[CST]-x(8)-G-[LM]-x(3)-[LIVMFYW].
- NAME: Multicopper oxidases signature 2.  
 35 CONSENSUS: H-C-H-x(3)-H-x(3)-[AG]-[LM].
- NAME: Peroxidases proximal heme-ligand signature.  
 40 CONSENSUS: [DET]-[LIVMTA]-x(2)-[LIVM]-[LIVMSTAG]-[SAG]-[LIVMSTAG]-H-[STA]-[LIVMFY].
- NAME: Peroxidases active site signature.  
 CONSENSUS: [SGATV]-x(3)-[LIVMA]-R-[LIVMA]-x-[FW]-H-x-[SAC].
- NAME: Catalase proximal heme-ligand signature.  
 45 CONSENSUS: R-[LIVMFSTAN]-F-[GASTNP]-Y-x-D-[AST]-[QEH].
- NAME: Catalase proximal active site signature.  
 CONSENSUS: [IF]-x-[RH]-x(4)-[EQ]-R-x(2)-H-x(2)-[GAS]-[GASTF]-[GAST].
- 50 NAME: Glutathione peroxidases selenocysteine active site.  
 CONSENSUS: [GN]-[RKHNFC]-x-[LIVMFC]-[LIVMF](2)-x-N-[VT]-x-[STC]-x-C-[GA]-x-T.
- NAME: Glutathione peroxidases signature 2.  
 55 CONSENSUS: [LIV]-[AGD]-F-P-[CS]-[NG]-Q-F.
- NAME: Lipoxygenases iron-binding region signature 1.

- CONSENSUS: H-[EQ]-x(3)-H-x-[LM]-[NQR]-[GST]-H-[LIVMSTAC](3)-E.
- 5 NAME: Lipoxygenases iron-binding region signature 2.  
 CONSENSUS: [LIVMA]-H-P-[LIVM]-x-[KRQ]-[LIVMF](2)-x-[AP]-H.
- NAME: Extradiol ring-cleavage dioxygenases signature.  
 CONSENSUS: [GNTIV]-x-H-x(5,7)-[LIVMF]-Y-x(2)-[DENTA]-P-x-[GP]-x(2,3)-E.
- 10 NAME: Intradiol ring-cleavage dioxygenases signature.  
 CONSENSUS: [LIVM]-x-G-x-[LIVM]-x(4)-[GS]-x(2)-[LIVM]-x(4)-[LIVM]-[DE]-[LIVMFY]-  
 CONSENSUS: x(6)-G-x-[FY].
- 15 NAME: Indoleamine 2,3-dioxygenase signature 1.  
 CONSENSUS: G-G-S-[AN]-[GA]-Q-S-S-x(2)-Q.
- 20 NAME: Indoleamine 2,3-dioxygenase signature 2.  
 CONSENSUS: [FY]-L-[DQ]-[DE]-[LIVM]-x(2)-Y-M-x(3)-H-[KR].
- NAME: Bacterial ring hydroxylating dioxygenases alpha-subunit signature.  
 CONSENSUS: C-x-H-R-[GA]-x(8)-G-N-x(5)-C-x-[FY]-H.
- 25 NAME: Bacterial luciferase subunits signature.  
 CONSENSUS: [GA]-[LIVM]-P-[LIVM]-x-[LIVMFY]-x-W-x(6)-[RK]-x(6)-Y-x(3)-[AR].
- 30 NAME: ubiH/C0Qb monooxygenase family signature.  
 CONSENSUS: H-P-[LIV]-[AG]-G-Q-G-x-N-x-G-x(2)-D.
- NAME: Biopterin-dependent aromatic amino acid hydroxylases signature.  
 35 CONSENSUS: P-D-x(2)-H-[DE]-[LI]-[LIVMF]-G-H-[LIVMC]-P.
- NAME: Copper type II, ascorbate-dependent monooxygenases signature 1.  
 CONSENSUS: H-H-M-x(2)-F-x-C.
- 40 NAME: Copper type II, ascorbate-dependent monooxygenases signature 2.  
 CONSENSUS: H-x-F-x(4)-H-T-H-x(2)-G.
- 45 NAME: Tyrosinase CuA-binding region signature.  
 CONSENSUS: H-x(4,5)-F-[LIVMFTP]-x-[FW]-H-R-x(2)-[LM]-x(3)-E.
- NAME: Tyrosinase and hemocyanins CuB-binding region signature.  
 50 CONSENSUS: D-P-x-F-[LIVMFYW]-x(2)-H-x(3)-D.
- NAME: Fatty acid desaturases family 1 signature.  
 CONSENSUS: G-E-x-[FY]-H-N-[FY]-H-H-x-F-P-x-D-Y.
- 55 NAME: Fatty acid desaturases family 2 signature.  
 CONSENSUS: [ST]-[SA]-x(3)-[QR]-[LI]-x(5,6)-D-Y-x(2)-[LIVMFYW]-[LIVM]-[DE].

- NAME: Cytochrome P450 cysteine heme-iron ligand signature.  
 CONSENSUS: [FW]-[SGNH]-x-[GD]-x-[RHPT]-x-C-[LIVMFAP]-[GAD].
- 5 NAME: Heme oxygenase signature.  
 CONSENSUS: L-L-V-A-H-A-Y-T-R.
- NAME: Copper/Zinc superoxide dismutase signature 1.  
 CONSENSUS: [GA]-[IFAT]-H-[LIVF]-H-x(2)-[GP]-[SDG]-x-[STAGD].
- 10 NAME: Copper/Zinc superoxide dismutase signature 2.  
 CONSENSUS: G-[GN]-[SGA]-G-x-R-x-[SGA]-C-x(2)-[IV].
- NAME: Manganese and iron superoxide dismutases signature.  
 CONSENSUS: D-x-W-E-H-[STA]-[FY](2).
- 15 NAME: Ribonucleotide reductase large subunit signature.  
 CONSENSUS: W-x(2)-[LF]-x(6,7)-G-[LIVM]-[FYRA]-[NH]-x(3)-  
 [STAQLIVM]-[ASC]-x(2)-  
 CONSENSUS: [PA].
- 20 NAME: Ribonucleotide reductase small subunit signature.  
 CONSENSUS: [IVMSEQ]-E-x(1,2)-[LIVTA]-[HY]-[GSA]-x-[STAVM]-Y-  
 x(2)-[LIVMQ]-x(3)-  
 CONSENSUS: [LIFY]-[IVFYCSA].
- 25 NAME: Nitrogenases component 1 alpha and beta subunits  
 signature 1.  
 CONSENSUS: [LIVMFYH]-[LIVMFST]-H-[AG]-[AGSP]-[LIVMNQA]-[AG]-  
 C.
- 30 NAME: Nitrogenases component 1 alpha and beta subunits  
 signature 2.  
 CONSENSUS: [STANQ]-[ET]-C-x(5)-G-D-[DN]-[LIVMT]-x-[STAGR]-  
 [LIVMFYST].
- 35 NAME: NifH/frxC family signature 1.  
 CONSENSUS: E-x-G-G-P-x(2)-[GA]-x-G-C-[AG]-G.
- NAME: NifH/frxC family signature 2.  
 CONSENSUS: D-x-L-G-D-V-V-C-G-G-F-[AG]-x-P.
- NAME: Nickel-dependent hydrogenases large subunit signature  
 1.  
 CONSENSUS: R-G-[LIVMF]-E-x(15)-[QESM]-R-x-C-G-[LIVM]-C.
- 45 NAME: Nickel-dependent hydrogenases large subunit signature  
 2.  
 CONSENSUS: [FY]-D-P-C-[LIM]-[ASG]-C-x(2,3)-H.
- 50 NAME: Glutamyl-tRNA reductase signature.  
 CONSENSUS: H-[LIVM]-x(2)-[LIVM]-[GSTAC](3)-[LIVM]-[DEQ]-S-  
 [LIVMA]-[LIVM](2)-[GF]-E-  
 CONSENSUS: x-[QR]-[IV]-[LIT]-[STAG]-Q-[LIVM]-[KR].
- 55 NAME: Bacterial-type phytoene dehydrogenase signature.  
 CONSENSUS: [NG]-x-[FYWV]-[LIVMF]-x-G-[AGC]-[GS]-[TA]-[HQT]-P-  
 G-[STAV]-G-[LIVM]-  
 CONSENSUS: x(5)-[GS].

- NAME: Glycine radical signature.  
 CONSENSUS: [[STIV]]-x-R-[[IVT]]-[[CSA]]-G-Y-x-[[GACV]].
- 5 NAME: Ergosterol biosynthesis ERG4/ERG24 family signature 1.  
 CONSENSUS: G-x(2)-[[LIVM]]-Y-D-x-[[FY]]-x-G-x(2)-L-N-P-R.
- NAME: Ergosterol biosynthesis ERG4/ERG24 family signature 2.  
 CONSENSUS: [[LIVM]](2)-H-R-x(2)-R-D-x(3)-C-x(2)-K-Y-G.
- 10 NAME: NNMT/PNMT/TEMT family of methyltransferases signature.  
 CONSENSUS: L-I-D-I-G-S-G-P-T-[[IV]]-Y-Q-L-L-S-A-C.
- NAME: RNA methyltransferase trmA family signature 1.  
 15 CONSENSUS: [[DN]]-P-[[PA]]-R-x-G-x(14,16)-[[LIVM]](2)-Y-x-S-C-N-x(2)-T.
- NAME: RNA methyltransferase trmA family signature 2.  
 CONSENSUS: [[LIVMF]]-D-x-F-P-[[QHY]]-[[ST]]-x-H-[[LIVMFY]]-E.
- 20 NAME: Thymidylate synthase active site.  
 CONSENSUS: R-x(2)-[[LIVM]]-x(3)-[[FW]]-[[QN]]-x(8,9)-[[LV]]-x-P-C-[[HAVM]]-x(3)-[[QMT]]-[[FYW]]-  
 CONSENSUS: x-[[LV]].
- 25 NAME: Ribosomal RNA adenine dimethylases signature.  
 CONSENSUS: [[LIVM]]-[[LIVMFY]]-[[DE]]-x-G-[[STAPV]]-G-x-[[GA]]-x-[[LIVMF]]-[[ST]]-x(2)-[[LIVM]]-  
 CONSENSUS: x(6)-[[LIVMY]]-x-[[STAGV]]-[[LIVMFYHC]]-E-x-D.
- 30 NAME: Methylated-DNA--protein-cysteine methyltransferase active site.  
 CONSENSUS: [[LIVMF]]-P-C-H-R-[[LIVMF]](2).
- 35 NAME: N-6 Adenine-specific DNA methylases signature.  
 CONSENSUS: [[LIVMAC]]-[[LIVFYWA]]-x-[[DN]]-P-P-[[FYW]].
- NAME: N-4 cytosine-specific DNA methylases signature.  
 CONSENSUS: [[LIVMF]]-T-S-P-P-[[FY]].
- 40 NAME: C-5 cytosine-specific DNA methylases active site.  
 CONSENSUS: [[DENKS]]-x-[[FLIV]]-x(2)-[[GSTC]]-x-P-C-x(2)-[[FYWLM]]-S.
- 45 NAME: C-5 cytosine-specific DNA methylases C-terminal signature.  
 CONSENSUS: [[RKQGTF]]-x(2)-G-N-[[STAG]]-[[LIVMF]]-x(3)-[[LIVMT]]-x(3)-[[LIVM]]-x(3)-[[LIVM]].
- 50 NAME: Protein-L-isoaspartate(D-aspartate) O-methyltransferase signature.  
 CONSENSUS: [[GSA]]-D-G-x(2)-G-[[FYWV]]-x(3)-[[AS]]-P-[[FY]]-[[DN]]-x-I.
- NAME: Uroporphyrin-III C-methyltransferase signature 1.  
 55 CONSENSUS: [[LIVM]]-[[GS]]-[[STAL]]-G-P-G-x(3)-[[LIVMFY]]-[[LIVM]]-T-[[LIVM]]-[[KRHQG]]-[[AG]].
- NAME: Uroporphyrin-III C-methyltransferase signature 2.



CONSENSUS: V-x(2)-[LI]-x(2)-G-D-x(3)-[FYW]-[GS]-x(8)-[LIVF]-  
x(5,b)-[LIVMFYWPAC]-  
CONSENSUS: x-[LIVMY]-x-P-G.

5 NAME: ubiE/C0Q5 methyltransferase family signature 1.  
CONSENSUS: Y-D-x-M-N-x(2)-[LIVM]-S-x(3)-H-x(2)-W.

NAME: ubiE/C0Q5 methyltransferase family signature 2.  
CONSENSUS: R-V-[LIVM]-K-[PV]-G-G-x-[LIVMF]-x(2)-[LIVM]-E-x-S.

10 NAME: Serine hydroxymethyltransferase pyridoxal-phosphate  
attachment site.

CONSENSUS: [DEH]-[LIVMFY]-x-[STMV]-[GST]-[ST](2)-H-K-[ST]-  
[LF]-x-G-[PAC]-[RQ]-

15 CONSENSUS: [GSA]-[GA].

NAME: Phosphoribosylglycinamide formyltransferase active  
site.

CONSENSUS: G-x-[STM]-[IVT]-x-[FYWVQ]-[VMAT]-x-[DEV]-x-  
20 [LIVMY]-D-x-G-x(2)-[LIVT]-  
CONSENSUS: x(b)-[LIVM].

NAME: Aspartate and ornithine carbamoyltransferases  
signature.

25 CONSENSUS: F-x-[EK]-x-S-[GT]-R-T.

NAME: Transketolase signature 1.

CONSENSUS: R-x(3)-[LIVMTA]-[DENQSTHKF]-x(5,b)-[GSN]-G-H-  
[PLIVMF]-[GSTA]-x(2)-  
30 CONSENSUS: [LIMC]-[GS].

NAME: Transketolase signature 2.

CONSENSUS: G-[DEQGS]-[DN]-G-[PAEQ]-[ST]-[HQ]-x-[PAGM]-  
[LIVMYAC]-[DEFYW]-x(2)-  
35 CONSENSUS: [STAP]-x(2)-[RGA].

NAME: Transaldolase signature 1.

CONSENSUS: [DG]-[IVSA]-T-[ST]-N-P-[STA]-[LIVMF](2).

40 NAME: Transaldolase active site.

CONSENSUS: [LIVM]-x-[LIVM]-K-[LIVM]-[PAS]-x-[ST]-x-[DENQPAS]-  
G-[LIVM]-x-[AGV]-x-  
CONSENSUS: [QEKIRST]-x-[LIVM].

45 NAME: Acyltransferases ChoActase / COT / CPT family  
signature 1.

CONSENSUS: [LI]-P-x-[LVP]-P-[IVTA]-P-x-[LIVM]-x-[DENQAS]-  
[ST]-[LIVM]-x(2)-[LY].

50 NAME: Acyltransferases ChoActase / COT / CPT family  
signature 2.

CONSENSUS: R-[FYW]-x-[DA]-[KA]-x(0,1)-[LIVMFY]-x-[LIVMFY](2)-  
x(3)-[DNS]-[GSA]-x(b)-  
CONSENSUS: [DE]-[HS]-x(3)-[DE]-[GA].

55

NAME: Thiolases acyl-enzyme intermediate signature.

CONSENSUS: [LIVM]-[NST]-x(2)-C-[SAGLI]-[ST]-[SAG]-[LIVMFYNS]-  
x-[STAG]-[LIVM]-x(b)-

- CONSENSUS: [LIVM].
- NAME: Thiolases signature 2.  
 5 CONSENSUS: N-x(2)-G-G-x-[LIVM]-[SA]-x-G-H-P-x-G-x-[ST]-G.
- NAME: Thiolases active site.  
 CONSENSUS: [AG]-[LIVMA]-[STAGLIVM]-[STAG]-[LIVMA]-C-x-[AG]-x-[AG]-x-[AG]-x-[SAG].
- 10 NAME: Chloramphenicol acetyltransferase active site.  
 CONSENSUS: Q-[LIV]-H-H-[SA]-x(2)-D-G-[FY]-H.
- NAME: Hexapeptide-repeat containing-transferases signature.  
 CONSENSUS: [LIV]-[GAED]-x(2)-[STAV]-x-[LIV]-x(3)-[LIVAC]-x-  
 15 [LIV]-[GAED]-x(2)-  
 CONSENSUS: [STAVR]-x-[LIV]-[GAED]-x(2)-[STAV]-x-[LIV]-x(3)-[LIV].
- NAME: Beta-ketoacyl synthases active site.  
 20 CONSENSUS: G-x(4)-[LIVMFAP]-x(2)-[AGC]-C-[STA](2)-[STAG]-x(3)-[LIVMF].
- NAME: Chalcone and stilbene synthases active site.  
 CONSENSUS: R-[LIVMFYS]-x-[LIVM]-x-[QHG]-x-G-C-[FYNA]-[GA]-G-  
 25 [GA]-[STAV]-x-[LIVMF]-  
 CONSENSUS: [RA].
- NAME: Myristoyl-CoA:protein N-myristoyltransferase signature 1.  
 30 CONSENSUS: E-I-N-F-L-C-x-H-K.
- NAME: Myristoyl-CoA:protein N-myristoyltransferase signature 2.  
 CONSENSUS: K-F-G-x-G-D-G.  
 35
- NAME: Gamma-glutamyltranspeptidase signature.  
 CONSENSUS: T-[STA]-H-x-[ST]-[LIVMA]-x(4)-G-[SN]-x-V-[STA]-x-T-x-T-[LIVM]-[NE]-  
 40 CONSENSUS: x(1,2)-[FY]-G.
- NAME: Transglutaminases active site.  
 CONSENSUS: [GT]-Q-[CA]-W-V-x-[SA]-[GA]-[IVT]-x(2)-T-x-[LMSC]-R-[CSA]-[LV]-G.
- 45 NAME: Phosphorylase pyridoxal-phosphate attachment site.  
 CONSENSUS: E-A-[SC]-G-x-[GS]-x-M-K-x(2)-[LM]-N.
- NAME: UDP-glycosyltransferases signature.  
 CONSENSUS: [FW]-x(2)-Q-x(2)-[LIVMYA]-[LIMV]-x(4,6)-[LVGAC]-  
 50 [LVFYA]-[LIVMF]-[STAGCM]-  
 CONSENSUS: [HNQ]-[STAGC]-G-x(2)-[STAG]-x(3)-[STAGL]-[LIVMFA]-x(4)-[PQR]-[LIVMT]-  
 CONSENSUS: x(3)-[PA]-x(3)-[DES]-[QEHN].
- 55 NAME: Purine/pyrimidine phosphoribosyl transferases signature.  
 CONSENSUS: [LIVMFYWCTA]-[LIVM]-[LIVMA]-[LIVMFC]-[DE]-D-[LIVMS]-[LIVM]-[STAVD]-

CONSENSUS: [ESTAR]-[GAC]-x-[ESTAR].

NAME: Glutamine amidotransferases class-I active site.

5 CONSENSUS: [PAS]-[LIVMFYT]-[LIVMFY]-G-[LIVMFY]-C-[LIVMFYN]-G-  
x-[QEH]-x-[LIVMFA].

NAME: Glutamine amidotransferases class-II active site.

CONSENSUS: <x(D,11)-C-[GS]-[IV]-[LIVMFYW]-[AG].

10 NAME: Purine and other phosphorylases family 1 signature.

CONSENSUS: [GST]-x-G-[LIVM]-G-x-[PA]-S-x-[GSTA]-I-x(3)-E-L.

NAME: Purine and other phosphorylases family 2 signature.

15 CONSENSUS: [LIV]-x(3)-G-x(2)-H-x-[LIVMFY]-x(4)-[LIVMF]-x(3)-  
[ATV]-x(1,2)-[LIVM]-x-  
CONSENSUS: [ATV]-x(4)-[GN]-x(3,4)-[LIVMF](2)-x(2)-[STN]-[SA]-  
x-G-[GS]-[LIVM].

20 NAME: Thymidine and pyrimidine-nucleoside phosphorylases  
signature.

CONSENSUS: S-[GS]-R-[GA]-[LIV]-x(2)-[TA]-[GA]-G-T-x-D-x-  
[LIV]-E.

NAME: ATP phosphoribosyltransferase signature.

25 CONSENSUS: E-x(5)-G-x-[SAG]-x(2)-[IV]-x-D-[LIV]-x(2)-[ST]-G-  
x-T-[LM].

NAME: NAD:arginine ADP-ribosyltransferases signature.

30 CONSENSUS: [FY]-x-[FY]-K-x(2)-H-[FY]-x-L-[ST]-x-A.

NAME: Prolipoprotein diacylglycerol transferase signature.

CONSENSUS: G-R-x-[GA]-N-F-[LIVMF]-N-x-E-x(2)-G.

NAME: S-adenosylmethionine synthetase signature 1.

35 CONSENSUS: G-A-G-D-Q-G-x(3)-G-Y.

NAME: S-adenosylmethionine synthetase signature 2.

CONSENSUS: G-[GA]-G-[ASC]-F-S-x-K-[DE].

40 NAME: Polyprenyl synthetases signature 1.

CONSENSUS: [LIVM](2)-x-D-D-x(2,4)-D-x(4)-R-R-[GH].

NAME: Polyprenyl synthetases signature 2.

45 CONSENSUS: [LIVMFY]-G-x(2)-[FYL]-Q-[LIVM]-x-D-D-[LIVMFY]-x-  
[DNG].

NAME: Squalene and phytoene synthases signature 1.

50 CONSENSUS: Y-[CSAM]-x(2)-[VSG]-A-[GSA]-[LIVAT]-[IV]-G-x(2)-  
[LMSC]-x(2)-[LIV].

NAME: Squalene and phytoene synthases signature 2.

CONSENSUS: [LIVM]-G-x(3)-Q-x(2,3)-N-[IF]-x-R-D-[LIVMFY]-x(2)-  
[DE]-x(4,7)-R-x-[FY]-  
55 CONSENSUS: x-P.

NAME: Protein prenyltransferases alpha subunit repeat  
signature.

CONSENSUS: [PSIAV]-x-[NDFV]-[NEQIY]-x-[LIVMAGP]-W-[NQSTHF]-  
[FYHQ]-[LIVMR].

5 NAME: Riboflavin synthase alpha chain family signature.  
CONSENSUS: [LIVMF]-x(5)-G-[STADNQ]-[KREQIYW]-V-N-[LIVM]-E.

NAME: Dihydropteroate synthase signature 1.  
CONSENSUS: [LIVM]-x-[AG]-[LIVMF](2)-N-x-T-x-D-S-F-x-D-x-[SG].

10 NAME: Dihydropteroate synthase signature 2.  
CONSENSUS: [GE]-[SA]-x-[LIVM](2)-D-[LIVM]-G-[GP]-x(2)-[STA]-  
x-P.

15 NAME: EPSP synthase signature 1.  
CONSENSUS: [LIVM]-x(2)-[GN]-N-[SA]-G-T-[STA]-x-R-x-[LIVMY]-x-  
[GSTA].

20 NAME: EPSP synthase signature 2.  
CONSENSUS: [KR]-x-[KH]-E-[CST]-[DNE]-R-[LIVM]-x-[STA]-  
[LIVMC]-x(2)-[EN]-[LIVMF]-x-  
CONSENSUS: [KRA]-[LIVMF]-G.

25 NAME: FLAP/GST2/LTC4S family signature.  
CONSENSUS: G-x(3)-F-E-R-V-[FY]-x-A-[NQ]-x-N-C.

30 NAME: Aminotransferases class-I pyridoxal-phosphate  
attachment site.  
CONSENSUS: [GS]-[LIVMFYTAC]-[GSTA]-K-x(2)-[GSALVN]-[LIVMFA]-  
x-[GNAR]-x-R-[LIVMA]-  
CONSENSUS: [GA].

35 NAME: Aminotransferases class-II pyridoxal-phosphate  
attachment site.  
CONSENSUS: T-[LIVMFYW]-[STAG]-K-[SAG]-[LIVMFYWR]-[SAG]-x(2)-  
[SAG].

40 NAME: Aminotransferases class-III pyridoxal-phosphate  
attachment site.  
CONSENSUS: [LIVMFYW](2)-x-D-E-[LIVMA]-x(2)-[GP]-x(0,1)-  
[LIVMFYWAG]-x(0,1)-[SACR]-x-  
CONSENSUS: [GSAD]-x(12,16)-D-[LIVMFYW](2,3)-[GSA]-K-x(3)-  
[GSTADN]-[GSA].

45 NAME: Aminotransferases class-IV signature.  
CONSENSUS: E-x-[STAGCI]-x(2)-N-[LIVMFAC]-[FY]-x(6,12)-  
[LIVMF]-x-T-x(6,8)-[LIVM]-x-  
CONSENSUS: [GS]-[LIVM]-x-[KR].

50 NAME: Aminotransferases class-V pyridoxal-phosphate  
attachment site.  
CONSENSUS: [LIVFYCHT]-[DGH]-[LIVMFYAC]-[LIVMFYA]-x(2)-  
[GSTAC]-[GSTA]-[HQR]-K-  
CONSENSUS: x(4,6)-G-x-[GSAT]-x-[LIVMFYSAC].

55 NAME: Hexokinases signature.  
CONSENSUS: [LIVM]-G-F-[TN]-F-S-[FY]-P-x(5)-[LIVM]-[DNST]-  
x(3)-[LIVM]-x(2)-W-T-K-x-  
CONSENSUS: [LF].

- NAME: Galactokinase signature.  
 CONSENSUS: G-R-x-N-[LIV]-I-G-E-H-x-D-Y.
- 5 NAME: GHMP kinases putative ATP-binding domain.  
 CONSENSUS: [LIVM]-[PK]-x-[GSTA]-x(0,1)-G-L-[GS]-S-S-[GSA]-[GSTAC].
- 10 NAME: Phosphofructokinase signature.  
 CONSENSUS: [RK]-x(4)-G-H-x-Q-[QR]-G-G-x(5)-D-R.
- NAME: pfkB family of carbohydrate kinases signature 1.  
 CONSENSUS: [AG]-G-x(0,1)-[GAP]-x-N-x-[STA]-x(6)-[GS]-x(9)-G.
- 15 NAME: pfkB family of carbohydrate kinases signature 2.  
 CONSENSUS: [DNSK]-[PSTV]-x-[SAG](2)-[GD]-D-x(3)-[SAGV]-[AG]-[LIVMFY]-[LIVMSTAP].
- NAME: ROK family signature.  
 20 CONSENSUS: [LIVM]-x(2)-G-[LIVMFACT]-G-x-[GA]-[LIVMFA]-x(8)-G-x(3,5)-[GATP]-x(2)-  
 CONSENSUS: G-[RKH].
- NAME: Phosphoribulokinase signature.  
 25 CONSENSUS: K-[LIVM]-x-R-D-x(3)-R-G-x-[ST]-x-E.
- NAME: Thymidine kinase cellular-type signature.  
 CONSENSUS: [GA]-x(1,2)-[DE]-x-Y-x-[STAP]-x-C-[NKR]-x-[CH]-[LIVMFYWH].
- 30 NAME: FGGY family of carbohydrate kinases signature 1.  
 CONSENSUS: [MFYGS]-x-[PST]-x(2)-K-[LIVMFYW]-x-W-[LIVMF]-x-[DENQTKR]-[ENQH].
- 35 NAME: FGGY family of carbohydrate kinases signature 2.  
 CONSENSUS: [GSA]-x-[LIVMFYW]-x-G-[LIVM]-x(7,8)-[HDENQ]-[LIVMF]-x(2)-[AS]-[STAIVM]-  
 CONSENSUS: [LIVMFY]-[DEQ].
- 40 NAME: Protein kinases ATP-binding region signature.  
 CONSENSUS: [LIV]-G-{P}-G-{P}-[FYWMGSTNH]-[SGA]-{PW}-[LIVCAT]-{PD}-x-[GSTACLIVMFY]-  
 CONSENSUS: x(5,18)-[LIVMFYWCSTAR]-[AIVP]-[LIVMFAGCKR]-K.
- 45 NAME: Serine/Threonine protein kinases active-site signature.  
 CONSENSUS: [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-K-x(2)-N-[LIVMFYCT](3).
- 50 NAME: Tyrosine protein kinases specific active-site signature.  
 CONSENSUS: [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-[RSTAC]-x(2)-N-[LIVMFYC](3).
- 55 NAME: Protein kinase domain profile.  
 NAME: Casein kinase II regulatory subunit signature.

CONSENSUS: C-P-x-[LIVMY]-x-C-x(5)-L-P-[LIVMC]-G-x(9)-V-[KR]-  
x(2)-C-P-x-C.

NAME: Pyruvate kinase active site signature.

5 CONSENSUS: [LIVAC]-x-[LIVM](2)-[SAPCV]-K-[LIV]-E-[NKRST]-x-  
[DEQH]-[GSTA]-[LIVM].

NAME: Shikimate kinase signature.

10 CONSENSUS: [KR]-x(2)-E-x(3)-[LIVMF]-x(8,12)-[LIVMF](2)-[SA]-  
x-G(3)-x-[LIVMF].

NAME: Prokaryotic diacylglycerol kinase signature.

CONSENSUS: E-x-[LIVM]-N-[ST]-[SA]-[LIV]-E-x(2)-V-D.

15 NAME: Phosphatidylinositol 3- and 4-kinases signature 1.

CONSENSUS: [LIVMFAC]-K-x(1,3)-[DEA]-[DE]-[LIVMC]-R-Q-[DE]-  
x(4)-Q.

NAME: Phosphatidylinositol 3- and 4-kinases signature 2.

20 CONSENSUS: [GS]-x-[AV]-x(3)-[LIVM]-x(2)-[FYH]-[LIVM](2)-x-  
[LIVMF]-x-D-R-H-x(2)-N.

NAME: Acetate and butyrate kinases family signature 1.

25 CONSENSUS: [LIVM](2)-x-[LIVM]-N-x-G-S-[ST]-S-x-[KE].

NAME: Acetate and butyrate kinases family signature 2.

CONSENSUS: [LIVMA](2)-x(2)-H-x-G-x-G-x-[ST]-[LIVM]-x-[AV]-  
x(3)-G.

30 NAME: Phosphoglycerate kinase signature.

CONSENSUS: [KRHGTCV]-[VT]-[LIVMF]-[LIVMC]-R-x-D-x-N-[SACV]-P.

NAME: Aspartokinase signature.

35 CONSENSUS: [LIVM]-x-K-[FY]-G-G-[ST]-[SC]-[LIVM].

NAME: Glutamate 5-kinase signature.

40 CONSENSUS: [GSTN]-x(2)-G-x-G-[GC]-[IM]-x-[STA]-K-[LIVM]-x-  
[SA]-[TCA]-x(2)-[GALV]-  
CONSENSUS: x(3)-G.

NAME: ATP:guanido phosphotransferases active site.

CONSENSUS: C-P-x(0,1)-[ST]-N-[IL]-G-T.

NAME: PTS HPR component histidine phosphorylation site  
signature.

45 CONSENSUS: G-[LIVM]-H-[STA]-R-[PA]-[GSTA]-[STAM].

NAME: PTS HPR component serine phosphorylation site  
signature.

50 CONSENSUS: [GSADE]-[KREQTV]-x(4)-[KRN]-S-[LIVMF](2)-x-[LIVM]-  
x(2)-[LIVM]-[GAD].

NAME: PTS EIIA domains phosphorylation site signature 1.

55 CONSENSUS: G-x(2)-[LIVMF](3)-H-[LIVMF]-G-[LIVMF]-x-T-[ALV].

NAME: PTS EIIA domains phosphorylation site signature 2.

CONSENSUS: [DENQ]-x(6)-[LIVMF]-[GA]-x(2)-[LIVM]-A-[LIVM]-P-H-  
[GAC].

- NAME: PTS EIIB domains cysteine phosphorylation site signature.  
 5 CONSENSUS: N-[LIVMFY]-x(5)-C-x-T-R-[LIVMF]-x-[LIVMF]-x-[LIVM]-x-[DQ].
- NAME: Adenylate kinase signature.  
 CONSENSUS: [LIVMFYW](3)-D-G-[FYI]-P-R-x(3)-[NQ].
- 10 NAME: Nucleoside diphosphate kinases active site.  
 CONSENSUS: N-x(2)-H-[GA]-S-D-[SA]-[LIVMPKNE].
- NAME: Guanylate kinase signature.  
 15 CONSENSUS: T-[ST]-R-x(2)-[KR]-x(2)-[DE]-x(2)-G-x(2)-Y-x-[FY]-[LIVMK].
- NAME: Guanylate kinase domain profile.
- NAME: Phosphoribosyl pyrophosphate synthetase signature.  
 20 CONSENSUS: D-[LI]-H-[SA]-x-Q-[IMST]-[QM]-G-[FY]-F-x(2)-P-[LIVMFC]-D.
- NAME: 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature.  
 25 CONSENSUS: G-[PE]-R-x(2)-D-L-D-[LIVM](2).
- NAME: Bacteriophage-type RNA polymerase family active site signature 1.  
 30 CONSENSUS: P-[LIVM]-x(2)-D-[GA]-[ST]-[AC]-[SN]-[GA]-[LIVMFY]-Q.
- NAME: Bacteriophage-type RNA polymerase family active site signature 2.  
 35 CONSENSUS: [LIVMF]-x-R-x(3)-K-x(2)-[LIVMF]-M-[PT]-x(2)-Y.
- NAME: Eukaryotic RNA polymerase II heptapeptide repeat.  
 CONSENSUS: Y-[ST]-P-[ST]-S-P-[STANK].
- NAME: RNA polymerases beta chain signature.  
 40 CONSENSUS: G-x-K-[LIVMFA]-[STAC]-[GSTN]-x-[HSTA]-[GS]-[QNH]-K-G-[IVT].
- NAME: RNA polymerases M / 15 Kd subunits signature.  
 45 CONSENSUS: F-C-x-[DEKST]-C-[GNK]-[DNSA]-[LIVMH]-[LIVM]-x(8,14)-C-x(2)-C.
- NAME: RNA polymerases D / 30 to 40 Kd subunits signature.  
 CONSENSUS: N-[SGA]-[LIVMF]-R-R-x(9)-[SA]-x(3)-V-x(4)-N-x-[STA]-x(3)-[DN]-E-x-[LI]-  
 50 CONSENSUS: [GA]-x-R-[LI]-[GA]-[LIVM](2)-P.
- NAME: RNA polymerases H / 23 Kd subunits signature.  
 CONSENSUS: H-[NEI]-[LIVM]-V-P-x-H-x(2)-[LIVM]-x(2)-[DE].
- 55 NAME: RNA polymerases K / 14 to 18 Kd subunits signature.  
 CONSENSUS: [ST]-x-[FY]-E-x-[AT]-R-x-[LIVM]-[GSA]-x-R-[SA]-x-Q.

- NAME: RNA polymerases L / 13 to 16 Kd subunits signature.  
 CONSENSUS: [DE](2)-H-[ST]-[LIVM]-[GAP]-N-x(11)-V-x-[FM]-x(2)-Y-x(3)-H-P.
- 5 NAME: RNA polymerases N / 8 Kd subunits signature.  
 CONSENSUS: [LIVMF](2)-P-[LIVM]-x-C-F-[ST]-C-G.
- NAME: DNA polymerase family A signature.  
 CONSENSUS: R-x(2)-[GSAV]-K-x(3)-[LIVMFY]-[AGQ]-x(2)-Y-x(2)-[GS]-x(3)-[LIVMA].
- 10 [GS]-x(3)-[LIVMA].
- NAME: DNA polymerase family B signature.  
 CONSENSUS: [YA]-[GLIVMSTAC]-D-T-D-[SG]-[LIVMFTC]-x-[LIVMSTAC].
- 15 NAME: DNA polymerase family X signature.  
 CONSENSUS: G-[SG]-[LFY]-x-R-[GE]-x(3)-[SGCL]-x-D-[LIVM]-D-[LIVMFY](3)-x(2)-[SAP].
- 20 NAME: Galactose-1-phosphate uridyl transferase family 1 active site signature.  
 CONSENSUS: F-E-N-[RK]-G-x(3)-G-x(4)-H-P-H-x-Q.
- NAME: Galactose-1-phosphate uridyl transferase family 2 signature.  
 25 CONSENSUS: D-L-P-I-V-G-G-[ST]-[LIVM](2)-[SA]-H-[DEN]-H-[FY]-Q-G-G.
- NAME: ADP-glucose pyrophosphorylase signature 1.  
 30 CONSENSUS: [AG]-G-G-x-G-[STK]-x-L-x(2)-L-[TA]-x(3)-A-x-P-A-[LV].
- NAME: ADP-glucose pyrophosphorylase signature 2.  
 CONSENSUS: W-[FY]-x-G-[ST]-A-[DNSh]-[AS]-[LIVMFYW].
- 35 NAME: ADP-glucose pyrophosphorylase signature 3.  
 CONSENSUS: [APV]-[GS]-M-G-[LIVMN]-Y-[IVC]-[LIVMFY]-x(2)-[DENPHK].
- 40 NAME: Phosphatidate cytidyltransferase signature.  
 CONSENSUS: S-x-[LIVMF]-K-R-x(4)-K-D-x-[GSA]-x(2)-[LI]-[PG]-x-H-G-G-[LIVM]-x-D-R-  
 CONSENSUS: [LIVMFT]-D.
- 45 NAME: Ribonuclease PH signature.  
 CONSENSUS: C-[DE]-[LIVM](2)-Q-[GTA]-D-G-[SG]-x(2)-[TA]-A.
- NAME: 2'-5'-oligoadenylate synthetases signature 1.  
 CONSENSUS: G-G-S-x-[AG]-[KR]-x-T-x-L-[KR]-[GST]-x-S-D-[AG].
- 50 NAME: 2'-5'-oligoadenylate synthetases signature 2.  
 CONSENSUS: R-P-V-I-L-D-P-x-[DE]-P-T.
- NAME: CDP-alcohol phosphatidyltransferases signature.  
 55 CONSENSUS: D-G-x(2)-A-R-x(8)-G-x(3)-D-x(3)-D.
- NAME: PEP-utilizing enzymes phosphorylation site signature.



CONSENSUS: G-[GA]-x-[TN]-x-H-[STA]-[STAV]-[LIVM](2)-[STAV]-[RG].

NAME: PEP-utilizing enzymes signature 2.

5 CONSENSUS: [DEQS]-x-[LIVMF]-S-[LIVMF]-G-[ST]-N-D-[LIVM]-x-Q-[LIVMFYGT]-[STALIV]-

CONSENSUS: [LIVMF]-[GAS]-x(2)-R.

NAME: Rhodanese signature 1.

10 CONSENSUS: [FY]-x(3)-H-[LIV]-P-G-A-x(2)-[LIVF].

NAME: Rhodanese C-terminal signature.

CONSENSUS: [AV]-x(2)-[FY]-[DEAP]-G-[GSA]-[WF]-x-E-[FYW].

15 NAME: CoA transferases signature 1.

CONSENSUS: [DN]-[GN]-x(2)-[LIVMFA](3)-G-G-F-x(3)-G-x-P.

NAME: CoA transferases signature 2.

20 CONSENSUS: [LF]-[HQ]-S-E-N-G-[LIVF](2)-[GA].

NAME: Phospholipase A2 histidine active site.

CONSENSUS: C-C-x(2)-H-x(2)-C.

NAME: Phospholipase A2 aspartic acid active site.

25 CONSENSUS: [LIVMA]-C-[LIVMFYWPCT]-C-D-x(5)-C.

NAME: Lipases, serine active site.

CONSENSUS: [LIV]-x-[LIVFY]-[LIVMST]-G-[HYWV]-S-x-G-[GSTAC].

30 NAME: Colipase signature.

CONSENSUS: Y-x(2)-Y-Y-x-C-x-C.

NAME: Lipolytic enzymes "G-D-S-L" family, serine active site.

35 CONSENSUS: [LIVMFYAG](4)-G-D-S-[LIVM]-x(1,2)-[TAG]-G.

NAME: Lipolytic enzymes "G-D-X-G" family, putative histidine active site.

40 CONSENSUS: [LIVMF](2)-x-[LIVMF]-H-G-G-[SAG]-[FY]-x(3)-[STDN]-x(2)-[ST]-H.

NAME: Lipolytic enzymes "G-D-X-G" family, putative serine active site.

45 CONSENSUS: [LIVM]-x-[LIVMF]-[SA]-G-D-S-[CA]-G-[GA]-x-L-[CA].

NAME: Carboxylesterases type-B serine active site.

CONSENSUS: F-[GR]-G-x(4)-[LIVM]-x-[LIV]-x-G-x-S-[STAG]-G.

NAME: Carboxylesterases type-B signature 2.

50 CONSENSUS: [ED]-D-C-L-[YT]-[LIV]-[DNS]-[LIV]-[LIVFYW]-x-[PQR].

NAME: Pectinesterase signature 1.

55 CONSENSUS: [GSTN]-x(5)-[LIVM]-x-[LIVM]-x(2)-G-x-Y-[DNK]-E-x-[LIVM]-x-[LIVM].

NAME: Pectinesterase signature 2.

CONSENSUS: G-[STAD]-[LIVMT]-D-F-I-F-G.

- NAME: Peptidyl-tRNA hydrolase signature 1.  
 CONSENSUS: [FY]-x(2)-T-R-H-N-x-G-x(2)-[LIVMFA](2)-[DE].
- 5 NAME: Peptidyl-tRNA hydrolase signature 2.  
 CONSENSUS: [GS]-x(3)-H-N-G-[LIVM]-[KR]-[DNS]-[LIVMT].
- NAME: Alkaline phosphatase active site.  
 CONSENSUS: [IV]-x-D-S-[GAS]-[GASC]-[GAST]-[GA]-T.
- 10 NAME: Histidine acid phosphatases phosphohistidine  
 signature.  
 CONSENSUS: [LIVM]-x(2)-[LIVMA]-x(2)-[LIVM]-x-R-H-[GN]-x-R-x-  
 [PAS].
- 15 NAME: Histidine acid phosphatases active site signature.  
 CONSENSUS: [LIVMF]-x-[LIVMFAG]-x(2)-[STAGI]-H-D-[STANQ]-x-  
 [LIVM]-x(2)-[LIVMFY]-x(2)-  
 CONSENSUS: [STA].
- 20 NAME: Class A bacterial acid phosphatases signature.  
 CONSENSUS: G-S-Y-P-S-G-H-T.
- NAME: 5'-nucleotidase signature 1.  
 25 CONSENSUS: [LIVM]-x-[LIVM](2)-[HEA]-[TI]-x-D-x-H-[GSA]-x-  
 [LIVMF].
- NAME: 5'-nucleotidase signature 2.  
 CONSENSUS: [FYP]-x(4)-[LIVM]-G-N-H-E-F-[DN].
- 30 NAME: Fructose-1,6-bisphosphatase active site.  
 CONSENSUS: [AG]-[RK]-L-x(1,2)-[LIV]-[FY]-E-x(2)-P-[LIVM]-  
 [GSA].
- 35 NAME: Serine/threonine specific protein phosphatases  
 signature.  
 CONSENSUS: [LIVM]-R-G-N-H-E.
- NAME: Protein phosphatase 2A regulatory subunit PR55  
 40 signature 1.  
 CONSENSUS: E-F-D-Y-L-K-S-L-E-I-E-E-K-I-N.
- NAME: Protein phosphatase 2A regulatory subunit PR55  
 signature 2.  
 45 CONSENSUS: N-[AG]-H-[TA]-Y-H-I-N-S-I-S-[LIVM]-N-S-D.
- NAME: Protein phosphatase 2C signature.  
 CONSENSUS: [LIVMFY]-[LIVMFYA]-[GSAC]-[LIVM]-[FYC]-D-G-H-  
 [GAV].
- 50 NAME: Tyrosine specific protein phosphatases active site.  
 CONSENSUS: [LIVMF]-H-C-x(2)-G-x(3)-[STC]-[STAGP]-x-[LIVMFY].
- NAME: Tyrosine specific protein phosphatases profile.
- 55 NAME: Dual specificity protein phosphatase profile.
- NAME: PTP type protein phosphatase profile.

- NAME: Inositol monophosphatase family signature 1.  
 5 CONSENSUS: [FWV]-x(0,1)-[LIVM]-D-P-[LIVM]-D-[SG]-[ST]-x(2)-  
 [FY]-x-[HKRNSTY].
- NAME: Inositol monophosphatase family signature 2.  
 CONSENSUS: [WV]-D-x-[AC]-[GSA]-[GSAPV]-x-[LIVACP]-[LIV]-  
 [LIVAC]-x(3)-[GH]-[GA].
- 10 NAME: Prokaryotic zinc-dependent phospholipase C signature.  
 CONSENSUS: H-Y-x-[GT]-D-[LIVM]-[DNS]-x-P-x-H-[PA]-x-N.
- NAME: Phosphatidylinositol-specific phospholipase X-box  
 domain profile.
- 15 NAME: Phosphatidylinositol-specific phospholipase Y-box  
 domain profile.
- NAME: 3'5'-cyclic nucleotide phosphodiesterases signature.  
 20 CONSENSUS: H-D-[LIVMFY]-x-H-x-[AG]-x(2)-[NQ]-x-[LIVMFY].
- NAME: cAMP phosphodiesterases class-II signature.  
 CONSENSUS: H-x-H-L-D-H-[LIVM]-x-[GS]-[LIVMA]-[LIVM](2)-x-S-  
 [AP].
- 25 NAME: Sulfatases signature 1.  
 CONSENSUS: [SAP]-[LIVMST]-[CS]-[STAC]-P-[STA]-R-x(2)-  
 [LIVMFW](2)-[TR]-G.
- 30 NAME: Sulfatases signature 2.  
 CONSENSUS: G-[YV]-x-[ST]-x(2)-[IVA]-G-K-x(0,1)-[FYWK]-[HL].
- NAME: AP endonucleases family 1 signature 1.  
 CONSENSUS: [APF]-D-[LIVMF](2)-x-[LIVM]-Q-E-x-K.
- 35 NAME: AP endonucleases family 1 signature 2.  
 CONSENSUS: D-[ST]-[FY]-R-[KH]-x(7,8)-[FYW]-[ST]-[FYW](2).
- NAME: AP endonucleases family 1 signature 3.  
 40 CONSENSUS: N-x-G-x-R-[LIVM]-D-[LIVMFYH]-x-[LV]-x-S.
- NAME: AP endonucleases family 2 signature 1.  
 CONSENSUS: H-x(2)-Y-[LIVMF]-[IM]-N-[LIVMCA]-[AG].
- 45 NAME: AP endonucleases family 2 signature 2.  
 CONSENSUS: [GR]-[LIVMF]-C-[LIVM]-D-T-C-H.
- NAME: AP endonucleases family 2 signature 3.  
 CONSENSUS: [LIVMW]-H-x-N-[DE]-[SA]-K-x(3)-G-[SA]-x(2)-D.
- 50 NAME: Deoxyribonuclease I signature 1.  
 CONSENSUS: [LIVM](2)-[AP]-L-H-[STA](2)-P-x(5)-E-[LIVM]-[DN]-  
 x-L-x-[DE]-V.
- 55 NAME: Deoxyribonuclease I signature 2.  
 CONSENSUS: G-D-F-N-A-x-C-[SA].
- NAME: Endonuclease III iron-sulfur binding region signature.

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- CONSENSUS: C-x(3)-[KRS]-P-[KRAL]-C-x(2)-C-x(5)-C.  
 NAME: Endonuclease III family signature.  
 CONSENSUS: [GST]-x-[LIVMF]-P-x(5)-[LIVMW]-x(2,3)-[LI]-[PAS]-  
 G-V-[GA]-x(3)-[GAC]-  
 CONSENSUS: x(3)-[LIVM]-x(2)-[SALV]-[LIVMFYW]-[GANK].  
 NAME: Ribonuclease II family signature.  
 CONSENSUS: [HI]-[FYE]-[GSTAM]-[LIVM]-x(4,5)-Y-[STAL]-x-  
 [FWVAC]-[TV]-[SA]-P-[LIVMA]-  
 CONSENSUS: [RQ]-[KR]-[FY]-x-D-x(3)-[HQ].  
 NAME: Ribonuclease III family signature.  
 CONSENSUS: [DEQ]-[RQ]-[LM]-E-[FYW]-[LV]-G-D-[SAR].  
 NAME: Bacterial Ribonuclease P protein component signature.  
 CONSENSUS: [LIVMFYS]-x(2)-A-x(2)-R-[NH]-[KRQL]-[LIVM]-[KRA]-  
 R-x-[LIVMTA]-[KR].  
 NAME: Ribonuclease T2 family histidine active site 1.  
 CONSENSUS: [FYWL]-x-[LIVM]-H-G-L-W-P.  
 NAME: Ribonuclease T2 family histidine active site 2.  
 CONSENSUS: [LIVMF]-x(2)-[HDGTY]-[EQ]-[FYW]-x-[KR]-H-G-x-C.  
 NAME: Pancreatic ribonuclease family signature.  
 CONSENSUS: C-K-x(2)-N-T-F.  
 NAME: DNA/RNA non-specific endonucleases active site.  
 CONSENSUS: D-R-G-H-[QIL]-x(3)-A.  
 NAME: Thermonuclease family signature 1.  
 CONSENSUS: D-G-D-T-[LIVM]-x-[LIVMC]-x(9,10)-R-[LIVM]-x(2)-  
 [LIVM]-D-x-P-E.  
 NAME: Thermonuclease family signature 2.  
 CONSENSUS: D-[KR]-Y-[GQ]-R-x-[LV]-[GA]-x-[IV]-[FYW].  
 NAME: Beta-amylase active site 1.  
 CONSENSUS: H-x-C-G-G-N-V-G-D.  
 NAME: Beta-amylase active site 2.  
 CONSENSUS: G-x-[SA]-G-E-[LIVM]-R-Y-P-S-Y.  
 NAME: Glucoamylase active site region signature.  
 CONSENSUS: [STN]-[GP]-x(1,2)-[DE]-x-W-E-E-x(2)-[GS].  
 NAME: Polygalacturonase active site.  
 CONSENSUS: [GSDENKRH]-x(2)-[VMFC]-x(2)-[GS]-H-G-[LIVMAG]-  
 x(1,2)-[LIVM]-G-S.  
 NAME: Clostridium cellulosome enzymes repeated domain  
 signature.  
 CONSENSUS: D-[LIVMFY]-[DNV]-x-[DNS]-x(2)-[LIVM]-[DN]-[SALM]-  
 x-D-x(3)-[LIVMF]-x-  
 CONSENSUS: [RKS]-x-[LIVMF].  
 NAME: Chitinases family 1B active site.

- CONSENSUS: [LIVMFY]-[DN]-G-[LIVMF]-[DN]-[LIVMF]-[DN]-x-E.
- NAME: Chitinases family 19 signature 1.  
 5 CONSENSUS: C-x(4,5)-F-Y-[ST]-x(3)-[FY]-[LIVMF]-x-A-x(3)-[YF]-x(2)-F-[GSA].
- NAME: Chitinases family 19 signature 2.  
 10 CONSENSUS: [LIVM]-[GSA]-F-x-[STAG](2)-[LIVMFY]-W-[FY]-W-[LIVM].
- NAME: Alpha-lactalbumin / lysozyme C signature.  
 CONSENSUS: C-x(3)-C-x(2)-[LMF]-x(3)-[DEN]-[LI]-x(5)-C.
- NAME: Alpha-galactosidase signature.  
 15 CONSENSUS: G-[LIVMFY]-x(2)-[LIVMFY]-x-[LIVM]-D-D-x-W-x(3,4)-R-[DNSF].
- NAME: Trehalase signature 1.  
 20 CONSENSUS: P-G-G-R-F-x-E-x-Y-x-W-D-x-Y.
- NAME: Trehalase signature 2.  
 CONSENSUS: Q-W-D-x-P-x-[GA]-W-[PA]-P.
- NAME: Alpha-L-fucosidase putative active site.  
 25 CONSENSUS: P-x(2)-L-x(3)-K-W-E-x-C.
- NAME: Glycosyl hydrolases family 1 active site.  
 30 CONSENSUS: [LIVMFSTC]-[LIVFYS]-[LIV]-[LIVMST]-E-N-G-[LIVMFAR]-[CSAGN].
- NAME: Glycosyl hydrolases family 1 N-terminal signature.  
 CONSENSUS: F-x-[FYWM]-[GSTA]-x-[GSTA]-x-[GSTA](2)-[FYNH]-[NQ]-x-E-x-[GSTA].
- NAME: Glycosyl hydrolases family 2 signature 1.  
 35 CONSENSUS: N-x-[LIVMFYWD]-R-[STACN](2)-H-Y-P-x(4)-[LIVMFYW](2)-x(3)-[DN]-x(2)-G-[LIVMFYW](4).
- NAME: Glycosyl hydrolases family 2 acid/base catalyst.  
 40 CONSENSUS: [DENQF]-[KRVW]-N-H-[AP]-[SAC]-[LIVMF](3)-W-[GS]-x(2,3)-N-E.
- NAME: Glycosyl hydrolases family 3 active site.  
 45 CONSENSUS: [LIVM](2)-[KR]-x-[EQK]-x(4)-G-[LIVMFT]-[LIVT]-[LIVMF]-[ST]-D-x(2)-[SGADNI].
- NAME: Glycosyl hydrolases family 5 signature.  
 50 CONSENSUS: [LIV]-[LIVMFYWGA](2)-[DNEQG]-[LIVMGST]-x-N-E-[PV]-[RHDNSTLIVFY].
- NAME: Glycosyl hydrolases family 6 signature 1.  
 55 CONSENSUS: V-x-Y-x(2)-P-x-R-D-C-[GSAF]-x(2)-[GSA](2)-x-G.
- NAME: Glycosyl hydrolases family 6 signature 2.  
 CONSENSUS: [LIVMYA]-[LIVA]-[LIVT]-[LIV]-E-P-D-[SAL]-[LI]-[PSAG].

- NAME: Glycosyl hydrolases family 8 signature.  
 5 CONSENSUS: A-[ST]-D-[AG]-D-x(2)-[IM]-A-x-[SA]-[LIVM]-[LIVMG]-  
 x-A-x(3)-[FW].
- NAME: Glycosyl hydrolases family 9 active sites signature 1.  
 CONSENSUS: [STV]-x-[LIVMFY]-[STV]-x(2)-G-x-[NKR]-x(4)-  
 [PLIVM]-H-x-R.
- 10 NAME: Glycosyl hydrolases family 9 active sites signature 2.  
 CONSENSUS: [FYW]-x-D-x(4)-[FYW]-x(3)-E-x-[STA]-x(3)-N-[STA].
- NAME: Glycosyl hydrolases family 10 active site.  
 15 CONSENSUS: [GTA]-x(2)-[LIVN]-x-[IVMF]-[ST]-E-[LIY]-[DN]-  
 [LIVMF].
- NAME: Glycosyl hydrolases family 11 active site signature 1.  
 CONSENSUS: [PSA]-[LQ]-x-E-Y-Y-[LIVM](2)-[DE]-x-[FYWHN].
- 20 NAME: Glycosyl hydrolases family 11 active site signature 2.  
 CONSENSUS: [LIVMF]-x(2)-E-[AG]-[YWG]-[QRFGS]-[SG]-[STAN]-G-x-  
 [SAF].
- NAME: Glycosyl hydrolases family 16 active sites.  
 25 CONSENSUS: E-[LIV]-D-[LIV]-x(0,1)-E-x(2)-[GQ]-[KRN]-x-  
 [PSTA].
- NAME: Glycosyl hydrolases family 17 signature.  
 30 CONSENSUS: [LIVM]-x-[LIVMFYWA](3)-[STAG]-E-[STA]-G-W-P-[STN]-  
 x-[SAGQ].
- NAME: Glycosyl hydrolases family 25 active sites signature.  
 CONSENSUS: D-[LIVM]-x(3)-[NQ]-[PG]-x(9,10)-G-x(4)-  
 [LIVMFY](2)-K-x-[ST]-E-[GS]-x(2)-  
 35 CONSENSUS: Y-x-[DN].
- NAME: Glycosyl hydrolases family 31 active site.  
 CONSENSUS: [GF]-[LIVMF]-W-x-D-M-[NSA]-E.
- 40 NAME: Glycosyl hydrolases family 31 signature 2.  
 CONSENSUS: G-[AV]-D-[LIVMT]-C-G-[FY]-x(3)-[ST]-x(3)-L-C-x-R-  
 W-x(2)-[LV]-[GS]-[SA]-  
 CONSENSUS: F-x-P-F-x-R-[DN].
- 45 NAME: Glycosyl hydrolases family 32 active site.  
 CONSENSUS: H-x(2)-P-x(4)-[LIVM]-N-D-P-N-G.
- NAME: Glycosyl hydrolases family 35 putative active site.  
 50 CONSENSUS: G-G-P-[LIVM](2)-x(2)-Q-x-E-N-E-[FY].
- NAME: Glycosyl hydrolases family 39 active site.  
 CONSENSUS: W-x-F-E-x-W-N-E-P-[DN].
- NAME: Glycosyl hydrolases family 45 active site.  
 55 CONSENSUS: [STA]-T-R-Y-[FYW]-D-x(5)-[CA].
- NAME: Prokaryotic transglycosylases signature.

- CONSENSUS: [LIVM]-x(3)-E-S-x(3)-[AP]-x(3)-S-x(5)-G-[LIVM]-  
 [LIVMFYW]-x-[LIVMFYW]-  
 CONSENSUS: x(4)-[SAG].
- 5 NAME: Inosine-uridine preferring nucleoside hydrolase family  
 signature.  
 CONSENSUS: D-x-D-[PT]-[GA]-x-D-D-[TAV]-[VI]-A.
- 10 NAME: Alkylbase DNA glycosidases alkA family signature.  
 CONSENSUS: G-I-G-x-W-[ST]-[AV]-x-[LIVMFY](2)-x-[LIVM]-x(8)-  
 [MF]-x(2)-[ED]-D.
- 15 NAME: Formamidopyrimidine-DNA glycosylase signature.  
 CONSENSUS: C-x(2,4)-C-x-[GTAQ]-x-[IV]-x(7)-R-[GSTAN]-[STA]-x-  
 [FYI]-C-x(2)-C-Q.
- NAME: Uracil-DNA glycosylase signature.  
 CONSENSUS: [KR]-[LIV]-[LIVC]-[LIVM]-x-G-[QI]-D-P-Y.
- 20 NAME: S-adenosyl-L-homocysteine hydrolase signature 1.  
 CONSENSUS: [CS]-N-x-[FYL]-S-[ST]-[QA]-[DEN]-x-[AV](2)-A-A-  
 [LIV]-[SAV].
- 25 NAME: S-adenosyl-L-homocysteine hydrolase signature 2.  
 CONSENSUS: G-K-x(3)-[LIV]-x-G-Y-G-x-V-G-[KR]-G-x-A.
- NAME: Cytosol aminopeptidase signature.  
 CONSENSUS: N-T-D-A-E-G-R-L.
- 30 NAME: Aminopeptidase P and proline dipeptidase signature.  
 CONSENSUS: [HA]-[GSYR]-[LIVMT]-[SG]-H-x-[LIV]-G-[LIVM]-x-  
 [IV]-H-[DE].
- 35 NAME: Methionine aminopeptidase subfamily 1 signature.  
 CONSENSUS: [MFY]-x-G-H-G-[LIVMC]-[GSH]-x(3)-H-x(4)-[LIVM]-x-  
 [HN]-[YWV].
- 40 NAME: Methionine aminopeptidase subfamily 2 signature.  
 CONSENSUS: [DA]-[LIVMY]-x-K-[LIVM]-D-x-G-x-[HQ]-[LIVM]-[DNS]-  
 G-x(3)-[DN].
- 45 NAME: Renal dipeptidase active site.  
 CONSENSUS: [LIVM]-E-G-[GA]-x(2)-[LIVMF]-x(6)-L-x(3)-Y-x(2)-G-  
 [LIVM]-R.
- NAME: Serine carboxypeptidases, serine active site.  
 CONSENSUS: [LIVM]-x-[GTA]-E-S-Y-[AG]-[GS].
- 50 NAME: Serine carboxypeptidases, histidine active site.  
 CONSENSUS: [LIVF]-x(2)-[LIVSTA]-x-[IVPST]-x-[GSDNQL]-[SAGV]-  
 [SG]-H-x-[IVAQ]-P-x(3)-  
 CONSENSUS: [PSA].
- 55 NAME: Zinc carboxypeptidases, zinc-binding region 1  
 signature.  
 CONSENSUS: [PK]-x-[LIVMFY]-x-[LIVMFY]-x(4)-H-[STAG]-x-E-x-  
 [LIVM]-[STAG]-x(6)-  
 CONSENSUS: [LIVMFYTA].

- NAME: Zinc carboxypeptidases, zinc-binding region 2  
signature.  
5 CONSENSUS: H-[[STAG]]-x(3)-[[LIVME]]-x(2)-[[LIVMFYW]]-P-[[FYW]].
- NAME: Serine proteases, trypsin family, histidine active site.  
CONSENSUS: [[LIVM]]-[[EST]]-A-[[STAG]]-H-C.
- 10 NAME: Serine proteases, trypsin family, serine active site.  
CONSENSUS: [[DNSTAGC]]-[[GSTAPIMVQH]]-x(2)-G-[[DEI]]-S-G-[[GS]]-  
[[SAPHV]]-[[LIVMFYWH]]-  
CONSENSUS: [[LIVMFYSTANQH]].
- 15 NAME: Serine proteases, subtilase family, aspartic acid active site.  
CONSENSUS: [[STAIV]]-x-[[LIVMF]]-[[LIVM]]-D-[[DSTA]]-G-[[LIVMFC]]-  
x(2,3)-[[DNH]].
- 20 NAME: Serine proteases, subtilase family, histidine active site.  
CONSENSUS: H-G-[[STM]]-x-[[VIC]]-[[STAGC]]-[[GS]]-x-[[LIVMA]]-  
[[STAGCLV]]-[[SAGM]].
- 25 NAME: Serine proteases, subtilase family, serine active site.  
CONSENSUS: G-T-S-x-[[SA]]-x-P-x(2)-[[STAVC]]-[[AG]].
- 30 NAME: Serine proteases, V8 family, histidine active site.  
CONSENSUS: [[ST]]-G-[[LIVMFYW]](3)-[[GN]]-x(2)-T-[[LIVM]]-x-T-x(2)-H.  
NAME: Serine proteases, V8 family, serine active site.  
CONSENSUS: T-x(2)-[[GC]]-[[NQ]]-S-G-S-x-[[LIVM]]-[[FY]].
- 35 NAME: Serine proteases, omptin family signature 1.  
CONSENSUS: W-T-D-x-S-x-H-P-x-T.  
NAME: Serine proteases, omptin family signature 2.  
40 CONSENSUS: A-G-Y-Q-E-[[ST]]-R-[[FYW]]-S-[[FYW]]-[[TN]]-A-x-G-G-[[ST]]-  
Y.
- NAME: Prolyl endopeptidase family serine active site.  
CONSENSUS: D-x(3)-A-x(3)-[[LIVMFYW]]-x(14)-G-x-S-x-G-G-  
[[LIVMFYW]](2).  
45
- NAME: Endopeptidase Clp serine active site.  
CONSENSUS: T-x(2)-[[LIVMF]]-G-x-A-[[SAC]]-S-[[MSA]]-[[PAG]]-[[STA]].
- NAME: Endopeptidase Clp histidine active site.  
50 CONSENSUS: R-x(3)-[[EAP]]-x(3)-[[LIVMFYT]]-M-[[LIVM]]-H-Q-P.
- NAME: ATP-dependent serine proteases, lon family, serine active site.  
CONSENSUS: D-G-[[PD]]-S-A-[[GS]]-[[LIVMCA]]-[[TA]]-[[LIVM]].  
55
- NAME: Eukaryotic thiol (cysteine) proteases cysteine active site.  
CONSENSUS: Q-x(3)-[[GE]]-x-C-[[YW]]-x(2)-[[STAGC]]-[[STAGCV]].



NAME: Eukaryotic thiol (cysteine) proteases histidine active site.  
 5 CONSENSUS: [LIVMGSTAN]-x-H-[GSACE]-[LIVM]-x-[LIVMAT](2)-G-x-[GSADNH].  
  
 NAME: Eukaryotic thiol (cysteine) proteases asparagine active site.  
 10 CONSENSUS: [FYCH]-[WII]-[LIVT]-x-[KRQAG]-N-[EST]-W-x(3)-[FYW]-G-x(2)-G-[LFYW]-  
 CONSENSUS: [LIVMFYGG]-x-[LIVMF].  
  
 NAME: Ubiquitin carboxyl-terminal hydrolase family 1 cysteine active-site.  
 15 CONSENSUS: Q-x(3)-N-[SA]-C-G-x(3)-[LIVM](2)-H-[SA]-[LIVM]-[SA].  
  
 NAME: Ubiquitin carboxyl-terminal hydrolases family 2 signature 1.  
 20 CONSENSUS: G-[LIVMFY]-x(1,3)-[AGC]-[NASM]-x-C-[FYW]-[LIVMC]-[NST]-[SACV]-x-[LIVMS]-  
 CONSENSUS: Q.  
  
 NAME: Ubiquitin carboxyl-terminal hydrolases family 2 signature 2.  
 25 CONSENSUS: Y-x-L-x-[SAG]-[LIVMFT]-x(2)-H-x-G-x(4,5)-G-H-Y.  
  
 NAME: Caspase family histidine active site.  
 30 CONSENSUS: H-x(2,4)-[SC]-x(4)-[LIVMF](2)-[EST]-H-G.  
  
 NAME: Caspase family cysteine active site.  
 CONSENSUS: K-P-K-[LIVMF](4)-Q-A-C-[RQG]-G.  
  
 NAME: Eukaryotic and viral aspartyl proteases active site.  
 35 CONSENSUS: [LIVMFGAC]-[LIVMTADN]-[LIVFSA]-D-[EST]-G-[ESTAV]-[STAPDENQ]-x-[LIVMFSTNC]-  
 CONSENSUS: x-[LIVMFGTA].  
  
 NAME: Neutral zinc metalloproteinases, zinc-binding region signature.  
 40 CONSENSUS: [GSTALIVN]-x(2)-H-E-[LIVMFYW]-[DEHRKP]-H-x-[LIVMFYWGSPQ].  
  
 NAME: Matrixins cysteine switch.  
 45 CONSENSUS: P-R-C-[GN]-x-P-[DR]-[LIVSAPKQ].  
  
 NAME: Insulinase family, zinc-binding region signature.  
 50 CONSENSUS: G-x(8,9)-G-x-[STA]-H-[LIVMFY]-[LIVMC]-[DERN]-[HRKL]-[LMFAT]-x-[LFSTH]-x-  
 CONSENSUS: [GSTAN]-[GST].  
  
 //

AC PS01016;  
 55 DE Glycoprotease family signature.  
 CONSENSUS: [KR]-[GSAT]-x(4)-[FYWHL]-[DQNGK]-x-P-x-[LIVMFY]-x(3)-H-x(2)-[AG]-H-  
 CONSENSUS: [LIVM].

NAME: Proteasome A-type subunits signature.

CONSENSUS: [FY]-x(4)-[STNV]-x-[FYW]-S-P-x-G-[RKH]-x(2)-Q-[LIVM]-[DE]-Y-[SAD]-x(2)-

5 CONSENSUS: [SAG].

NAME: Proteasome B-type subunits signature.

CONSENSUS: [LIVMA]-[GSA]-[LIVMF]-x-[FYLVGAC]-x(2)-[GSACFY]-[LIVMSTAC](3)-[GAC]-

10 CONSENSUS: [GSTACV]-[DES]-x(15)-[RK]-x(12,13)-G-x(2)-[GSTA]-D.

NAME: Signal peptidases I serine active site.

CONSENSUS: [GS]-x-S-M-x-[PS]-[AT]-[LF].

15

NAME: Signal peptidases I lysine active site.

CONSENSUS: K-R-[LIVMSTA](2)-G-x-[PG]-G-[DE]-x-[LIVM]-x-[LIVMFY].

20 NAME: Signal peptidases I signature 3.

CONSENSUS: [LIVMFYW](2)-x(2)-G-D-[NH]-x(3)-[SND]-x(2)-[SG].

NAME: Signal peptidases II signature.

CONSENSUS: [GAF]-[GA]-[GAS]-[LIVM]-[GAS]-N-[LVMFG]-[LIVMFY]-D-R-[LIMFA].

25

NAME: Peptidase family U32 signature.

CONSENSUS: E-x-F-x(2)-G-[SA]-[LIVM]-C-x(4)-G-x-C-x-[LIVM]-S.

30 NAME: Amidases signature.

CONSENSUS: G-[GA]-S-S-[GS]-G-x-[GSA]-[GSAVY]-x-[LIVM]-[GSA]-x(6)-[GSA]-x-[GA]-x-D-

CONSENSUS: x-[GA]-x-S-[LIVM]-R-x-P-[GSAC].

35 NAME: Asparaginase / glutaminase active site signature 1.

CONSENSUS: [LIVM]-x(2)-T-G-G-T-[IV]-[AGS].

NAME: Asparaginase / glutaminase active site signature 2.

CONSENSUS: G-x-[LIVM]-x(2)-H-G-T-D-T-[LIVM].

40

NAME: Urease nickel ligands signature.

CONSENSUS: T-[AY]-[GA]-[GAT]-[LIVM]-D-x-H-[LIVM]-H-x(3)-P.

NAME: Urease active site.

45 CONSENSUS: [LIVM](2)-[CT]-H-[HN]-L-x(3)-[LIVM]-x(2)-D-[LIVM]-x-F-A.

NAME: ArgE / dapE / ACY1 / CPG2 / yscS family signature 1.

CONSENSUS: [LIV]-[GALMY]-[LIVMF]-x-[GSA]-H-x-D-[TV]-[STAV].

50

NAME: ArgE / dapE / ACY1 / CPG2 / yscS family signature 2.

CONSENSUS: [GSTAI]-[SANQ]-D-x-K-[GSACN]-x(2)-[LIVMA]-x(2)-[LIVMFY]-x(14,17)-[LIVM]-

CONSENSUS: x-[LIVMF]-[LIVMSTAG]-[LIVMFA]-x(2)-[DNG]-E-E-x-

55

[EGSTN].

NAME: Dihydroorotase signature 1.

CONSENSUS: D-[LIVMFYWSAP]-H-[LIVA]-H-[LIVF]-[RN]-x-[PGN].

- NAME: Dihydroorotase signature 2.  
 CONSENSUS: [GA]-[ST]-D-x-A-P-H-x(4)-K.
- 5 NAME: Beta-lactamase class-A active site.  
 CONSENSUS: [FY]-x-[LIVMFY]-x-S-[TV]-x-K-x(4)-[AGLM]-x(2)-[LC].
- 10 NAME: Beta-lactamase class-C active site.  
 CONSENSUS: F-E-[LIVM]-G-S-[LIVMG]-[SA]-K.
- NAME: Beta-lactamase class-D active site.  
 CONSENSUS: [PA]-x-S-[ST]-F-K-[LIV]-[PAL]-x-[STA]-[LI].
- 15 NAME: Beta-lactamases class B signature 1.  
 CONSENSUS: [LI]-x-[STN]-[HN]-x-H-[GSTA]-D-x(2)-G-[GP]-x(7,8)-[GS].
- 20 NAME: Beta-lactamases class B signature 2.  
 CONSENSUS: P-x(3)-[LIVM](2)-x-G-x-C-[LIVMF](2)-K.
- NAME: Arginase family signature 1.  
 CONSENSUS: [LIVMF]-G-G-x-H-x-[LIVMT]-[STAV]-x-[PAG]-x(3)-[GSTA].
- 25 NAME: Arginase family signature 2.  
 CONSENSUS: [LIVM](2)-x-[LIVMFY]-D-[AS]-H-x-D.
- 30 NAME: Arginase family signature 3.  
 CONSENSUS: [ST]-[LIVMFY]-D-[LIVM]-D-x(3)-[PAQ]-x(3)-P-[GSA]-x(7)-G.
- NAME: Adenosine and AMP deaminase signature.  
 CONSENSUS: [SA]-[LIVM]-[NGS]-[STA]-D-D-P.
- 35 NAME: Cytidine and deoxycytidylate deaminases zinc-binding region signature.  
 CONSENSUS: [CH]-[AGV]-E-x(2)-[LIVMFGAT]-[LIVM]-x(17,33)-P-C-x(2,8)-C-x(3)-[LIVM].
- 40 NAME: GTP cyclohydrolase I signature 1.  
 CONSENSUS: [EN]-[LIVM](2)-x(2)-[KRQN]-[DN]-[LIVM]-x(3)-[ST]-x-C-E-H-H.
- 45 NAME: GTP cyclohydrolase I signature 2.  
 CONSENSUS: [SA]-x-[RK]-x-Q-[LIVM]-Q-E-[RN]-[LI]-[TSN].
- NAME: Nitrilases / cyanide hydratase signature 1.  
 CONSENSUS: G-x(2)-[LIVMFY](2)-x-[IF]-x-E-x(2)-[LIVM]-x-G-Y-P.
- 50 NAME: Nitrilases / cyanide hydratase active site signature.  
 CONSENSUS: G-[GAQ]-x(2)-C-[WA]-E-[NH]-x(2)-[PST]-[LIVMFYS]-x-[KR].
- 55 NAME: Inorganic pyrophosphatase signature.  
 CONSENSUS: D-[SGDN]-D-[PE]-[LIVMF]-D-[LIVMGAC].
- NAME: Acylphosphatase signature 1.

- CONSENSUS: [LIV]-x-G-x-V-Q-G-V-x-[FM]-R.
- NAME: Acylphosphatase signature 2.  
 5 CONSENSUS: G-[FYW]-[AVC]-[KRQAM]-N-x(3)-G-x-V-x(5)-G.
- NAME: ATP synthase alpha and beta subunits signature.  
 CONSENSUS: P-[SAP]-[LIV]-[DNH]-x(3)-S-x-S.
- NAME: ATP synthase gamma subunit signature.  
 10 CONSENSUS: [IV]-T-x-E-x(2)-[DE]-x(3)-G-A-x-[SAKR].
- NAME: ATP synthase delta (OSCP) subunit signature.  
 CONSENSUS: [LIVM]-x-[LIVMFYT]-x(3)-[LIVMT]-[DENQK]-x(2)-  
 [LIVM]-x-[GSA]-G-[LIVMFYGA]-  
 15 CONSENSUS: x-[LIVM]-[KRHENQ]-x-[GSEN].
- NAME: ATP synthase a subunit signature.  
 CONSENSUS: [STAGN]-x-[STAG]-[LIVMF]-R-L-x-[SAGV]-N-[LIVMT].
- NAME: ATP synthase c subunit signature.  
 20 CONSENSUS: [GSTA]-R-[NQ]-P-x(10)-[LIVMFYW](2)-x(3)-[LIVMFYW]-  
 x-[DE].
- NAME: E1-E2 ATPases phosphorylation site.  
 25 CONSENSUS: D-K-T-G-T-[LI]-[TI].
- NAME: Sodium and potassium ATPases beta subunits signature  
 1. CONSENSUS: [FYW]-x(2)-[FYW]-x-[FYW]-[DN]-x(6)-[LIVM]-G-R-T-  
 30 x(3)-W.
- NAME: Sodium and potassium ATPases beta subunits signature  
 2. CONSENSUS: [RK]-x(2)-C-[RKQWI]-x(5)-L-x(2)-C-[SA]-G.
- NAME: GDA1/CD39 family of nucleoside phosphatases signature.  
 35 CONSENSUS: [LIVM]-x-G-x(2)-E-G-x-[FY]-x-[FW]-[LIVA]-[TAG]-x-  
 N-[HY].
- NAME: Iodothyronine deiodinases active site.  
 40 CONSENSUS: R-P-L-V-x-N-F-G-S-[CA]-T-C-P-x-F.
- NAME: Cutinase, serine active site.  
 45 CONSENSUS: P-x-[STA]-x-[LIV]-[IVT]-x-[GS]-G-Y-S-[QL]-G.
- NAME: Cutinase, aspartate and histidine active sites.  
 CONSENSUS: C-x(3)-D-x-[IV]-C-x-G-[GST]-x(2)-[LIVM]-x(2,3)-H.
- NAME: DDC / GAD / HDC / TyrDC pyridoxal-phosphate attachment  
 50 site.  
 CONSENSUS: S-[LIVMFYW]-x(5)-K-[LIVMFYWG](2)-x(3)-[LIVMFYW]-x-  
 [CA]-x(2)-[LIVMFYWQ]-  
 CONSENSUS: x(2)-[RK].
- NAME: Orn/Lys/Arg decarboxylases family 1 pyridoxal-P  
 55 attachment site.  
 CONSENSUS: [STAV]-x-S-x-H-K-x(2)-[GSTAN](2)-x-[STA]-Q-  
 [STA](2).

- NAME: Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment site.  
 5 CONSENSUS: [FY]-[PA]-x-K-[SACV]-[NHCLFW]-x(4)-[LIVMF]-[LIVMTA]-x(2)-[LIVMA]-x(3)-  
 CONSENSUS: [GTE].
- NAME: Orn/DAP/Arg decarboxylases family 2 signature 2.  
 10 CONSENSUS: [GS]-x(2,6)-[LIVMSCP]-x(2)-[LIVMF]-[DNS]-[LIVMCA]-G-G-G-[LIVMFY]-  
 CONSENSUS: [GSTPCEQ].
- NAME: Orotidine 5'-phosphate decarboxylase active site.  
 15 CONSENSUS: [LIVMFTA]-[LIVMF]-x-D-x-K-x(2)-D-I-[GP]-x-T-[LIVMTA].
- NAME: Phosphoenolpyruvate carboxylase active site 1.  
 CONSENSUS: [VT]-x-T-A-H-P-T-[EQ]-x(2)-R-[KRH].
- 20 NAME: Phosphoenolpyruvate carboxylase active site 2.  
 CONSENSUS: [IV]-M-[LIVM]-G-Y-S-D-S-x-K-D-[STAG]-G.
- NAME: Phosphoenolpyruvate carboxykinase (GTP) signature.  
 25 CONSENSUS: F-P-S-A-C-G-K-T-N.
- NAME: Phosphoenolpyruvate carboxykinase (ATP) signature.  
 CONSENSUS: L-I-G-D-D-E-H-x-W-x-[DE]-x-G-[IV]-x-N.
- NAME: Uroporphyrinogen decarboxylase signature 1.  
 30 CONSENSUS: P-x-W-x-M-R-Q-A-G-R.
- NAME: Uroporphyrinogen decarboxylase signature 2.  
 35 CONSENSUS: G-F-[STAGCV]-[STAGC]-x-P-[FYW]-T-[LV]-x(2)-Y-x(2)-[AE]-[GK].
- NAME: Indole-3-glycerol phosphate synthase signature.  
 CONSENSUS: [LIVMFY]-[LIVMC]-x-E-[LIVMFYC]-K-[KRSP]-[STAK]-S-P-[ST]-x(3)-[LIVMFYST].
- 40 NAME: Ribulose biphosphate carboxylase large chain active site.  
 CONSENSUS: G-x-[DN]-F-x-K-x-D-E.
- NAME: Fructose-bisphosphate aldolase class-I active site.  
 45 CONSENSUS: [LIVM]-x-[LIVMFYW]-E-G-x-[LS]-L-K-P-[SN].
- NAME: Fructose-bisphosphate aldolase class-II signature 1.  
 50 CONSENSUS: [FYVM]-x(1,3)-[LIVMH]-[APN]-[LIVM]-x(1,2)-[LIVM]-H-x-D-H-[GACH].
- NAME: Fructose-bisphosphate aldolase class-II signature 2.  
 CONSENSUS: [LIVM]-E-x-E-[LIVM]-G-x(2)-[GM]-[GSTA]-x-E.
- NAME: Malate synthase signature.  
 55 CONSENSUS: [KR]-[DENQ]-H-x(2)-G-L-N-x-G-x-W-D-Y-[LIVM]-F.
- NAME: Hydroxymethylglutaryl-coenzyme A lyase active site.  
 CONSENSUS: S-V-A-G-L-G-G-C-P-Y.

- NAME: Hydroxymethylglutaryl-coenzyme A synthase active site.  
 CONSENSUS: N-x-[DN]-[IV]-E-G-[IV]-D-x(2)-N-A-C-[FY]-x-G.
- 5 NAME: Citrate synthase signature.  
 CONSENSUS: G-[FYA]-[GA]-H-x-[IV]-x(1,2)-[RKT]-x(2)-D-[PS]-R.
- NAME: Alpha-isopropylmalate and homocitrate synthases signature 1.  
 10 CONSENSUS: L-R-[DE]-G-x-Q-x(10)-K.
- NAME: Alpha-isopropylmalate and homocitrate synthases signature 2.  
 CONSENSUS: [LIVMFV]-x(2)-H-x-H-[DN]-D-x-G-x-[GAS]-x-[GASLI].
- 15 NAME: KDPG and KHG aldolases active site.  
 CONSENSUS: G-[LIVM]-x(3)-E-[LIV]-T-[LF]-R.
- NAME: KDPG and KHG aldolases Schiff-base forming residue.  
 20 CONSENSUS: G-x(3)-[LIVMF]-K-[LF]-F-P-[SA]-x(3)-G.
- NAME: Isocitrate lyase signature.  
 CONSENSUS: K-[KR]-C-G-H-[LMQ].
- 25 NAME: Beta-eliminating lyases pyridoxal-phosphate attachment site.  
 CONSENSUS: Y-x-D-x(3)-M-S-[GA]-K-K-D-x-[LIVM](2)-x-[LIVM]-G-G.
- 30 NAME: DNA photolyases class 1 signature 1.  
 CONSENSUS: T-G-x-P-[LIVM](2)-D-A-x-M-[RA]-x-[LIVM].
- NAME: DNA photolyases class 1 signature 2.  
 CONSENSUS: [DN]-R-x-R-[LIVM](2)-x-[STA](2)-F-[LIVMFA]-x-K-x-L-x(2,3)-W-[KRQ].
- 35 NAME: DNA photolyases class 2 signature 1.  
 CONSENSUS: F-x-E-E-x-[LIVM](2)-R-R-E-L-x(2)-N-F.
- 40 NAME: DNA photolyases class 2 signature 2.  
 CONSENSUS: G-x-H-D-x(2)-W-x-E-R-x-[LIVM]-F-G-K-[LIVM]-R-[FY]-M-N.
- NAME: Eukaryotic-type carbonic anhydrases signature.  
 45 CONSENSUS: S-E-H-x-[LIVM]-x(4)-[FYH]-x(2)-E-[LIVM]-H-[LIVMFA](2).
- NAME: Prokaryotic-type carbonic anhydrases signature 1.  
 CONSENSUS: C-[SA]-D-S-R-[LIVM]-x-[AP].
- 50 NAME: Prokaryotic-type carbonic anhydrases signature 2.  
 CONSENSUS: [EQ]-Y-A-[LIVM]-x(2)-[LIVM]-x(4)-[LIVMF](3)-x-G-H-x(2)-C-G.
- 55 NAME: Fumarate lyases signature.  
 CONSENSUS: G-S-x(2)-M-x(2)-K-x-N.
- NAME: Aconitase family signature 1.

CONSENSUS: [LIVM]-x(2)-[GSACIVM]-x-[LIV]-[GTIV]-[STP]-C-  
x(0,1)-T-N-[GSTANI]-x(4)-  
CONSENSUS: [LIVMA].

5 NAME: Aconitase family signature 2.  
CONSENSUS: G-x(2)-[LIVWPQ]-x(3)-[GAC]-C-[GSTAM]-[LIMPTA]-C-  
[LIMV]-[GA].

10 NAME: Dihydroxy-acid and L-phosphogluconate dehydratases  
signature 1.  
CONSENSUS: C-D-K-x(2)-P-[GA]-x(3)-[GA].

NAME: Dihydroxy-acid and L-phosphogluconate dehydratases  
signature 2.  
15 CONSENSUS: [SA]-L-[LIVM]-T-D-[GA]-R-[LIVMF]-S-[GA]-[GAV]-  
[ST].

NAME: Dehydroquinase class I active site.  
CONSENSUS: D-[LIVM]-[DE]-[LIVN]-x(18,20)-[LIVM](2)-x-[SC]-  
20 [NHY]-H-[DN].

NAME: Dehydroquinase class II signature.  
CONSENSUS: [LIVM]-[NQ]-G-P-N-[LV]-x(2)-L-G-x-R-[QED]-P-x(2)-  
[FY]-G.  
25

NAME: Enolase signature.  
CONSENSUS: [LIV](3)-K-x-N-Q-I-G-[ST]-[LIV]-[ST]-[DE]-[STA].

30 NAME: Serine/threonine dehydratases pyridoxal-phosphate  
attachment site.  
CONSENSUS: [DESH]-x(4,5)-[STVG]-x-[AS]-[FYI]-K-[DLIFSA]-  
[RVMF]-[GA]-[LIVMGA].

NAME: Enoyl-CoA hydratase/isomerase signature.  
35 CONSENSUS: [LIVM]-[STA]-x-[LIVM]-[DENQRHSTA]-G-x(3)-[AG](3)-  
x(4)-[LIVMST]-x-[CSTA]-  
CONSENSUS: [DQHP]-[LIVMFY].

NAME: Imidazoleglycerol-phosphate dehydratase signature 1.  
40 CONSENSUS: [LIVMY]-[DE]-x-H-H-x(2)-E-x(2)-[GCA]-[LIVM]-  
[STAC]-[LIVM].

NAME: Imidazoleglycerol-phosphate dehydratase signature 2.  
CONSENSUS: G-x-[DN]-x-H-H-x(2)-E-[STAGC]-x-[FY]-K.  
45

NAME: Tryptophan synthase alpha chain signature.  
CONSENSUS: [LIVM]-E-[LIVM]-G-x(2)-[FYC]-[ST]-[DE]-[PA]-  
[LIVMY]-[AGLI]-[DE]-G.

50 NAME: Tryptophan synthase beta chain pyridoxal-phosphate  
attachment site.  
CONSENSUS: [LIVM]-x-H-x-G-[STA]-H-K-x-N.

NAME: Delta-aminolevulinic acid dehydratase active site.  
55 CONSENSUS: G-x-D-x-[LIVM](2)-[IV]-K-P-[GSA]-x(2)-Y.

NAME: Urocanase active site.  
CONSENSUS: F-Q-G-L-P-x-R-I-C-W.

- NAME: Prephenate dehydratase signature 1.  
 5 CONSENSUS: [FY]-x-[LIVM]-x(2)-[LIVM]-x(5)-[DN]-x(5)-T-R-F-[LIVM]-x-[LIVM].
- NAME: Prephenate dehydratase signature 2.  
 CONSENSUS: [LIVM]-[ST]-[KR]-[LIVM]-E-[ST]-R-P.
- NAME: Dihydrodipicolinate synthetase signature 1.  
 10 CONSENSUS: [GSA]-[LIVM]-[LIVMFY]-x(2)-G-[ST]-[TG]-G-E-[GASNF]-x(6)-[EQ].
- NAME: Dihydrodipicolinate synthetase signature 2.  
 15 CONSENSUS: Y-[DNS]-[LIVMF]-P-x(2)-[ST]-x(3)-[LIVM]-x(13,14)-[LIVM]-x-[SGA]-[LIVMF]-  
 CONSENSUS: K-[DEQAF]-[STAC].
- NAME: RsuA family of pseudouridine synthase signature.  
 20 CONSENSUS: G-R-L-D-x(2)-[ST]-x-G-[LIVMF](4)-[ST]-[DNT].
- NAME: Cysteine synthase/cystathionine beta-synthase P-phosphate attachment site.  
 25 CONSENSUS: K-x-E-x(3)-[PA]-[STAGC]-x-S-[IVAP]-K-x-R-x-[STAG]-x(2)-[LIVM].
- NAME: Phenylalanine and histidine ammonia-lyases signature.  
 CONSENSUS: G-[STG]-[LIVM]-[STG]-[AC]-S-G-[DH]-L-x-P-L-[SA]-x(2)-[SA].
- NAME: Porphobilinogen deaminase cofactor-binding site.  
 30 CONSENSUS: E-R-x-[LIVMFA]-x(3)-[LIVMF]-x-G-[GSA]-C-x-[IVT]-P-[LIVMF]-[GSA].
- NAME: Cys/Met metabolism enzymes pyridoxal-phosphate attachment site.  
 35 CONSENSUS: [DQ]-[LIVMF]-x(3)-[STAGC]-[STAGCI]-T-K-[FYWQ]-[LIVMF]-x-G-[HQ]-[SGNH].
- NAME: Glyoxalase I signature 1.  
 40 CONSENSUS: [HQ]-[IVT]-x-[LIVFY]-x-[IV]-x(5)-[STA]-x(2)-F-[YM]-x(2,3)-[LMF]-G-[LMF].
- NAME: Glyoxalase I signature 2.  
 45 CONSENSUS: G-[ENTKQ]-x(0,5)-[GA]-[LVFY]-[GH]-H-[IVF]-[CGA]-x-[STAGL]-x(2)-[DNC].
- NAME: Cytochrome c and c1 heme lyases signature 1.  
 CONSENSUS: H-N-x(2)-N-E-x(2)-W-[NQKR]-x(4)-W-E.
- NAME: Cytochrome c and c1 heme lyases signature 2.  
 50 CONSENSUS: P-F-D-R-H-D-W.
- NAME: Adenylate cyclases class-I signature 1.  
 55 CONSENSUS: E-Y-F-G-[SA](2)-L-W-x-L-Y-K.
- NAME: Adenylate cyclases class-I signature 2.  
 CONSENSUS: Y-R-N-x-W-[NS]-E-[LIVM]-R-T-L-H-F-x-G.



- NAME: Guanylate cyclases signature.  
 CONSENSUS: G-V-[[LIVM]]-x(0,1)-G-x(5)-[[FY]]-x-[[LIVM]]-[[FYW]]-[[GS]]-  
 [[DNTHKW]]-[[DNT]]-[[IV]]-  
 CONSENSUS: [[DNTA]]-x(5)-[[DE]].
- 5 NAME: Chorismate synthase signature 1.  
 CONSENSUS: G-E-S-H-[[GC]]-x(2)-[[LIVM]]-[[GTV]]-x-[[LIVM]](2)-[[DE]]-G-  
 x-[[PV]].
- 10 NAME: Chorismate synthase signature 2.  
 CONSENSUS: [[GE]]-R-[[SA]](2)-[[SAG]]-R-[[EV]]-[[ST]]-x(2)-[[RH]]-V-x(2)-  
 G.
- 15 NAME: Chorismate synthase signature 3.  
 CONSENSUS: R-[[SH]]-D-[[PSV]]-[[CSAV]]-x(4)-[[GAI]]-x-[[IVGSP]]-[[LIVM]]-  
 x-E-[[STAH]]-[[LIVM]].
- 20 NAME: b-pyruvoyl tetrahydropterin synthase signature 1.  
 CONSENSUS: C-N-N-x(2)-G-H-G-H-N-Y.
- NAME: b-pyruvoyl tetrahydropterin synthase signature 2.  
 CONSENSUS: D-H-K-N-L-D-x-D.
- 25 NAME: Ferrochelatase signature.  
 CONSENSUS: [[LIVMF]](2)-x-S-x-H-[[GS]]-[[LIVM]]-P-x(4,5)-[[DENQKR]]-  
 x-G-D-x-Y.
- 30 NAME: Alanine racemase pyridoxal-phosphate attachment site.  
 CONSENSUS: V-x-K-A-[[DN]]-[[GA]]-Y-G-H-G.
- NAME: Aspartate and glutamate racemases signature 1.  
 CONSENSUS: [[IVA]]-[[LIVM]]-x-C-x(0,1)-N-[[ST]]-[[MSA]]-[[STH]]-  
 [[LIVFYSTANK]].
- 35 NAME: Aspartate and glutamate racemases signature 2.  
 CONSENSUS: [[LIVM]](2)-x-[[AG]]-C-T-[[DEH]]-[[LIVMFY]]-[[PNGRS]]-x-  
 [[LIVM]].
- 40 NAME: Mandelate racemase / muconate lactonizing enzyme  
 family signature 1.  
 CONSENSUS: A-x-[[SAG]](2)-[[LIVM]]-[[DE]]-x-A-x(2)-D-x(2)-[[GA]]-  
 [[KR]].
- 45 NAME: Mandelate racemase / muconate lactonizing enzyme  
 family signature 2.  
 CONSENSUS: G-x(7)-D-x(9)-A-x(14)-[[LIVM]]-E-[[DENQ]]-P-x(4)-  
 [[DENQ]].
- 50 NAME: Ribulose-phosphate 3-epimerase family signature 1.  
 CONSENSUS: [[LIVMF]]-H-[[LIVMFY]]-D-[[LIVM]]-x-D-x(1,2)-[[FY]]-  
 [[LIVM]]-x-N-x-[[STAV]].
- 55 NAME: Ribulose-phosphate 3-epimerase family signature 2.  
 CONSENSUS: [[LIVMA]]-x-[[LIVM]]-M-[[ST]]-[[VS]]-x-P-x(3)-G-Q-x-F-  
 x(6)-[[NK]]-[[LIVMC]].
- NAME: Aldose 1-epimerase putative active site.  
 CONSENSUS: [[NS]]-x-T-N-H-x-Y-[[FW]]-N-[[LI]].

- NAME: Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.  
 5 CONSENSUS: [FY]-x(2)-[STCNLV]-x-F-H-[RH]-[LIVMN]-[LIVM]-x(2)-F-[LIVM]-x-Q-[AG]-G.
- NAME: Cyclophilin-type peptidyl-prolyl cis-trans isomerase profile.
- 10 NAME: FKBP-type peptidyl-prolyl cis-trans isomerase signature 1.  
 CONSENSUS: [LIVMC]-x-[YF]-x-[GVL]-x(1,2)-[LFT]-x(2)-G-x(3)-[DE]-[STAEQK]-[STAN].
- 15 NAME: FKBP-type peptidyl-prolyl cis-trans isomerase signature 2.  
 CONSENSUS: [LIVMFY]-x(2)-[GA]-x(3,4)-[LIVMF]-x(2)-[LIVMFHK]-x(2)-G-x(4)-[LIVMF]-  
 20 CONSENSUS: x(3)-[PSGAQ]-x(2)-[AG]-[FY]-G.
- NAME: FKBP-type peptidyl-prolyl cis-trans isomerase domain profile.
- 25 NAME: PpiC-type peptidyl-prolyl cis-trans isomerase signature.  
 CONSENSUS: F-[GSADEI]-x-[LVAQ]-A-x(3)-[ST]-x(3,4)-[STQ]-x(3,5)-[GER]-G-x-[LIVM]-  
 CONSENSUS: [GS].
- 30 NAME: Triosephosphate isomerase active site.  
 CONSENSUS: [AV]-Y-E-P-[LIVM]-W-[SA]-I-G-T-[GK].
- NAME: Xylose isomerase signature 1.  
 35 CONSENSUS: [LI]-E-P-K-P-x(2)-P.
- NAME: Xylose isomerase signature 2.  
 CONSENSUS: [FL]-H-D-x-D-[LIV]-x-[PD]-x-[GDE].
- NAME: Phosphomannose isomerase type I signature 1.  
 40 CONSENSUS: Y-x-D-x-N-H-K-P-E.
- NAME: Phosphomannose isomerase type I signature 2.  
 CONSENSUS: H-A-Y-[LIVM]-x-G-x(2)-[LIVM]-E-x-M-A-x-S-D-N-x-[LIVM]-R-A-G-x-T-P-K.
- 45 NAME: Phosphoglucose isomerase signature 1.  
 CONSENSUS: [DENS]-x-[LIVM]-G-G-R-[FY]-S-[LIVMT]-x-[STA]-[PSAC]-[LIVMA]-G.
- 50 NAME: Phosphoglucose isomerase signature 2.  
 CONSENSUS: [GS]-x-[LIVM]-[LIVMFYW]-x(4)-[FY]-[DN]-Q-x-G-V-E-x(2)-K.
- NAME: Glucosamine/galactosamine-6-phosphate isomerases signature.  
 55 CONSENSUS: [LIVM]-x(3)-G-x-[LIT]-x-[LIV]-x-[LIVM]-x-G-[LIVM]-G-x-[DEN]-G-H.

- NAME: Phosphoglycerate mutase family phosphohistidine  
signature.  
CONSENSUS: [LIVM]-x-R-H-G-[EQ]-x(3)-N.
- 5 NAME: Phosphoglucumutase and phosphomannomutase  
phosphoserine signature.  
CONSENSUS: [GSA]-[LIVM]-x-[LIVM]-[ST]-[PGA]-S-H-x-P-x(4)-  
[GNHE].
- 10 NAME: Methylmalonyl-CoA mutase signature.  
CONSENSUS: R-I-A-R-N-[TQ]-x(2)-[LIVMFY](2)-x-[EQ]-E-x(4)-  
[KRN]-x(2)-D-P-x-[GSA]-  
CONSENSUS: G-S.
- 15 NAME: Terpene synthases signature.  
CONSENSUS: [DE]-G-S-W-x-G-x-W-[GA]-[LIVM]-x-[FY]-x-Y-[GA].
- NAME: Eukaryotic DNA topoisomerase I active site.  
CONSENSUS: [DEN]-x(6)-[GS]-[IT]-S-K-x(2)-Y-[LIVM]-x(3)-  
20 [LIVM].
- NAME: Prokaryotic DNA topoisomerase I active site.  
CONSENSUS: [EQ]-x-L-Y-[DEQT]-x(3,12)-[LI]-[ST]-Y-x-R-[ST]-  
[DEQS].
- 25 NAME: DNA topoisomerase II signature.  
CONSENSUS: [LIVMA]-x-E-G-[DN]-S-A-x-[STAG].
- NAME: Aminoacyl-transfer RNA synthetases class-I signature.  
30 CONSENSUS: P-x(D,2)-[GSTAN]-[DENQGAPK]-x-[LIVMFP]-[HT]-  
[LIVMYAC]-G-[HNTG]-  
CONSENSUS: [LIVMFYSTAGPC].
- NAME: Aminoacyl-transfer RNA synthetases class-II signature  
1.  
35 CONSENSUS: [FYH]-R-x-[DE]-x(4,12)-[RH]-x(3)-F-x(3)-[DE].
- NAME: Aminoacyl-transfer RNA synthetases class-II signature  
2.  
40 CONSENSUS: [GSTALVF]-[DENQHRKP]-[GSTA]-[LIVMF]-[DE]-R-  
[LIVMF]-x-[LIVMSTAG]-[LIVMFY].
- NAME: WHEP-TRS domain signature.  
CONSENSUS: [QY]-G-[DNEA]-x-[LIV]-[KR]-x(2)-K-x(2)-[KRNQ]-  
45 [AS]-x(4)-[LIV]-[DENK]-  
CONSENSUS: x(2)-[IV]-x(2)-L-x(3)-K.
- NAME: ATP-citrate lyase / succinyl-CoA ligases family  
signature 1.  
50 CONSENSUS: S-[KR]-S-G-[GT]-[LIVM]-[GST]-x-[EQ]-x(8,10)-G-  
x(4)-[LIVM]-[GA]-[LIVM]-G-  
CONSENSUS: G-D.
- NAME: ATP-citrate lyase / succinyl-CoA ligases family active  
site.  
55 CONSENSUS: G-x(2)-A-x(4,7)-[RQT]-[LIVMF]-G-H-[AS]-[GH].

- NAME: ATP-citrate lyase / succinyl-CoA ligases family  
signature 3.  
CONSENSUS: G-x-[IV]-x(2)-[LIVMF]-x-[NA]-G-[GA]-G-[LA]-[STAV]-  
x(4)-D-x-[LIVM]-x(3)-  
5 CONSENSUS: G-[GRE].
- NAME: Glutamine synthetase signature 1.  
CONSENSUS: [FYWL]-D-G-S-S-x(6,8)-[DENQSTAK]-[SA]-[DE]-x(2)-  
[LIVMFY].  
10
- NAME: Glutamine synthetase putative ATP-binding region  
signature.  
CONSENSUS: K-P-[LIVMFYA]-x(3,5)-[NPAT]-G-[GSTAN]-G-x-H-x(3)-  
S.  
15
- NAME: Glutamine synthetase class-I adenylation site.  
CONSENSUS: K-[LIVM]-x(5)-[LIVMA]-D-[RK]-[DN]-[LI]-Y.
- NAME: D-alanine--D-alanine ligase signature 1.  
20 CONSENSUS: H-G-x(2)-G-E-D-G-x-[LIVMA]-[QSA]-[GSA].
- NAME: D-alanine--D-alanine ligase signature 2.  
CONSENSUS: [LIV]-x(3)-[GA]-x-[GSAIV]-R-[LIVCA]-D-[LIVMF](2)-  
x(7,9)-[LI]-x-E-  
25 CONSENSUS: [LIVA]-N-[STP]-x-P-[GA].
- NAME: SAICAR synthetase signature 1.  
CONSENSUS: [LIVMF](2)-P-[LIVM]-E-x-[LIVM]-[LIVMCA]-R-x(3)-  
[TA]-G-S.  
30
- NAME: SAICAR synthetase signature 2.  
CONSENSUS: [LIVM]-[LIVMA]-D-x-K-[LIVMFY]-E-F-G.
- NAME: Folylpolyglutamate synthase signature 1.  
35 CONSENSUS: [LIVMFY]-x-[LIVM]-[STAG]-G-T-[NK]-G-K-x-[ST]-x(?)~  
[LIVM](2)-x(3)-[GSK].
- NAME: Folylpolyglutamate synthase signature 2.  
CONSENSUS: [LIVMFY](2)-E-x-G-[LIVM]-[GA]-G-x(2)-D-x-[GST]-x-  
40 [LIVM](2).
- NAME: Ubiquitin-activating enzyme signature 1.  
CONSENSUS: K-A-C-S-G-K-F-x-P.
- 45 NAME: Ubiquitin-activating enzyme active site.  
CONSENSUS: P-[LIVM]-C-T-[LIVM]-[KRH]-x-[FT]-P.
- NAME: Ubiquitin-conjugating enzymes active site.  
CONSENSUS: [FYWLSP]-H-[PC]-[NH]-[LIV]-x(3,4)-G-x-[LIV]-C-  
50 [LIV]-x-[LIV].
- NAME: Formate--tetrahydrofolate ligase signature 1.  
CONSENSUS: G-[LIVM]-K-G-G-A-A-G-G-G-Y.
- 55 NAME: Formate--tetrahydrofolate ligase signature 2.  
CONSENSUS: V-A-T-[IV]-R-A-L-K-x-[HN]-G-G.
- NAME: Adenylosuccinate synthetase GTP-binding site.

- CONSENSUS: Q-W-G-D-E-G-K-G.
- NAME: Adenylosuccinate synthetase active site.  
 5 CONSENSUS: G-I-[GR]-P-x-Y-x(2)-K-x(2)-R.
- NAME: Argininosuccinate synthase signature 1.  
 CONSENSUS: A-[FY]-S-G-G-L-D-T-S.
- NAME: Argininosuccinate synthase signature 2.  
 10 CONSENSUS: G-x-T-x-K-G-N-D-x(2)-R-F.
- NAME: Phosphoribosylglycinamide synthetase signature.  
 CONSENSUS: R-F-G-D-P-E-x-[QM].
- NAME: Carbamoyl-phosphate synthase subdomain signature 1.  
 15 CONSENSUS: [FYV]-[PS]-[LIVMC]-[LIVMA]-[LIVM]-[KR]-[PSA]-[STA]-x(3)-[SG]-G-x-[AG].
- NAME: Carbamoyl-phosphate synthase subdomain signature 2.  
 20 CONSENSUS: [LIVMF]-[LIMN]-E-[LIVMCA]-N-[PATLIVM]-[KR]-[LIVMSTAC].
- NAME: ATP-dependent DNA ligase AMP-binding site.  
 CONSENSUS: [EDQH]-x-K-x-[DN]-G-x-R-[GACIVM].
- NAME: ATP-dependent DNA ligase signature 2.  
 25 CONSENSUS: E-G-[LIVMA]-[LIVM](2)-[KR]-x(5,8)-[YW]-[QNEK]-x(2,6)-[KRH]-x(3,5)-K-  
 CONSENSUS: [LIVMFY]-K.
- NAME: NAD-dependent DNA ligase signature 1.  
 30 CONSENSUS: K-[LIVM]-D-G-[LIVM]-[SA]-x(4)-Y-x(2)-G-x-L-x(4)-[ST]-R-G-[DN]-G-x(2)-G-  
 CONSENSUS: [DE]-[DENL].
- NAME: NAD-dependent DNA ligase signature 2.  
 35 CONSENSUS: [IV]-G-[KR]-[ST]-G-x-[LIVM]-[STNK]-x-[VT]-x(2)-L-x-[PS]-V.
- NAME: RNA 3'-terminal phosphate cyclase signature.  
 40 CONSENSUS: [RH]-G-x(2)-P-x-G(3)-x-[LIV].
- NAME: Lipoate-protein ligase B signature.  
 45 CONSENSUS: R-G-G-x(2)-T-[FYW]-H-x(2)-[GH]-Q-x-[LIV]-x-Y.
- NAME: Isopenicillin N synthetase signature 1.  
 CONSENSUS: [RK]-x-[STA]-x(2)-S-x-C-Y-[SL].
- NAME: Isopenicillin N synthetase signature 2.  
 50 CONSENSUS: [LIVM](2)-x-C-G-[STA]-x(2)-[STAG]-x(2)-T-x-[DNG].
- NAME: Site-specific recombinases active site.  
 CONSENSUS: Y-[LIVAC]-R-[VA]-S-[ST]-x(2)-Q.
- NAME: Site-specific recombinases signature 2.  
 55 CONSENSUS: G-[DE]-x(2)-[LIVM]-x(3)-[LIVM]-[DT]-R-[LIVM]-[GSA].

- NAME: Transposases, Mutator family, signature.  
 CONSENSUS: D-x(3)-G-[LIVMF]-x(6)-[STAV]-[LIVMFYW]-[PT]-x-  
 [STAV]-x(2)-[QR]-x-C-x(2)-  
 CONSENSUS: H.
- 5 NAME: Transposases, IS30 family, signature.  
 CONSENSUS: R-G-x(2)-E-N-x-N-G-[LIVM](2)-R-[QE]-[LIVMFY](2)-P-  
 K.
- 10 NAME: Autoinducers synthetases family signature.  
 CONSENSUS: [LMFY]-R-x(3)-F-x(2)-[KR]-x(2)-W-x-[LIVM]-x(6,9)-  
 E-x-D-x-[FY]-D.
- 15 NAME: Thiamine pyrophosphate enzymes signature.  
 CONSENSUS: [LIVMF]-[GSA]-x(5)-P-x(4)-[LIVMFYW]-x-[LIVMF]-x-G-  
 D-[GSA]-[GSAC].
- NAME: Biotin-requiring enzymes attachment site.  
 CONSENSUS: [GN]-[DEQTR]-x-[LIVMFY]-x(2)-[LIVM]-x-[AIV]-M-K-  
 20 [LMAT]-x(3)-[LIVM]-x-  
 CONSENSUS: [SAV].
- NAME: 2-oxo acid dehydrogenases acyltransferase component  
 lipoyl binding site.  
 25 CONSENSUS: [GN]-x(2)-[LIVF]-x(5)-[LIVFC]-x(2)-[LIVFA]-x(3)-K-  
 [STAIV]-[STAVQDN]-  
 CONSENSUS: x(2)-[LIVMFS]-x(5)-[GCN]-x-[LIVMFY].
- NAME: Putative AMP-binding domain signature.  
 30 CONSENSUS: [LIVMFY]-x(2)-[STG]-[STAG]-G-[ST]-[STEI]-[SG]-x-  
 [PASLIVM]-[KR].
- NAME: Molybdenum cofactor biosynthesis proteins signature 1.  
 CONSENSUS: [LIVM](3)-[LIT](2)-G-G-T-G-x(4)-D.
- 35 NAME: Molybdenum cofactor biosynthesis proteins signature 2.  
 CONSENSUS: S-x-[GS]-x(2)-D-x(5)-[LIVW]-x(10,12)-[LIV]-x(2)-  
 [KR]-P-G-[KRL]-P-x(2)-  
 CONSENSUS: [LIVMF]-[GA].
- 40 NAME: moaA / nifB / pqqE family signature.  
 CONSENSUS: [LIV]-x(3)-C-[NP]-[LIVMF]-[QRS]-C-x-[FYM]-C.
- NAME: Radical activating enzymes signature.  
 45 CONSENSUS: [GV]-x-G-x-[KR]-x(3)-F-x(2)-G-x(0,1)-C-x(3)-C-  
 x(2)-C-x-[NL].
- NAME: Tpx family signature.  
 CONSENSUS: S-x-D-L-P-F-A-x(2)-[KR]-[FW]-C.
- 50 NAME: Cytochrome c family heme-binding site signature.  
 CONSENSUS: C-{CPWHF}-{CPWR}-C-H-{CFYW}.
- NAME: Cytochrome b5 family, heme-binding domain signature.  
 55 CONSENSUS: [FY]-[LIVMK]-x(2)-H-P-[GA]-G.
- NAME: Cytochrome b/bb heme-ligand signature.  
 CONSENSUS: [DENQ]-x(3)-G-[FYWMQ]-x-[LIVMF]-R-x(2)-H.

- NAME: Cytochrome b/b<sub>6</sub>  $\alpha_0$  site signature.  
 CONSENSUS: P-[DE]-W-[FY]-[LFY](2).
- 5 NAME: Cytochrome b<sub>559</sub> subunits heme-binding site signature.  
 CONSENSUS: [LIV]-x-[ST]-[LIVF]-R-[FYW]-x(2)-[IV]-H-[STGA]-  
 [LIV]-[STGA]-[IV]-P.
- 10 NAME: Nickel-dependent hydrogenases b-type cytochrome  
 subunit signature 1.  
 CONSENSUS: R-[LIVMFYW]-x-H-W-[LIVM]-x(2)-[LIVMF]-[STAC]-  
 [LIVM]-x(2)-L-x-[LIVM]-T-G.
- 15 NAME: Nickel-dependent hydrogenases b-type cytochrome  
 subunit signature 2.  
 CONSENSUS: [RH]-[STA]-[LIVMFYW]-H-[RH]-[LIVM]-x(2)-W-x-  
 [LIVMF]-x(2)-F-x(3)-H.
- 20 NAME: Succinate dehydrogenase cytochrome b subunit signature  
 1.  
 CONSENSUS: R-P-[LIVMT]-x(3)-[LIVM]-x(6)-[LIVMWPk]-x(4)-S-  
 x(2)-H-R-x-[ST].
- 25 NAME: Succinate dehydrogenase cytochrome b subunit signature  
 2.  
 CONSENSUS: H-x(3)-[GA]-[LIVMT]-R-[HF]-[LIVMF]-x-[FYWM]-D-x-  
 [GVA].
- 30 NAME: Thioredoxin family active site.  
 CONSENSUS: [LIVMF]-[LIVMSTA]-x-[LIVMFYC]-[FYWSTHE]-x(2)-  
 [FYWGTN]-C-[GATPLVE]-  
 CONSENSUS: [PHYWSTA]-C-x(6)-[LIVMFYWT].
- 35 NAME: Glutaredoxin active site.  
 CONSENSUS: [LIVD]-[FYSA]-x(4)-C-[PV]-[FYW]-C-x(2)-[TAV]-  
 x(2,3)-[LIV].
- 40 NAME: Type-1 copper (blue) proteins signature.  
 CONSENSUS: [GA]-x(0,2)-[YSA]-x(0,1)-[VFY]-x-C-x(1,2)-[PG]-  
 x(0,1)-H-x(2,4)-[MQ].
- 45 NAME: 2Fe-2S ferredoxins, iron-sulfur binding region  
 signature.  
 CONSENSUS: C-[C]-[C]-[GA]-[C]-C-[GAST]-[CPDEKRHFYW]-C.
- NAME: Adrenodoxin family, iron-sulfur binding region  
 signature.  
 CONSENSUS: C-x(2)-[STAQ]-x-[STAMV]-C-[STA]-T-C-[HR].
- 50 NAME: 4Fe-4S ferredoxins, iron-sulfur binding region  
 signature.  
 CONSENSUS: C-x(2)-C-x(2)-C-x(3)-C-[PEG].
- 55 NAME: High potential iron-sulfur proteins signature.  
 CONSENSUS: C-x(6,9)-[LIVM]-x(3)-G-[YW]-C-x(2)-[FYW].
- NAME: Rieske iron-sulfur protein signature 1.  
 CONSENSUS: C-[TK]-H-L-G-C-[LIVT].

- NAME: Rieske iron-sulfur protein signature 2.  
 CONSENSUS: C-P-C-H-x-[GSA].
- 5 NAME: Flavodoxin signature.  
 CONSENSUS: [LIV]-[LIVFY]-[FY]-x-[ST]-x(2)-[AGC]-x-T-x(3)-A-x(2)-[LIV].
- 10 NAME: Rubredoxin signature.  
 CONSENSUS: [LIVM]-x(3)-W-x-C-P-x-C-[AGD].
- NAME: Electron transfer flavoprotein alpha-subunit signature.  
 15 CONSENSUS: [LI]-Y-[LIVM]-[AT]-x-G-[IV]-[SD]-G-x-[IV]-Q-H-x(2)-G-x(6)-[IV]-x-A-  
 CONSENSUS: [IV]-N.
- NAME: Electron transfer flavoprotein beta-subunit signature.  
 20 CONSENSUS: [IVA]-x-[KR]-x(2)-[DE]-[GD]-[GDE]-x(1,2)-[EQ]-x-[LIV]-x(4)-P-x-[LIVM](2)-  
 CONSENSUS: [TAC].
- NAME: Vertebrate metallothioneins signature.  
 25 CONSENSUS: C-x-C-[GSTAP]-x(2)-C-x-C-x(2)-C-x-C-x(2)-C-x-K.
- NAME: Ferritin iron-binding regions signature 1.  
 CONSENSUS: E-x-[KR]-E-x(2)-E-[KR]-[LF]-[LIVMA]-x(2)-Q-N-x-R-x-G-R.
- 30 NAME: Ferritin iron-binding regions signature 2.  
 CONSENSUS: D-x(2)-[LIVMF]-[STAC]-[DH]-F-[LI]-[EN]-x(2)-[FY]-L-x(6)-[LIVM]-[KN].
- NAME: Bacterioferritin signature.  
 35 CONSENSUS: <M-x-G-x(3)-V-[LIV]-x(2)-[LM]-x(3)-L-x(3)-L.
- NAME: Transferrins signature 1.  
 40 CONSENSUS: Y-x(0,1)-[VAS]-V-[IVAC]-[IVA]-[IVA]-[RKH]-[RKS]-[GDENSA].
- NAME: Transferrins signature 2.  
 CONSENSUS: Y-x-G-A-[FL]-[KRHNQ]-C-L-x(3,4)-G-[DENQ]-V-[GA]-[FYW].
- 45 NAME: Transferrins signature 3.  
 CONSENSUS: [DENQ]-[YF]-x-[LY]-L-C-x-[DN]-x(5,8)-[LIV]-x(4,5)-C-x(2)-A-x(4)-[HQR]-x-  
 CONSENSUS: [LIVMFYW]-[LIVM].
- 50 NAME: Globins profile.
- NAME: Protozoan/cyanobacterial globins signature.  
 CONSENSUS: F-[LF]-x(5)-G-[PA]-x(4)-G-[KRA]-x-[LIVM]-x(3)-H.
- 55 NAME: Plant hemoglobins signature.  
 CONSENSUS: [SN]-P-x-L-x(2)-H-A-x(3)-F.
- NAME: Hemerythrins signature.



CONSENSUS: W-L-x-[NQ]-H-I-x(3)-D-F.

NAME: Arthropod hemocyanins / insect LSPs signature 1.

CONSENSUS: Y-[FYW]-x-E-D-[LIVM]-x(2)-N-x(6)-H-x(3)-P.

NAME: Arthropod hemocyanins / insect LSPs signature 2.

CONSENSUS: T-x(2)-R-D-P-x-[FY]-[FYW].

NAME: Heavy-metal-associated domain.

CONSENSUS: [LIVN]-x(2)-[LIVMFA]-x-C-x-[STAGCDNH]-C-x(3)-

[LIVFG]-x(3)-[LIV]-x(9,11)-

CONSENSUS: [IVA]-x-[LVFYS].

NAME: ABC transporters family signature.

CONSENSUS: [LIVMFYC]-[SA]-[SAPGLVFYKQH]-G-[DENQMW]-

[KRQASPCLIMFW]-[KRNQSTAVM]-

CONSENSUS: [KRACLVM]-[LIVMFYPAN]-[PHY]-[LIVMFW]-[SAGCLIVP]-

[FYWHP]-[KRHP]-

CONSENSUS: [LIVMFYWSTA].

NAME: Binding-protein-dependent transport systems inner membrane comp. sign.

CONSENSUS: [LIVMFY]-x(8)-[EQR]-[STAGV]-[STAG]-x(3)-G-

[LIVMFYSTAC]-x(5)-[LIVMFYSTA]-

CONSENSUS: x(4)-[LIVMFY]-[PKR].

NAME: ABC-2 type transport system integral membrane proteins signature.

CONSENSUS: [LIMST]-x(2)-[LIMW]-x(2)-[LIMCA]-[GSTC]-x-[GSAIV]-

x(6)-[LIMGAI]-[PGSNQ]-

CONSENSUS: x(9,12)-P-[LIMFT]-x-[HRSY]-x(5)-[RQ].

NAME: Bacterial extracellular solute-binding proteins, family 1 signature.

CONSENSUS: [GAP]-[LIVMFA]-[STAVDN]-x(4)-[GSAV]-[LIVMFY](2)-Y-

[ND]-x(3)-[LIVMF]-x-

CONSENSUS: [KNDE].

NAME: Bacterial extracellular solute-binding proteins, family 3 signature.

CONSENSUS: G-[FYIL]-[DE]-[LIVMT]-[DE]-[LIVMF]-x(3)-[LIVMA]-

[VAGC]-x(2)-[LIVMAGN].

NAME: Bacterial extracellular solute-binding proteins, family 5 signature.

CONSENSUS: [AG]-x(6,7)-[DNEG]-x(2)-[STAVE]-[LIVMFYWA]-x-

[LIVMFY]-x-[LIVM]-[KR]-

CONSENSUS: [KRHDE]-[GDN]-[LIVMA]-[KNGSP]-[FW].

NAME: Serum albumin family signature.

CONSENSUS: [FY]-x(6)-C-C-x(7)-C-[LFY]-x(6)-[LIVMFYW].

NAME: Transthyretin signature 1.

CONSENSUS: S-K-C-P-L-M-V-K-V-L-D-[AS]-V-R-G.

NAME: Transthyretin signature 2.

CONSENSUS: S-P-[FY]-S-[FY]-S-T-T-A-[LIVM]-V-[ST]-x-P.

- NAME: Avidin / Streptavidin family signature.  
 CONSENSUS: [DEN]-x(2)-[KR]-[STA]-x(2)-V-G-x-[DN]-x-[FW]-T-[KR].
- 5 NAME: Eukaryotic cobalamin-binding proteins signature.  
 CONSENSUS: [SN]-V-D-T-[GA]-A-[LIVM]-A-x-L-A-[LIVMF]-T-C.
- NAME: Lipocalin signature.  
 CONSENSUS: [DENG]-x-[DENQGSTARK]-x(0,2)-[DENQARK]-[LIVFY]-  
 10 {CP}-G-{C}-W-[FYWLRH]-x-  
 CONSENSUS: [LIVMTA].
- NAME: Cytosolic fatty-acid binding proteins signature.  
 CONSENSUS: [GSAIVK]-x-[FYW]-x-[LIVMF]-x(4)-[NHG]-[FY]-[DE]-x-  
 15 [LIVMFY]-[LIVM]-x(2)-  
 CONSENSUS: [LIVMAKR].
- NAME: Acyl-CoA-binding protein signature.  
 CONSENSUS: P-[STA]-x-[DEN]-x-[LIVMF]-x(2)-[LIVMFY]-Y-[GSTA]-  
 20 x-[FY]-K-Q-[STA](2)-x-G.
- NAME: LBP / BPI / CETP family signature.  
 CONSENSUS: [PA]-[GA]-[LIVMC]-x(2)-R-[IV]-[ST]-x(3)-L-x(5)-  
 25 [EQ]-x(4)-[LIVM]-[EQK]-  
 CONSENSUS: x(8)-P.
- NAME: Phosphatidylethanolamine-binding protein family  
 signature.  
 CONSENSUS: [FY]-x-[LIVMF](3)-x-[DC]-P-D-x-P-[SN]-x(10)-H.  
 30
- NAME: Plant lipid transfer proteins signature.  
 CONSENSUS: [LIVM]-[PA]-x(2)-C-x-[LIVM]-x-[LIVM]-x-[LIVMFY]-x-  
 [LIVM]-[ST]-x(3)-  
 35 CONSENSUS: [DN]-C-x(2)-[LIVM].
- NAME: Uteroglobin family signature 1.  
 CONSENSUS: [GA]-x(3)-I-C-P-x-[LIVMF]-x(3)-[LIVM]-[DE]-x-  
 [LIVMF](2).
- 40 NAME: Uteroglobin family signature 2.  
 CONSENSUS: [DEQ]-x(4)-[SN]-x(5)-[DEQ]-x-I-x(2)-S-[PSE]-[LS]-  
 C.
- NAME: Mitochondrial energy transfer proteins signature.  
 45 CONSENSUS: P-x-[DE]-x-[LIVAT]-[RK]-x-[LRH]-[LIVMFY]-[QMAIGV].
- NAME: Sugar transport proteins signature 1.  
 CONSENSUS: [LIVMSTAG]-[LIVMFSAG]-x(2)-[LIVMSA]-[DE]-x-  
 [LIVMFYWA]-G-R-[RK]-x(4,6)-  
 50 CONSENSUS: [GSTA].
- NAME: Sugar transport proteins signature 2.  
 CONSENSUS: [LIVMF]-x-G-[LIVMFA]-x(2)-G-x(8)-[LIFY]-x(2)-[EQ]-  
 x(6)-[RK].
- 55 NAME: LacY family proton/sugar symporters signature 1.  
 CONSENSUS: G-[LIVM](2)-x-D-[RK]-L-G-L-[RK](2)-x-[LIVM](2)-W.

- NAME: LacY family proton/sugar symporters signature 2.  
 CONSENSUS: P-x-[[LIVMF]](2)-N-R-[[LIVM]]-G-x-K-N-[[STA]]-[[LIVM]](3).
- 5 NAME: PTR2 family proton/oligopeptide symporters signature 1.  
 CONSENSUS: [[GA]]-[[GAS]]-[[LIVMFYWA]]-[[LIVM]]-[[GAS]]-D-x-[[LIVMFYWT]]-[[LIVMFYW]]-G-x(3)-[[TAV]]-  
 CONSENSUS: [[IV]]-x(3)-[[GSTAV]]-x-[[LIVMF]]-x(3)-[[GA]].
- 10 NAME: PTR2 family proton/oligopeptide symporters signature 2.  
 CONSENSUS: [[FYT]]-x(2)-[[LMFY]]-[[FYV]]-[[LIVMFYWA]]-x-[[IVG]]-N-[[LIVMAG]]-G-[[GSA]]-[[LIMF]].
- 15 NAME: Amiloride-sensitive sodium channels signature.  
 CONSENSUS: Y-x(2)-[[EQTF]]-x-C-x(2)-[[GSTDNL]]-C-x-[[QT]]-x(2)-[[LIVMT]]-[[LIVMS]]-x(2)-C-x-C.
- 20 NAME: Sodium:alanine symporter family signature.  
 CONSENSUS: G-G-x-[[GA]](2)-[[LIVM]]-F-W-M-W-[[LIVM]]-x-[[STAV]]-[[LIVMFA]](2)-G.
- 25 NAME: Sodium:dicarboxylate symporter family signature 1.  
 CONSENSUS: P-x(0,1)-G-[[DE]]-x-[[LIVMF]](2)-x-[[LIVM]](2)-[[KREQ]]-[[LIVM]](3)-x-P.
- 30 NAME: Sodium:dicarboxylate symporter family signature 2.  
 CONSENSUS: P-x-G-x-[[STA]]-x-[[NT]]-[[LIVMC]]-D-G-[[STAN]]-x-[[LIVM]]-[[FY]]-x(2)-[[LIVM]]-x(2)-  
 CONSENSUS: [[LIVM]]-[[FY]]-[[LI]]-[[SA]]-Q.
- 35 NAME: Sodium:galactoside symporter family signature.  
 CONSENSUS: D-x(3)-G-x(3)-[[DN]]-x(6,8)-G-[[KH]]-F-[[KR]]-P-[[FYW]]-[[LIVM]](2)-x-[[GSTA]](2).
- NAME: Sodium:neurotransmitter symporter family signature 1.  
 CONSENSUS: W-R-F-[[GP]]-Y-x(4)-N-G-G-G-x-[[FY]].
- 40 NAME: Sodium:neurotransmitter symporter family signature 2.  
 CONSENSUS: Y-[[LIVMFY]]-x(2)-[[SC]]-[[LIVMFY]]-[[STQ]]-x(2)-L-P-W-x(2)-C-x(4)-N-[[GST]].
- 45 NAME: Sodium:solute symporter family signature 1.  
 CONSENSUS: [[GS]]-x(2)-[[LIY]]-x(3)-[[LIVMFYSTAG]](10)-[[LIY]]-[[TAV]]-x(2)-G-G-[[LMF]]-x-  
 CONSENSUS: [[SAP]].
- 50 NAME: Sodium:solute symporter family signature 2.  
 CONSENSUS: [[GAST]]-[[LIVM]]-x(3)-[[KR]]-x(4)-G-A-x(2)-[[GAS]]-[[LIVMGS]]-[[LIVMW]]-[[LIVMGAT]]-G-  
 CONSENSUS: x-[[LIVMG]].
- 55 NAME: Sodium:sulfate symporter family signature.  
 CONSENSUS: [[STACP]]-S-x(2)-F-x(2)-P-[[LIVM]]-[[GSA]]-x(3)-N-x-[[LIVM]]-V.
- NAME: glpT family of transporters signature.  
 CONSENSUS: R-G-x(5)-W-N-x(2)-H-N-x-G-G.

- NAME: Ammonium transporters signature.  
 5 CONSENSUS: D-[FYWS]-A-G-[GSC]-x(2)-[IV]-x(3)-[SAG](2)-x(2)-  
 [SAG]-[LIVMF]-x(3)-  
 CONSENSUS: [LIVMFYWA](2)-x-[GK]-x-R.
- NAME: BCCT family of transporters signature.  
 CONSENSUS: [GSDN]-W-T-[LIVM]-x-[FY]-W-x-W-W.
- 10 NAME: Flagellar motor protein motA family signature.  
 CONSENSUS: A-[LMF]-x-[GAT]-T-[LIVF]-x-G-x-[LIVMF]-x(7)-P.
- NAME: Formate and nitrite transporters signature 1.  
 15 CONSENSUS: [LIVMA]-[LIVMY]-x-G-[GSTA]-[DES]-L-[FI]-[TN]-[GS].
- NAME: Formate and nitrite transporters signature 2.  
 CONSENSUS: [GA]-x(2)-[CA]-N-[LIVMFYW](2)-V-C-[LV]-A.
- NAME: Prokaryotic sulfate-binding proteins signature 1.  
 20 CONSENSUS: K-x-[NQEK]-[GT]-G-[DQ]-x-[LIVM]-x(3)-Q-S.
- NAME: Prokaryotic sulfate-binding proteins signature 2.  
 CONSENSUS: N-P-K-[ST]-S-G-x-A-R.
- 25 NAME: Sulfate transporters signature.  
 CONSENSUS: P-x-Y-[GS]-L-Y-[STAG](2)-x(4)-[LIVMFY](3)-x(3)-  
 [GSTA](2)-S-[KR].
- NAME: Amino acid permeases signature.  
 30 CONSENSUS: [STAGC]-G-[PAG]-x(2,3)-[LIVMFYWA](2)-x-[LIVMFYW]-  
 x-[LIVMFYSTAGC](2)-  
 CONSENSUS: [STAGC]-x(3)-[LIVMFYW]-x-[LIVMST]-x(3)-[LIMCTA]-  
 [GA]-E-x(5)-[PSAL].
- 35 NAME: Aromatic amino acids permeases signature.  
 CONSENSUS: I-G-[GA]-G-M-[LF]-[SA]-x-P-x(3)-[SA]-G-x(2)-F.
- NAME: Xanthine/uracil permeases family signature.  
 40 CONSENSUS: [LIVM]-P-x-[PASIF]-V-[LIVM]-G-G-x(4)-[LIVM]-[FY]-  
 [GSA]-x-[LIVM]-x(3)-G.
- NAME: Anion exchangers family signature 1.  
 CONSENSUS: F-G-G-[LIVM](2)-[KR]-D-[LIVM]-[RK]-R-R-Y.
- 45 NAME: Anion exchangers family signature 2.  
 CONSENSUS: [FI]-L-I-S-L-I-F-I-Y-E-T-F-x-K-L.
- NAME: MIP family signature.  
 50 CONSENSUS: [HNQA]-x-N-P-[STA]-[LIVMF]-[ST]-[LIVMF]-[GSTAFY].
- NAME: General diffusion Gram-negative porins signature.  
 CONSENSUS: [LIVMFY]-x(2)-G-x(2)-Y-x-F-x-K-x(2)-[SN]-[STAV]-  
 [LIVMFYW]-V.
- 55 NAME: OmpA-like domain.  
 CONSENSUS: [LIVMA]-x-[GT]-x-[TA]-[DA]-x(2)-[DG]-[GSTP]-x(2)-  
 [LFYDE]-[NQSS]-x(2)-

- CONSENSUS: [LI]-[SG]-[QE]-[KRQE]-R-A-x(2)-[LV]-x(3)-[LIVMF]-  
 x(4,5)-[LIVM]-x(4)-  
 CONSENSUS: [LIVM]-x(3)-[SG]-x-G.
- 5 NAME: Eukaryotic mitochondrial porin signature.  
 CONSENSUS: [YH]-x(2)-D-[SPA]-x-[STA]-x(3)-[TAG]-[KR]-[LIVMF]-  
 [DNSTA]-[DNS]-x(4)-  
 CONSENSUS: [GSTAN]-[LIVMA]-x-[LIVMY].
- 10 NAME: Insulin-like growth factor binding proteins signature.  
 CONSENSUS: G-C-[GS]-C-C-x(2)-C-A-x(6)-C.
- NAME: GPR1/FUN34/yaaH family signature.  
 CONSENSUS: N-P-[AV]-P-[LF]-G-L-x-[GSA]-F.
- 15 NAME: GNS1/SUR4 family signature.  
 CONSENSUS: L-x-F-L-H-x-Y-H-H.
- NAME: 43 Kd postsynaptic protein signature.  
 20 CONSENSUS: G-Q-D-Q-T-K-Q-Q-I.
- NAME: Actins signature 1.  
 CONSENSUS: [FY]-[LIV]-G-[DE]-E-A-Q-x-[RKQ](2)-G.
- 25 NAME: Actins signature 2.  
 CONSENSUS: W-[IV]-[STA]-[RK]-x-[DE]-Y-[DNE]-[DE].
- NAME: Actins and actin-related proteins signature.  
 CONSENSUS: [LM]-[LIVM]-T-E-[GAPQ]-x-[LIVMFYWHQ]-N-[PSTAQ]-  
 30 x(2)-N-[KR].
- NAME: Annexins repeated domain signature.  
 CONSENSUS: [TG]-[STV]-x(8)-[LIVMF]-x(2)-R-x(3)-[DEQNH]-x(7)-  
 [IFY]-x(7)-[LIVMF]-  
 35 CONSENSUS: x(3)-[LIVMF]-x(11)-[LIVMFA]-x(2)-[LIVMF].
- NAME: Caveolins signature.  
 CONSENSUS: F-E-D-V-I-A-E-P.
- 40 NAME: Clathrin light chain signature 1.  
 CONSENSUS: F-L-A-Q-Q-E-S.
- NAME: Clathrin light chain signature 2.  
 CONSENSUS: [KR]-D-x-S-[KR]-[LIVM]-[KR]-x-[LIVM](3)-x-L-K.
- 45 NAME: Clusterin signature 1.  
 CONSENSUS: C-K-P-C-L-K-x-T-C.
- NAME: Clusterin signature 2.  
 50 CONSENSUS: C-L-[RK]-M-[RK]-x-[EQ]-C-[ED]-K-C.
- NAME: Connexins signature 1.  
 CONSENSUS: C-[DN]-T-x-Q-P-G-C-x(2)-V-C-Y-D.
- 55 NAME: Connexins signature 2.  
 CONSENSUS: C-x(3,4)-P-C-x(3)-[LIVM]-[DEN]-C-[FY]-[LIVM]-[SA]-  
 [KR]-P.

- NAME: Crystallins beta and gamma 'Greek key' motif signature.  
 CONSENSUS: [LIVMFYWA]-x-{DEHRKSTP}-[FY]-[DEQHKY]-x(3)-[FY]-x-G-x(4)-[LIVMFCST].
- 5 NAME: Dynamin family signature.  
 CONSENSUS: L-P-[RK]-G-[STN]-[GN]-[LIVM]-V-T-R.
- 10 NAME: Dynein light chain type 1 signature.  
 CONSENSUS: H-x-I-x-G-[KR]-x-F-[GA]-S-x-V-[ST]-[HY]-E.
- NAME: FtsZ protein signature 1.  
 CONSENSUS: N-[ST]-D-x-Q-x-L-x(16,18)-G-x-G-[ATV]-G-[GSAN]-x-P-x(2)-G.
- 15 NAME: FtsZ protein signature 2.  
 CONSENSUS: [DNHKR]-[LIVMF]-x-[LIVMF](2)-[VSTAC]-[STAC]-G-x-G-[GK]-G-T-G-[ST]-G-  
 CONSENSUS: [GSAR]-[STA]-P-[LIVMFT]-[LIVMF]-[SGAV].
- 20 NAME: Fungal hydrophobins signature.  
 CONSENSUS: [GN]-[DNQPSA]-x-C-[GSTANK]-[GSTADNQ]-[STNQI]-[PTIV]-x-C-C-[DENQKPST].
- 25 NAME: Intermediate filaments signature.  
 CONSENSUS: [IV]-x-[TACI]-Y-[RKH]-x-[LM]-L-[DE].
- NAME: Involucrin signature.  
 CONSENSUS: <M-S-[QH]-Q-x-T-[LV]-P-V-T-[LV].
- 30 NAME: Kinesin motor domain signature.  
 CONSENSUS: [GSA]-[KRHPSTQVM]-[LIVMF]-x-[LIVMF]-[IVC]-D-L-[AH]-G-[SAN]-E.
- 35 NAME: Kinesin motor domain profile.
- NAME: Kinesin light chain repeat.  
 CONSENSUS: [DEQR]-A-L-x(3)-[GEQ]-x(3)-G-x-[DNS]-x-P-x-V-A-x(3)-N-x-L-[AS]-  
 40 CONSENSUS: x(5)-[QR]-x-[KR]-[FY]-x(2)-[AV]-x(4)-[HKNQ].
- NAME: Myelin basic protein signature.  
 CONSENSUS: V-V-H-F-F-K-N.
- 45 NAME: Myelin PO protein signature.  
 CONSENSUS: S-[KR]-S-x-K-[AG]-x-[SA]-E-K-K-[STA]-K.
- NAME: Myelin proteolipid protein signature 1.  
 CONSENSUS: G-[MV]-A-L-F-C-G-C-G-H.
- 50 NAME: Myelin proteolipid protein signature 2.  
 CONSENSUS: C-x-[ST]-x-[DE]-x(3)-[ST]-[FY]-x-L-[FY]-I-x(4)-G-A.
- 55 NAME: Neuromodulin (GAP-43) signature 1.  
 CONSENSUS: <M-L-C-C-[LIVM]-R-R.
- NAME: Neuromodulin (GAP-43) signature 2.

- CONSENSUS: S-F-R-G-H-I-x-R-K-K-[[LIVM]].
- NAME: Osteopontin signature.  
 5 CONSENSUS: [[KQ]]-x-[[TA]]-x(2)-[[GA]]-S-S-E-E-K.
- NAME: Peripherin / rom-1 signature.  
 CONSENSUS: D-[[GS]]-V-P-F-[[ST]]-C-C-N-P-x-S-P-R-P-C.
- NAME: Profilin signature.  
 10 CONSENSUS: <x(0,1)-[[STA]]-x(0,1)-W-[[DENQH]]-x-[[YI]]-x-[[DEQ]].
- NAME: Surfactant associated polypeptide SP-C palmitoylation sites.  
 CONSENSUS: I-P-C-C-P-V.  
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- NAME: Synapsins signature 1.  
 CONSENSUS: L-R-R-R-L-S-D-S.
- NAME: Synapsins signature 2.  
 20 CONSENSUS: G-H-A-H-S-G-M-G-K-V-K.
- NAME: Synaptobrevin signature.  
 CONSENSUS: N-[[LIVM]]-[[DENS]]-[[KL]]-V-x-[[DEQ]]-R-x(2)-[[KR]]-[[LIVM]]-[[STD]]-x-[[LIVM]]-x-[[DE]].  
 25 CONSENSUS: [[KR]]-[[TA]]-[[DE]].
- NAME: Synaptophysin / synaptoporin signature.  
 CONSENSUS: L-S-V-[[DE]]-C-x-N-K-T.
- NAME: Tropomyosins signature.  
 30 CONSENSUS: L-K-E-A-E-x-R-A-E.
- NAME: Tubulin subunits alpha, beta, and gamma signature.  
 CONSENSUS: [[SAG]]-G-G-T-G-[[SA]]-G.  
 35
- NAME: Tubulin-beta mRNA autoregulation signal.  
 CONSENSUS: <M-R-[[DE]]-[[IL]].
- NAME: Tau and MAP proteins tubulin-binding domain signature.  
 40 CONSENSUS: G-S-x(2)-N-x(2)-H-x-[[PA]]-[[AG]]-G(2).
- NAME: Neuraxin and MAP1B proteins repeated region signature.  
 CONSENSUS: [[STAGDN]]-Y-x-Y-E-x(2)-[[DE]]-[[KR]]-[[STAGCI]].
- NAME: F-actin capping protein alpha subunit signature 1.  
 45 CONSENSUS: V-H-[[FY]](2)-E-D-G-N-V.
- NAME: F-actin capping protein alpha subunit signature 2.  
 CONSENSUS: F-K-[[AE]]-L-R-R-x-L-P.  
 50
- NAME: F-actin capping protein beta subunit signature.  
 CONSENSUS: C-D-Y-N-R-D.
- NAME: Vinculin family talin-binding region signature.  
 55 CONSENSUS: [[KR]]-x-[[LIVMF]]-x(3)-[[LIVMA]]-x(2)-[[LIVM]]-x(6)-R-Q-Q-E-L.
- NAME: Vinculin repeated domain signature.

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- NAME: Amyloidogenic glycoprotein extracellular domain signature.  
 CONSENSUS: G-[VT]-E-[FY]-V-C-C-P.  
 NAME: Amyloidogenic glycoprotein intracellular domain signature.  
 CONSENSUS: G-Y-E-N-P-T-Y-[KR].  
 NAME: Cadherins extracellular repeated domain signature.  
 CONSENSUS: [LIV]-x-[LIV]-x-D-x-N-D-[NH]-x-P.  
 NAME: Insect cuticle proteins signature.  
 CONSENSUS: G-x(7)-[DEN]-G-x(6)-Y-x-A-[DNG]-x(2,3)-G-[FY]-x-[AP].  
 NAME: Gas vesicles protein GVPa signature 1.  
 CONSENSUS: [LIVM]-x-[DE]-[LIVMFYT]-[LIVM]-[DE]-x-[LIVM](2)-[DKR](2)-G-x-[LIVM](2).  
 NAME: Gas vesicles protein GVPa signature 2.  
 CONSENSUS: R-[LIVA](3)-A-[GS]-[LIVMFY]-x-T-x(3)-Y-[AG].  
 NAME: Gas vesicles protein GVPC repeated domain signature.  
 CONSENSUS: F-L-x(2)-T-x(3)-R-x(3)-A-x(2)-Q-x(3)-L-x(2)-F.  
 NAME: Bacterial microcompartments proteins signature.  
 CONSENSUS: D-x(0,1)-M-x-K-[SAG](2)-x-[IV]-x-[LIVM]-[LIVMA]-[GCS]-x(4)-[GD]-[SGPD]-  
 CONSENSUS: [GA].  
 NAME: Flagella basal body rod proteins signature.  
 CONSENSUS: [GTARYQ]-x(9)-[LIVMYSTA](2)-[GSTA]-[STADEN]-N-[LIVM]-[SAN]-N-x-[SADNFR]-  
 CONSENSUS: [STV].  
 NAME: Flagella transport protein fliP family signature 1.  
 CONSENSUS: [PA]-A-[FY]-x-[LIVT]-[ESTH]-[EQ]-[LI]-x(2)-[GA]-F-[KREQ]-[IM]-G-[LIF].  
 NAME: Flagella transport protein fliP family signature 2.  
 CONSENSUS: P-[LIVMF]-K-[LIVMF](5)-x-[LIVMA]-[DNGS]-G-W.  
 NAME: Plant viruses icosahedral capsid proteins 'S' region signature.  
 CONSENSUS: [FYW]-x-[PSTA]-x(7)-G-x-[LIVM]-x-[LIVM]-x-[FYWI]-x(2)-D-x(5)-P.  
 NAME: Potexviruses and carlaviruses coat protein signature.  
 CONSENSUS: [RK]-[FYW]-A-[GAP]-F-D-x-F-x(2)-[LV]-x(3)-[GAST](2).  
 NAME: Neurotransmitter-gated ion-channels signature.  
 CONSENSUS: C-x-[LIVMFQ]-x-[LIVMF]-x(2)-[FY]-P-x-D-x(3)-C.  
 NAME: ATP P2X receptors signature.



CONSENSUS: G-G-x-[LIVM]-G-[LIVM]-x-[IV]-x-W-x-C-[DN]-L-D-x(5)-C-x-P-x-Y-x-F.

NAME: G-protein coupled receptors signature.

5 CONSENSUS: [GSTALIVMFYWC]-[GSTANCPDE]-[EDPKRH]-x(2)-[LIVMNQGA]-x(2)-[LIVMFT]-

CONSENSUS: [GSTANC]-[LIVMFYWSTAC]-[DENH]-R-[FYWCSH]-x(2)-[LIVM].

10 NAME: G-protein coupled receptors family 2 signature 1.

CONSENSUS: C-x(3)-[FYWLIV]-D-x(3,4)-C-[FW]-x(2)-[STAGV]-x(8,9)-C-[PF].

NAME: G-protein coupled receptors family 2 signature 2.

15 CONSENSUS: Q-G-[LMFCA]-[LIVMFT]-[LIV]-x-[LIVFST]-[LIF]-[VIFYH]-C-[LFY]-x-N-x(2)-V.

NAME: G-protein coupled receptors family 3 signature 1.

20 CONSENSUS: [LV]-x-N-[LIVM](2)-x-L-F-x-I-[PA]-Q-[LIVM]-[STA]-x-[STA](3)-[STAN].

NAME: G-protein coupled receptors family 3 signature 2.

CONSENSUS: C-C-[FYW]-x-C-x(2)-C-x(4)-[FYW]-x(2,4)-[DN]-x(2)-[STAH]-C-x(2)-C.

25 NAME: G-protein coupled receptors family 3 signature 3.

CONSENSUS: F-N-E-[STA]-K-x-I-[STAG]-F-[ST]-M.

NAME: Visual pigments (opsins) retinal binding site.

30 CONSENSUS: [LIVMWAC]-[PGAC]-x(3)-[SAC]-K-[STALIMR]-[GSACPNV]-[STACP]-x(2)-[DENF]-

CONSENSUS: [AP]-x(2)-[IY].

NAME: Bacterial rhodopsins signature 1.

35 CONSENSUS: R-Y-x-[DT]-W-x-[LIVMF]-[ST]-T-P-[LIVM](3).

NAME: Bacterial rhodopsins retinal binding site.

CONSENSUS: [FYIV]-x-[FYVG]-[LIVM]-D-[LIVMF]-x-[STA]-K-x(2)-[FY].

40 NAME: Receptor tyrosine kinase class II signature.

CONSENSUS: [DN]-[LIV]-Y-x(3)-Y-Y-R.

NAME: Receptor tyrosine kinase class III signature.

45 CONSENSUS: G-x-H-x-N-[LIVM]-V-N-L-L-G-A-C-T.

NAME: Receptor tyrosine kinase class V signature 1.

CONSENSUS: F-x-[DN]-x-[GAW]-[GA]-C-[LIVM]-[SA]-[LIVM](2)-[SA]-[LV]-[KRHQ]-[LIV]-

50 CONSENSUS: x(3)-[KR]-C-[PSAW].

NAME: Receptor tyrosine kinase class V signature 2.

CONSENSUS: C-x(2)-[DE]-G-[DEQ]-W-x(2,3)-[PAQ]-[LIVMT]-[GT]-x-C-x-C-x(2)-G-[HFY]-

55 CONSENSUS: [EQ].

NAME: Growth factor and cytokines receptors family signature 1.

- CONSENSUS: C-[LVFYR]-x(7,8)-[STIVDN]-C-x-W.
- NAME: Growth factor and cytokines receptors family signature 2.
- 5 CONSENSUS: [STGL]-x-W-[SG]-x-W-S.
- NAME: TNFR/NGFR family cysteine-rich region signature.
- CONSENSUS: C-x(4,6)-[FYH]-x(5,10)-C-x(0,2)-C-x(2,3)-C-x(7,11)-C-x(4,6)-[DNEQSKP]-
- 10 CONSENSUS: x(2)-C.
- NAME: TNFR/NGFR family cysteine-rich region domain.
- NAME: Integrins alpha chain signature.
- 15 CONSENSUS: [FYWS]-[RK]-x-G-F-F-x-R.
- NAME: Integrins beta chain cysteine-rich domain signature.
- CONSENSUS: C-x-[GNQ]-x(1,3)-G-x-C-x-C-x(2)-C-x-C.
- 20 NAME: Natriuretic peptides receptors signature.
- CONSENSUS: G-P-x-C-x-Y-x-A-A-x-V-x-R-x(3)-H-W.
- NAME: Photosynthetic reaction center proteins signature.
- 25 CONSENSUS: [NH]-x(4)-P-x-H-x(2)-[SAG]-x(11)-[SAGC]-x-H-[SAG](2).
- NAME: Antenna complexes alpha subunits signature.
- CONSENSUS: [LIVFAG]-x-[GASV]-[LIVFA]-x-[IV]-H-x(3)-[LIVM]-[GSTAE]-[STANH]-x(1,3)-
- 30 CONSENSUS: [STN]-W-[LIVMFYW].
- NAME: Antenna complexes beta subunits signature.
- CONSENSUS: [EQ]-x(4)-H-x(5)-[GSTA]-x(3)-[FY]-x(3)-[AG]-x(2)-[AV]-H-x(7)-P.
- 35 NAME: Photosystem I psaA and psaB proteins signature.
- CONSENSUS: C-D-G-P-G-R-G-G-T-C.
- NAME: Photosystem I psaG and psaK proteins signature.
- 40 CONSENSUS: G-F-x-[LIVM]-x-[DEA]-x(2)-[GA]-x-[GTA]-[SA]-x-G-H-x-[LIVM]-[GA].
- NAME: Phytochrome chromophore attachment site signature.
- 45 CONSENSUS: [RGS]-[GSA]-[PV]-H-x-C-H-x(2)-Y.
- NAME: Phytochrome chromophore attachment site domain profile.
- NAME: Speract receptor repeated domain signature.
- 50 CONSENSUS: G-x(5)-G-x(2)-E-x(6)-W-G-x(2)-C-x(3)-[FYW]-x(8)-C-x(3)-G.
- NAME: TonB-dependent receptor proteins signature 1.
- 55 CONSENSUS: <x(10,115)-[DENF]-[ST]-[LIVMF]-[LIVSTEQ]-V-x-[AGP]-[STANEQPK].
- NAME: TonB-dependent receptor proteins signature 2.

CONSENSUS: [LYGSTANE]-x(3)-[GSTAENQ]-x-[PGE]-R-x-[LIVFYWA]-x-  
[LIVMFTA]-[STAGNQ]-  
CONSENSUS: [LIVMFYGT]-x-[LIVMFYWGTAQ]-x-F>.

5 NAME: Transmembrane 4 family signature.

CONSENSUS: G-x(3)-[LIVMF]-x(2)-[GSA]-[LIVMF](2)-G-C-x-[GA]-  
[STA]-x(2)-[EG]-x(2)-

CONSENSUS: [CWNI]-[LIVM](2).

10 NAME: Bacterial chemotaxis sensory transducers signature.

CONSENSUS: R-T-E-[EQ]-Q-x(2)-[SA]-[LIVM]-x-[EQ]-T-A-A-S-M-E-  
Q-L-T-A-T-V.

NAME: ER lumen protein retaining receptor signature 1.

15 CONSENSUS: G-I-S-x-[KR]-x-Q-x-L-[FY]-x-[LIV](2)-F-x(2)-R-Y.

NAME: ER lumen protein retaining receptor signature 2.

CONSENSUS: L-E-[SA]-V-A-I-[LM]-P-Q-L.

20 NAME: Ephrins signature.

CONSENSUS: [KRQ]-[LF]-[CST]-x-K-[IF]-Q-x-[FY]-[ST]-[PA]-x(3)-  
G-x-E-F-x(5)-[FY](2)-

CONSENSUS: x(2)-[SA].

25 NAME: Granulins signature.

CONSENSUS: C-x-D-x(2)-H-C-C-P-x(4)-C.

NAME: HBGF/FGF family signature.

30 CONSENSUS: G-x-L-x-[STAGP]-x(6,7)-[DE]-C-x-[FM]-x-E-x(6)-Y.

NAME: PTN/MK heparin-binding protein family signature 1.

CONSENSUS: S-[DE]-C-x-[DE]-W-x-W-x(2)-C-x-P-x-[SN]-x-D-C-G-  
[LIVMA]-G-x-R-E-G.

35 NAME: PTN/MK heparin-binding protein family signature 2.

CONSENSUS: C-[KR]-[LIVM]-P-C-N-W-K-K-x-F-G-A-[DE]-C-K-Y-x-F-  
[EQ]-x-W-G-x-C.

NAME: Nerve growth factor family signature.

40 CONSENSUS: G-C-[KR]-G-[LIV]-[DE]-x(3)-[YW]-x-S-x-C.

NAME: Platelet-derived growth factor (PDGF) family  
signature.

45 CONSENSUS: P-[PS]-C-V-x(3)-R-C-[GSTA]-G-C-C.

NAME: Small cytokines (intercrine/chemokine) C-x-C subfamily  
signature.

CONSENSUS: C-x-C-[LIVM]-x(5,6)-[LIVMFY]-x(2)-[RKSEQ]-x-  
[LIVM]-x(2)-[LIVM]-x(5)-

50 CONSENSUS: [SAG]-x(2)-C-x(3)-[EQ]-[LIVM](2)-x(9,10)-C-L-[DN].

NAME: Small cytokines (intercrine/chemokine) C-C subfamily  
signature.

55 CONSENSUS: C-C-[LIFYT]-x(5,6)-[LI]-x(4)-[LIVMF]-x(2)-[FYW]-  
x(6,8)-C-x(3,4)-[SAG]-

CONSENSUS: [LIVM](2)-[FL]-x(8)-C-[STA].

NAME: TGF-beta family signature.

CONSENSUS: [LIVM]-x(2)-P-x(2)-[FY]-x(4)-C-x-G-x-C.  
 NAME: TNF family signature.  
 CONSENSUS: [LV]-x-[LIVM]-x(3)-G-[LIVMF]-Y-[LIVMFY](2)-x(2)-  
 5 [QEKHL]-[LIVMGT]-x-  
 CONSENSUS: [LIVMFY].  
 NAME: TNF family profile.  
 10 NAME: Wnt-1 family signature.  
 CONSENSUS: C-K-C-H-G-[LIVMT]-S-G-x-C.  
 NAME: Interferon alpha, beta and delta family signature.  
 CONSENSUS: [FYH]-[FY]-x-[GNRC]-[LIVM]-x(2)-[FY]-L-x(7)-[CY]-  
 15 A-W.  
 NAME: Granulocyte-macrophage colony-stimulating factor  
 signature.  
 CONSENSUS: C-P-[LP]-T-x-E-[EST]-x-C.  
 20 NAME: Interleukin-1 signature.  
 CONSENSUS: [FC]-x-S-[ASLV]-x(2)-P-x(2)-[FYLIV]-[LI]-[SCA]-T-  
 x(7)-[LIVM].  
 25 NAME: Interleukin-2 signature.  
 CONSENSUS: T-E-[LF]-x(2)-L-x-C-L-x(2)-E-L.  
 NAME: Interleukins -4 and -13 signature.  
 CONSENSUS: L-x-E-[LIVM](2)-x(4,5)-[LIVM]-[TL]-x(5,7)-C-x(4)-  
 30 [IVA]-x-[DNS]-[LIVMA].  
 NAME: Interleukin-6 / G-CSF / MGF signature.  
 CONSENSUS: C-x(9)-C-x(6)-G-L-x(2)-[FY]-x(3)-L.  
 35 NAME: Interleukin-7 and -9 signature.  
 CONSENSUS: N-x-[LAP]-[SCT]-F-L-K-x-L-L.  
 NAME: Interleukin-10 family signature.  
 CONSENSUS: [GS]-C-x(2)-[LV]-x(2)-[LIVM](2)-x-F-Y-L-x(2)-V.  
 40 NAME: LIF / OSM family signature.  
 CONSENSUS: [PST]-x(4)-F-[NQ]-x-K-x(3)-C-x-[LF]-L-x(2)-Y-[HK].  
 NAME: Macrophage migration inhibitory factor family  
 signature.  
 45 CONSENSUS: [DE]-P-C-A-x(3)-[LIVM]-x-S-I-G-x-[LIVM]-G.  
 NAME: Adipokinetic hormone family signature.  
 CONSENSUS: Q-[LV]-[NT]-[FY]-[EST]-x(2)-W.  
 50 NAME: Bombesin-like peptides family signature.  
 CONSENSUS: W-A-x-G-[SH]-[LF]-M.  
 NAME: Calcitonin / CGRP / IAPP family signature.  
 55 CONSENSUS: C-[SAGDN]-[ESTN]-x(0,1)-[SA]-T-C-[VMA]-x(3)-[LYF]-  
 x(3)-[LYF].  
 NAME: Corticotropin-releasing factor family signature.

- CONSENSUS: [PQ]-x-[LIVM]-S-[LIVM]-x(2)-[PST]-[LIVMF]-x-[LIVM]-L-R-x(2)-[LIVM].
- 5 NAME: Crustacean CHH/MIH/GIH neurohormones family signature.  
CONSENSUS: C-[DENK]-D-C-x-N-[LIV]-[FY]-R-x(7)-C-[KR]-x(2)-C.
- NAME: Erythropoietin / thrombopoietin signature.  
CONSENSUS: P-x(4)-C-D-x-R-[LIVM](2)-x-[KR]-x(14)-C.
- 10 NAME: Granins signature 1.  
CONSENSUS: [DE]-[SN]-L-[SAN]-x(2)-[DE]-x-E-L.
- NAME: Granins signature 2.  
CONSENSUS: C-[LIVM](2)-E-[LIVM](2)-S-[DN]-[STA]-L-x-K-x-S-x(3)-[LIVM]-[STA]-x-E-C.
- 15 NAME: Galanin signature.  
CONSENSUS: G-W-T-L-N-S-A-G-Y-L-L-G-P-H.
- 20 NAME: Gastrin / cholecystokinin family signature.  
CONSENSUS: Y-x(0,1)-[GD]-[WH]-M-[DR]-F.
- NAME: Glucagon / GIP / secretin / VIP family signature.  
CONSENSUS: [YH]-[STAIVGD]-[DEQ]-[AGF]-[LIVMSTE]-[FYLR]-x-[DENSTAK]-[DENSTA]-  
25 CONSENSUS: [LIVMFYGG]-x(9)-[KREQL]-[KRDENQL]-[LVFYWG]-[LIVQ].
- NAME: Glycoprotein hormones alpha chain signature 1.  
CONSENSUS: C-x-G-C-C-[FY]-S-R-A-[FY]-P-T-P.
- 30 NAME: Glycoprotein hormones alpha chain signature 2.  
CONSENSUS: N-H-T-x-C-x-C-x-T-C-x(2)-H-K.
- NAME: Glycoprotein hormones beta chain signature 1.  
CONSENSUS: C-[STAGM]-G-[HFYL]-C-x-[ST].
- 35 NAME: Glycoprotein hormones beta chain signature 2.  
CONSENSUS: [PA]-V-A-x(2)-C-x-C-x(2)-C-x(4)-[STD]-[DEY]-C-x(6,8)-[PGSTAVM]-x(2)-C.
- 40 NAME: Gonadotropin-releasing hormones signature.  
CONSENSUS: Q-H-[FYW]-S-x(4)-P-G.
- NAME: Insulin family signature.  
CONSENSUS: C-C-[P]-x(2)-C-[STDNEKPI]-x(3)-[LIVMFS]-x(3)-C.
- 45 NAME: Natriuretic peptides signature.  
CONSENSUS: C-F-G-x(3)-D-R-I-x(3)-S-x(2)-G-C.
- 50 NAME: Neurohypophysial hormones signature.  
CONSENSUS: C-[LIFY](2)-x-N-[CS]-P-x-G.
- NAME: Neuromedin U signature.  
CONSENSUS: F-[LIVMF]-F-R-P-R-N.
- 55 NAME: Endogenous opioids neuropeptides precursors signature.  
CONSENSUS: C-x(3)-C-x(2)-C-x(2)-[KRH]-x(6,7)-[LIF]-[DN]-x(3)-C-x-[LIVM]-[EQ]-C-

- CONSENSUS: [EQ]-x(8)-W-x(2)-C.
- NAME: Pancreatic hormone family signature.  
 5 CONSENSUS: [FY]-x(3)-[LIVM]-x(2)-Y-x(3)-[LIVMFY]-x-R-x-R-[YF].
- NAME: Parathyroid hormone family signature.  
 CONSENSUS: V-S-E-x-Q-x(2)-H-x(2)-G.
- 10 NAME: Pyrokinins signature.  
 CONSENSUS: F-[GSTV]-P-R-L-[G>].
- NAME: Somatotropin, prolactin and related hormones signature 1.  
 15 CONSENSUS: C-x-[ST]-x(2)-[LIVMFY]-x-[LIVMSTA]-P-x(5)-[TALIV]-x(7)-[LIVMFY]-x(6)-  
 CONSENSUS: [LIVMFY]-x(2)-[STA]-W.
- NAME: Somatotropin, prolactin and related hormones signature 2.  
 20 CONSENSUS: C-[LIVMFY]-x(2)-D-[LIVMFYSTA]-x(5)-[LIVMFY]-x(2)-[LIVMFYT]-x(2)-C.
- NAME: Tachykinin family signature.  
 25 CONSENSUS: F-[IVFY]-G-[LM]-M-[G>].
- NAME: Thymosin beta-4 family signature.  
 CONSENSUS: K-L-K-K-T-E-T-Q-E-K-N.
- 30 NAME: Urotensin II signature.  
 CONSENSUS: C-F-W-K-Y-C.
- NAME: Cecropin family signature.  
 35 CONSENSUS: W-x(D,2)-[KDN]-x(2)-K-[KRE]-[LI]-E-[RKN].
- NAME: Mammalian defensins signature.  
 CONSENSUS: C-x-C-x(3,5)-C-x(7)-G-x-C-x(9)-C-C.
- NAME: Arthropod defensins signature.  
 40 CONSENSUS: C-x(2,3)-[HN]-C-x(3,4)-[GR]-x(2)-G-G-x-C-x(4,7)-C-x-C.
- NAME: Cathelcidins signature 1.  
 45 CONSENSUS: Y-x-[ED]-x-V-x-[RQ]-A-[LIVMA]-[DQG]-x-[LIVMFY]-N-[EQ].
- NAME: Cathelcidins signature 2.  
 CONSENSUS: F-x-[LIVM]-K-E-T-x-C-x(10)-C-x-F-[KR]-[KE].
- 50 NAME: Endothelin family signature.  
 CONSENSUS: C-x-C-x(4)-D-x(2)-C-x(2)-[FY]-C.
- NAME: Plant thionins signature.  
 CONSENSUS: C-C-x(5)-R-x(2)-[FY]-x(2)-C.
- 55 NAME: Gamma-thionins family signature.  
 CONSENSUS: [KR]-x-C-x(3)-[SV]-x(2)-[FYWH]-x-[GF]-x-C-x(5)-C-x(3)-C.

- NAME: Snake toxins signature.  
 CONSENSUS: G-C-x(1,3)-C-P-x(8,10)-C-C-x(2)-[P]DEN].
- 5 NAME: Myotoxins signature.  
 CONSENSUS: K-x-C-H-x-K-x(2)-H-C-x(2)-K-x(3)-C-x(8)-K-x(2)-C-x(2)-[RK]-x-K-C-C-K-K.
- 10 NAME: Scorpion short toxins signature.  
 CONSENSUS: C-x(3)-C-x(6,9)-[GAS]-K-C-[IMQT]-x(3)-C-x-C.
- NAME: Heat-stable enterotoxins signature.  
 CONSENSUS: C-C-x(2)-C-C-x-P-A-C-x-G-C.
- 15 NAME: Aerolysin type toxins signature.  
 CONSENSUS: [KT]-x(2)-N-W-x(2)-T-[DN]-T.
- NAME: Shiga/ricin ribosomal inactivating toxins active site signature.  
 20 CONSENSUS: [LIVMA]-x-[LIVMSTA](2)-x-E-[SAGV]-[STAL]-R-[FY]-[RKNQS]-x-[LIVM]-[EQS]-  
 CONSENSUS: x(2)-[LIVMF].
- NAME: Channel forming colicins signature.  
 25 CONSENSUS: T-x(2)-W-x-P-[LIVMFY](3)-x(2)-E.
- NAME: Hok/gef family cell toxic proteins signature.  
 CONSENSUS: [LIVMA](4)-C-[LIVMFA]-T-[LIVMA](2)-x(4)-[LIVM]-x-[RG]-x(2)-L-[CY].
- 30 NAME: Staphylococcal enterotoxin/Streptococcal pyrogenic exotoxin signature 1.  
 CONSENSUS: Y-G-G-[LIV]-T-x(4)-N.
- 35 NAME: Staphylococcal enterotoxin/Streptococcal pyrogenic exotoxin signature 2.  
 CONSENSUS: K-x(2)-[LIV]-x(4)-[LIV]-D-x(3)-R-x(2)-L-x(5)-[LIV]-Y.
- 40 NAME: Thiol-activated cytolysins signature.  
 CONSENSUS: [RK]-E-C-T-G-L-x-W-E-W-W-[RK].
- NAME: Membrane attack complex components / perforin signature.  
 45 CONSENSUS: Y-x(6)-[FY]-G-T-H-[FY].
- NAME: Pancreatic trypsin inhibitor (Kunitz) family signature.  
 CONSENSUS: F-x(3)-G-C-x(6)-[FY]-x(5)-C.
- 50 NAME: Bowman-Birk serine protease inhibitors family signature.  
 CONSENSUS: C-x(5,6)-[DENQKRHSTA]-C-[PASTDH]-[PASTDK]-[ASTDV]-C-[NDKS]-[DEKRHSTA]-C.
- 55 NAME: Kazal serine protease inhibitors family signature.  
 CONSENSUS: C-x(7)-C-x(6)-Y-x(3)-C-x(2,3)-C.

- NAME: Soybean trypsin inhibitor (Kunitz) protease inhibitors family signature.  
 5 CONSENSUS: [LIVM]-x-D-x-[EDNTY]-[DG]-[RKHDENQ]-x-[LIVM]-x(5)-Y-x-[LIVM].
- NAME: Serpins signature.  
 10 CONSENSUS: [LIVMFY]-x-[LIVMFYAC]-[DNQ]-[RKHQSS]-[PST]-F-[LIVMFY]-[LIVMFYC]-x-  
 CONSENSUS: [LIVMFAH].
- NAME: Potato inhibitor I family signature.  
 15 CONSENSUS: [FYW]-P-[EQH]-[LIV](2)-G-x(2)-[STAGV]-x(2)-A.
- NAME: Squash family of serine protease inhibitors signature.  
 CONSENSUS: C-P-x(5)-C-x(2)-D-x-D-C-x(3)-C-x-C.
- NAME: Streptomyces subtilisin-type inhibitors signature.  
 CONSENSUS: C-x-P-x(2,3)-G-x-H-P-x(4)-A-C-[ATD]-x-L.
- 20 NAME: Cysteine proteases inhibitors signature.  
 CONSENSUS: [GSTEQRV]-Q-[LIVT]-[VAF]-[SAGQ]-G-x-[LIVMNK]-x(2)-[LIVMFY]-x-[LIVMFYA]-  
 CONSENSUS: [DENQKRHSIV].
- 25 NAME: Tissue inhibitors of metalloproteinases signature.  
 CONSENSUS: C-x-C-x-P-x-H-P-Q-x-A-F-C.
- NAME: Cereal trypsin/alpha-amylase inhibitors family signature.  
 30 CONSENSUS: C-x(4)-[SAGD]-x(4)-[SPAL]-[LF]-x(2)-C-[RH]-x-[LIVMFY](2)-x(3,4)-C.
- NAME: Alpha-2-macroglobulin family thiolester region signature.  
 35 CONSENSUS: [PG]-x-[GS]-C-[GA]-E-[EQ]-x-[LIVM].
- NAME: Disintegrins signature.  
 CONSENSUS: C-x(2)-G-x-C-C-x-[NQRS]-C-x-[FM]-x(6)-C-[RK].
- 40 NAME: Lambdoid phages regulatory protein CIII signature.  
 CONSENSUS: E-S-x-L-x-R-x(2)-[KR]-x-L-x(4)-[KR](2)-x(2)-[DE]-x-L.
- NAME: Chaperonins cpn60 signature.  
 45 CONSENSUS: A-[AS]-x-[DEQ]-E-x(4)-G-G-[GA].
- NAME: Chaperonins cpn10 signature.  
 CONSENSUS: [LIVMFY]-x-P-[ILT]-x-[DEN]-[KR]-[LIVMFA](3)-[KREQ]-x(8,9)-[SG]-x-  
 50 CONSENSUS: [LIVMFY](3).
- NAME: Chaperonins TCP-1 signature 1.  
 CONSENSUS: [RKEL]-[ST]-x-[LMFY]-G-P-x-[GSA]-x-x-K-[LIVMF](2).
- 55 NAME: Chaperonins TCP-1 signature 2.  
 CONSENSUS: [LIVM]-[TS]-[NK]-D-[GA]-[AVNHK]-[TAV]-[LIVM](2)-x(2)-[LIVM]-x-[LIVM]-x-  
 CONSENSUS: [SNH]-[PQH].



- NAME: Chaperonins TCP-1 signature 3.  
 CONSENSUS: Q-[DEK]-x-x-[LIVMGTA]-[GA]-D-G-T.
- 5 NAME: Heat shock hsp20 proteins family profile.  
 NAME: Heat shock hsp70 proteins family signature 1.  
 CONSENSUS: [IV]-D-L-G-T-[ST]-x-[SC].
- 10 NAME: Heat shock hsp70 proteins family signature 2.  
 CONSENSUS: [LIVMF]-[LIVMFY]-[DN]-[LIVMFS]-G-[GSH]-[GS]-[AST]-  
 x(3)-[ST]-[LIVM]-  
 CONSENSUS: [LIVMFC].
- 15 NAME: Heat shock hsp70 proteins family signature 3.  
 CONSENSUS: [LIVMY]-x-[LIVMF]-x-G-G-x-[ST]-x-[LIVM]-P-x-  
 [LIVM]-x-[DEQKRSTA].
- 20 NAME: Heat shock hsp90 proteins family signature.  
 CONSENSUS: Y-x-[NQH]-K-[DE]-[IVA]-F-L-R-[ED].  
 NAME: Chaperonins clpA/B signature 1.  
 CONSENSUS: D-[AI]-[SGA]-N-[LIVMF](2)-K-[PT]-x-L-x(2)-G.
- 25 NAME: Chaperonins clpA/B signature 2.  
 CONSENSUS: R-[LIVMFY]-D-x-S-E-[LIVMFY]-x-E-[KRQ]-x-[STA]-x-  
 [STA]-[KR]-[LIVM]-x-G-  
 CONSENSUS: [STA].
- 30 NAME: Nt-dnaJ domain signature.  
 CONSENSUS: [FY]-x(2)-[LIVMA]-x(3)-[FYWHNT]-[DENQSA]-x-L-x-  
 [DN]-x(3)-[KR]-x(2)-[FYI].  
 NAME: dnaJ domain profile.
- 35 NAME: CXXCXGXG dnaJ domain signature.  
 CONSENSUS: C-[DEGSTHKR]-x-C-x-G-x-[GK]-[AGSDM]-x(2)-[GSNKR]-  
 x(4,6)-C-x(2,3)-C-x-G-x-G.
- 40 NAME: grpE protein signature.  
 CONSENSUS: [FL]-[DN]-[PHEA]-x(2)-[HM]-x-A-[LIVMTN]-x(16,20)-  
 G-[FY]-x(3)-[DEG]-x(2)-  
 CONSENSUS: [LIVM]-[RI]-x-[SA]-x-V-x-[IV].
- 45 NAME: Bacterial type II secretion system protein C  
 signature.  
 CONSENSUS: P-x(6)-F-x(4)-L-x(3)-D-[LIVM]-A-[LIVM]-x-[LIVM]-N-  
 x-[LIVM]-x-L.
- 50 NAME: Bacterial type II secretion system protein D  
 signature.  
 CONSENSUS: [GR]-[DEQKG]-[STVM]-[LIVMA](3)-[GA]-G-[LIVMFY]-  
 x(11)-[LIVM]-P-  
 CONSENSUS: [LIVMFYWGS]-[LIVMF]-[GSAE]-x-[LIVM]-P-  
 55 [LIVMFYW](2)-x(2)-[LV]-F.  
 NAME: Bacterial type II secretion system protein E  
 signature.

CONSENSUS: [LIVM]-R-x(2)-P-D-x-[LIVM](3)-G-E-[LIVM]-R-D.

NAME: Bacterial type II secretion system protein F signature.

5 CONSENSUS: [KRQ]-[LIVMA]-x(2)-[SAIV]-[LIVM]-x-[TY]-P-x(2)-[LIVM]-x(3)-[STAGV]-x(6)-

CONSENSUS: [LMY]-x(3)-[LIVMF](2)-P.

10 NAME: Bacterial type II secretion system protein N signature.

CONSENSUS: G-T-L-W-x-G-x(11)-L-x(4)-W.

NAME: Bacterial export FHIPEP family signature.

15 CONSENSUS: R-[LIVM]-[GSA]-E-V-[GSA]-A-R-F-[STV]-L-D-[GSA]-M-P-G-K-Q-M-[GSA]-I-D-

CONSENSUS: [GSA]-D.

NAME: Protein secA signatures.

20 CONSENSUS: [IV]-x-[IV]-[SA]-T-[NQ]-M-A-G-R-G-x-D-I-x-L.

NAME: Protein secY signature 1.

CONSENSUS: [GST]-[LIVMF](2)-x-[LIVM]-G-[LIVM]-x-P-[LIVMFY](2)-x-[AS]-[GSTQ]-

25 CONSENSUS: [LIVMFAT](3)-Q-[LIVMFA](2).

NAME: Protein secY signature 2.

CONSENSUS: [LIVMFYW](2)-x-[DE]-x-[LIVMF]-[STN]-x(2)-G-[LIVMF]-[GST]-[NST]-G-x-[GST]-

30 CONSENSUS: [LIVMF](3).

NAME: Protein secE/secB-gamma signature.

35 CONSENSUS: [LIVMFY]-x(2)-[DENQGA]-x(4)-[LIVMTA]-x-[KRV]-x(2)-[KW]-P-x(3)-[SEQ]-x(7)-

CONSENSUS: [LIVT]-[LIVGA]-[LIVFGAST].

NAME: Gram-negative pili assembly chaperone signature.

40 CONSENSUS: [LIVMFY]-[APN]-x-[DNS]-[KREQ]-E-[STR]-[LIVMAR]-x-[FYWT]-x-[NC]-[LIVM]-

CONSENSUS: x(2)-[LIVM]-P-[PAS].

NAME: Fimbrial biogenesis outer membrane usher protein signature.

45 CONSENSUS: [VL]-[PASQ]-[PAS]-G-[PAD]-[FY]-x-[LI]-[DNQSTAP]-[DNH]-[LIVMFY].

NAME: SRP54-type proteins GTP-binding domain signature.

CONSENSUS: P-[LIVM]-x-[FYL]-[LIVMAT]-[GS]-x-[GS]-[EQ]-x(4)-[LIVMF].

50 NAME: Cytochrome c oxidase assembly factor COX10/ctaB/cyoE signature.

CONSENSUS: [ED]-x-D-x(2)-M-x-R-T-x(2)-R-x(4)-G.

NAME: Cyclin-dependent kinases regulatory subunits signature 1.

55 CONSENSUS: Y-S-x-[KR]-Y-x-[DE](2)-x-[FY]-E-Y-R-H-V-x-[LV]-[PT]-[KRP].

- NAME: Cyclin-dependent kinases regulatory subunits signature 2.  
 CONSENSUS: H-x-P-E-x-H-[IV]-L-L-F-[KR].
- 5 NAME: Pentaxin family signature.  
 CONSENSUS: H-x-C-x-[ST]-W-x-[ST].
- NAME: Immunoglobulins and major histocompatibility complex proteins signature.  
 10 CONSENSUS: [FY]-x-C-x-[VA]-x-H.
- NAME: Prion protein signature 1.  
 CONSENSUS: A-G-A-A-A-A-G-A-V-V-G-G-L-G-G-Y.
- 15 NAME: Prion protein signature 2.  
 CONSENSUS: E-x-[ED]-x-K-[LIVM](2)-x-[KR]-[LIVM](2)-x-[QE]-M-C-x(2)-Q-Y.
- NAME: Cyclins signature.  
 20 CONSENSUS: R-x(2)-[LIVMSA]-x(2)-[FYWS]-[LIVM]-x(8)-[LIVMFC]-x(4)-[LIVMFYA]-x(2)-  
 CONSENSUS: [STAGC]-[LIVMFYQ]-x-[LIVMFYC]-[LIVMFY]-D-[RKH]-[LIVMFYW].
- 25 NAME: Proliferating cell nuclear antigen signature 1.  
 CONSENSUS: [GA]-[LIVMF]-x-[LIVMA]-x-[SAV]-[LIVM]-D-x-[NSAE]-[HKR]-[VI]-x-[LY]-  
 CONSENSUS: [VGA]-x-[LIVM]-x-[LIVM]-x(4)-F.
- 30 NAME: Proliferating cell nuclear antigen signature 2.  
 CONSENSUS: [RKA]-C-[DE]-[RH]-x(3)-[LIVMF]-x(3)-[LIVM]-x-[SGAN]-[LIVMF]-x-K-  
 CONSENSUS: [LIVMF](2).
- 35 NAME: Actin-depolymerizing proteins signature.  
 CONSENSUS: P-[DE]-x-[SA]-x-[LIVMT]-[KR]-x-[KR]-M-[LIVM]-[YA]-[STA](3)-x(3)-[LIVMF]-  
 CONSENSUS: [KR].
- 40 NAME: BCL2-like apoptosis inhibitors (spans part of BH3, BH1 and BH2).  
 NAME: Apoptosis regulator, Bcl-2 family BH1 domain signature.  
 45 CONSENSUS: [LVME]-[FT]-x-[GSD]-[GL]-x(1,2)-[NS]-[YW]-G-R-[LIV]-[LIVC]-[GAT]-  
 CONSENSUS: [LIVMF](2)-x-F-[GSAE]-[GSARY].
- NAME: Apoptosis regulator, Bcl-2 family BH2 domain signature.  
 50 CONSENSUS: W-[LIM]-x(3)-[GR]-G-[WQ]-[DENSAV]-x-[FLGA]-[LIVFTC].
- NAME: Apoptosis regulator, Bcl-2 family BH3 domain signature.  
 55 CONSENSUS: [LIVAT]-x(3)-L-[KARQ]-x-[IVAL]-G-D-[DESG]-[LIMFV]-[DENSHQ]-[LVSHRQ]-  
 CONSENSUS: [NSR].

- NAME: Apoptosis regulator, Bcl-2 family BH4 domain signature.  
 5 CONSENSUS: [DS]-[NT]-R-[AE]-[LI]-V-x-[K]-[FY]-[LIV]-[GHS]-Y-K-L-[SR]-Q-[RK]-G-  
 CONSENSUS: [HY]-x-[CW].
- NAME: Apoptosis regulator, Bcl-2 family BH4 domain profile.
- 10 NAME: Arrestins signature.  
 CONSENSUS: [FY]-R-Y-G-x-[DE](2)-x-[DE]-[LIVM](2)-G-[LIVM]-x-F-x-[RK]-[DEQ]-[LIVM].
- 15 NAME: AAA-protein family signature.  
 CONSENSUS: [LIVMT]-x-[LIVMT]-[LIVMF]-x-[GATMC]-[EST]-[NS]-x(4)-[LIVM]-D-x-A-[LIFA]-  
 CONSENSUS: x-R.
- 20 NAME: Ubiquitin domain signature.  
 CONSENSUS: K-x(2)-[LIVM]-x-[DESAK]-x(3)-[LIVM]-[PA]-x(3)-Q-x-[LIVM]-[LIVMC]-  
 CONSENSUS: [LIVMFY]-x-G-x(4)-[DE].
- 25 NAME: Ubiquitin domain profile.
- NAME: ADP-ribosylation factors family signature.  
 CONSENSUS: [HRQT]-x-[FYWI]-x-[LIVM]-x(4)-A-x(2)-G-x(2)-[LIVM]-x(2)-[GSA]-[LIVMF]-x-  
 CONSENSUS: [WK]-[LIVM].
- 30 NAME: GTP-binding nuclear protein ran signature.  
 CONSENSUS: D-T-A-G-Q-E-K-[LF]-G-G-L-R-[DE]-G-Y-Y.
- NAME: SAR1 family signature.  
 35 CONSENSUS: R-x-[LIVM]-E-V-F-M-C-S-[LIVM](2)-x-[KRQ]-x-G-Y-x-E-[AG]-[FI]-x-W-[LIVM]-  
 CONSENSUS: x-Q-Y.
- NAME: Band 7 protein family signature.  
 40 CONSENSUS: R-x(2)-[LIV]-[SAN]-x(6)-[LIV]-D-x(2)-T-x(2)-W-G-[LIV]-[KRH]-[LIV]-x-  
 CONSENSUS: [KR]-[LIV]-E-[LIV]-[KR].
- NAME: Trp-Asp (WD) repeats signature.  
 45 CONSENSUS: [LIVMSTAC]-[LIVMFYWSTAGC]-[LIMSTAG]-[LIVMSTAGC]-x(2)-[DN]-x(2)-  
 CONSENSUS: [LIVWSTAC]-x-[LIVMFSTAG]-W-[DEN]-[LIVMFSTAGCN].
- NAME: G-protein gamma subunit profile.
- 50 NAME: Ras GTPase-activating proteins signature.  
 CONSENSUS: [GSN]-x-[LIVMF]-[FY]-[LIVMFY]-R-[LIVMFY](2)-[GACN]-P-[AV]-[LIV](2)-  
 CONSENSUS: [SGAN]-P.
- 55 NAME: Ras GTPase-activating proteins profile.

NAME: Guanine-nucleotide dissociation stimulators CD24 family signature.

CONSENSUS: L-x(2)-[LIVMFYW]-L-x(2)-P-[LIVM]-x(2)-[LIVM]-x-[KRS]-x(2)-L-x-[LIVM]-x-

5 CONSENSUS: [DEQ]-[LIVM]-x(3)-[ST].

NAME: Guanine-nucleotide dissociation stimulators CD25 family signature.

10 CONSENSUS: [GAP]-[CT]-V-P-[FY]-x(4)-[LIVMFY]-x-[DN]-[LIVM].

NAME: MARCKS family signature 1.

CONSENSUS: G-Q-E-N-G-H-V-[KR].

NAME: MARCKS family phosphorylation site domain.

15 CONSENSUS: E-T-P-K(5)-x(0,1)-F-S-F-K-K-x-F-K-L-S-G-x-S-F-K-[KR]-[NS]-[KR]-K-E.

NAME: Stathmin family signature 1.

20 CONSENSUS: P-[KQ]-[KR](2)-[DE]-x-S-L-[EG]-E.

NAME: Stathmin family signature 2.

CONSENSUS: A-E-K-R-E-H-E-[KR]-E-V.

NAME: GTP-binding elongation factors signature.

25 CONSENSUS: D-[KRSTGANQFYW]-x(3)-E-[KRAQ]-x-[RKQD]-[GC]-[IVMK]-[ST]-[IV]-x(2)-

CONSENSUS: [GSTACKRNQ].

NAME: Elongation factor 1 beta/beta'/delta chain signature 1.

30 CONSENSUS: [DE]-[DEG]-[DE](2)-[LIVMF]-D-L-F-G.

NAME: Elongation factor 1 beta/beta'/delta chain signature 2.

35 CONSENSUS: V-Q-S-x-D-[LIVM]-x-A-[FWM]-[NQ]-K-[LIVM].

NAME: Elongation factor 1 gamma chain profile.

NAME: Elongation factor Ts signature 1.

40 CONSENSUS: L-R-x(2)-T-[GDQ]-x-[GS]-[LIVMF]-x(0,1)-[DENKAC]-x-K-[KRNEQS]-[AV]-L.

NAME: Elongation factor Ts signature 2.

45 CONSENSUS: E-[LIVM]-N-[SCV]-[QE]-T-D-F-V-[SA]-[KRN].

NAME: Elongation factor P signature.

CONSENSUS: K-x-A-x(4)-G-x(2)-[LIV]-x-V-P-x(2)-[LIV]-x(2)-G.

NAME: Eukaryotic initiation factor 1A signature.

50 CONSENSUS: [IM]-x-G-x-[GS]-[KRH]-x(4)-[CL]-x-D-G-x(2)-R-x(2)-[RH]-I-x-G.

NAME: Eukaryotic initiation factor 4E signature.

55 CONSENSUS: [DE]-[IFY]-x(2)-F-[KR]-x(2)-[LIVM]-x-P-x-W-E-[DV]-x(5)-G-G-[KR]-W.

NAME: Eukaryotic initiation factor 5A hypusine signature.

CONSENSUS: [PT]-G-K-H-G-x-A-K.

- NAME: Initiation factor 2 signature.  
 5 CONSENSUS: G-x-[LIVM]-x(2)-L-[KR]-[KRHNS]-x-K-x(5)-[LIVM]-x(2)-G-x-[DEN]-C-G.
- NAME: Initiation factor 3 signature.  
 CONSENSUS: [KR]-[LIVM](2)-[DN]-[FY]-[GSN]-[KR]-[LIVMFYS]-x-[FY]-[DEQT]-x(2)-[KR].
- 10 NAME: Translation initiation factor SUI1 signature.  
 CONSENSUS: [LIVM]-[EQ]-[LIVM]-Q-G-[DEN]-[KHQ]-[KRV].
- NAME: Prokaryotic-type class I peptide chain release factors signature.  
 15 CONSENSUS: [AR]-[STA]-x-G-x-G-G-Q-[HNGCS]-V-N-x(3)-[ST]-A-[IV].
- NAME: Transcription termination factor nusG signature.  
 20 CONSENSUS: [LIVM]-F-G-[KRW]-x-T-P-[IV]-x-[LIVM].
- NAME: Calponin family repeat.  
 CONSENSUS: [LIVM]-x-[LS]-Q-[MAS]-G-[STY]-[NT]-[KRQ]-x(2)-[STN]-Q-x-G-x(3,4)-G.
- 25 NAME: CAP protein signature 1.  
 CONSENSUS: [LIVM](2)-x-R-L-[DE]-x(4)-R-L-E.
- NAME: CAP protein signature 2.  
 30 CONSENSUS: D-[LIVMFY]-x-E-x-[PA]-x-P-E-Q-[LIVMFY]-K.
- NAME: Calreticulin family signature 1.  
 CONSENSUS: [KRHN]-x-[EQN]-[EQNK]-x(3)-C-G-G-[AG]-[FY]-[LIVM]-[KN]-[LIVMFY](2).
- 35 NAME: Calreticulin family signature 2.  
 CONSENSUS: [LIVM](2)-F-G-P-D-x-C-[AG].
- NAME: Calreticulin family repeated motif signature.  
 40 CONSENSUS: [IV]-x-D-x-[DENST]-x(2)-K-P-[DEH]-D-W-[DEN].
- NAME: Calsequestrin signature 1.  
 CONSENSUS: [EQ]-[DE]-G-L-[DN]-F-P-x-Y-D-G-x-D-R-V.
- NAME: Calsequestrin signature 2.  
 45 CONSENSUS: [DE]-L-E-D-W-[LIVM]-E-D-V-L-x-G-x-[LIVM]-N-T-E-D-D-D.
- NAME: S-100/ICaBP type calcium binding protein signature.  
 50 CONSENSUS: [LIVMFYW](2)-x(2)-[LK]-D-x(3)-[DN]-x(3)-[DNSG]-[FY]-x-[ES]-[FYVC]-x(2)-  
 CONSENSUS: [LIVMFS]-[LIVMF].
- NAME: Hemolysin-type calcium-binding region signature.  
 55 CONSENSUS: D-x-[LI]-x(4)-G-x-D-x-[LI]-x-G-G-x(3)-D.
- NAME: HlyD family secretion proteins signature.  
 CONSENSUS: [LIVM]-x(2)-G-[LM]-x(3)-[STGAV]-x-[LIVMT]-x-[LIVMT]-[GE]-x-[KR]-x-

- CONSENSUS: [LIVMFYW](2)-x-[LIVMFYW](3).
- NAME: P-II protein urydylatation site.  
 5 CONSENSUS: Y-[KR]-G-[AS]-[AE]-Y.
- NAME: P-II protein C-terminal region signature.  
 CONSENSUS: [ST]-x(3)-G-[DY]-G-[KR]-[IV]-[FW]-[LIVM]-x(2)-[LIVM].
- 10 NAME: 14-3-3 proteins signature 1.  
 CONSENSUS: R-N-L-[LIV]-S-[VG]-[GA]-Y-[KN]-N-[IVA].
- NAME: 14-3-3 proteins signature 2.  
 CONSENSUS: Y-K-[DE]-S-T-L-I-[IM]-Q-L-[LF]-[RH]-D-N-[LF]-T-  
 15 [LS]-W-[TAN]-[SAD].
- NAME: ATP1G1 / PLM / MATB family signature.  
 CONSENSUS: [DNS]-x-F-x-Y-D-x(2)-[ST]-[LIVM]-[RQ]-x(2)-G.
- 20 NAME: BTG1 family signature 1.  
 CONSENSUS: Y-x(2)-[HP]-W-[FY]-[AP]-E-x-P-x-K-G-x-[GA]-[FY]-R-  
 C-[IV]-[RH]-[IV].
- NAME: BTG1 family signature 2.  
 25 CONSENSUS: [LV]-P-x-[DE]-[LM]-[ST]-[LIVM]-W-[IV]-D-P-x-E-V-  
 [SC]-x-[RQ]-x-G-E.
- NAME: Cullin family signature.  
 CONSENSUS: [LIV]-K-x(2)-[LIV]-x(2)-L-I-[DEQ]-[KRHNQ]-x-Y-  
 30 [LIVM]-x-R-x(6,7)-[FY]-x-  
 CONSENSUS: Y-x-[SA]>.
- NAME: Cullin family profile.
- 35 NAME: Enhancer of rudimentary signature.  
 CONSENSUS: Y-D-I-[SA]-x-L-[FY]-x-F-[IV]-D-x(3)-D-[LIV]-S.
- NAME: G1D protein signature 1.  
 CONSENSUS: L-C-C-x-[KR]-C-x(4)-[DE]-x-N-x(4)-C-x-C-R-V-P.  
 40
- NAME: G1D protein signature 2.  
 CONSENSUS: C-x-H-C-G-C-[KRH]-G-C-[SA].
- NAME: Glucokinase regulatory protein family signature.  
 45 CONSENSUS: G-[PA]-E-x-[LIV]-[STA]-G-S-[ST]-R-[LIVM]-K-  
 [STGA](3)-x(2)-K.
- NAME: GTP1/0BG family signature.  
 CONSENSUS: D-[LIVM]-P-G-[LIVM](2)-[DEY]-[GN]-A-x(2)-G-x-G.  
 50
- NAME: HIT family signature.  
 CONSENSUS: [NQA]-x(4)-[GAV]-x-[QF]-x-[LIVM]-x-H-[LIVMFYT]-H-  
 [LIVMFT]-H-[LIVMF](2)-  
 CONSENSUS: [PSGA].
- 55 NAME: Caseins alpha/beta signature.  
 CONSENSUS: C-L-[LV]-A-x-A-[LVF]-A.

NAME: Clathrin adaptor complexes medium chain signature 1.  
 CONSENSUS: [IVT]-[GSP]-W-R-x(2,3)-[GAD]-x(2)-[HY]-x(2)-N-x-  
 [LIVMAFY](3)-D-[LIVM]-  
 CONSENSUS: [LIVMT]-E.

5

NAME: Clathrin adaptor complexes medium chain signature 2.  
 CONSENSUS: [LIV]-x-F-I-P-P-x-G-x-[LIVMFY]-x-L-x(2)-Y.

10 NAME: Clathrin adaptor complexes small chain signature.  
 CONSENSUS: [LIVM](2)-Y-[KR]-x(4)-L-Y-F.

NAME: Ependymins signature 1.  
 CONSENSUS: F-E-E-G-x-[LIVMF]-Y-[ED]-I-D-x(2)-N-[QE]-S-C-  
 [RKH](2).

15

NAME: Ependymins signature 2.  
 CONSENSUS: [QE]-[LIVMA]-F-x(2)-P-[STA]-[FY]-C-[DE]-[GA]-  
 [LIVM]-x(2)-[DE](2).

20 NAME: Syntaxin / epimorphin family signature.  
 CONSENSUS: [RQ]-x(3)-[LIVMA]-x(2)-[LIVM]-[ESH]-x(2)-[LIVMT]-  
 x-[DEV]-[LIVM]-x(2)-  
 CONSENSUS: [LIVM]-[FS]-x(2)-[LIVM]-x(3)-[LIVT]-x(2)-Q-  
 [GADEQ]-x(2)-[LIVM]-[DNQT]-x-  
 25 CONSENSUS: [LIVMF]-[DESV]-x(2)-[LIVM].

NAME: Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7  
 signature 1.  
 CONSENSUS: [GDER]-H-[FYWH]-T-Q-[LIVM](2)-W-x(2)-[STN].

30

NAME: Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7  
 signature 2.  
 CONSENSUS: [LIVMFYH]-[LIVMFY]-x-C-[NQRHS]-Y-x-[PARH]-x-[GL]-  
 N-[LIVMFYWDN].

35

NAME: Fetuin family signature 1.  
 CONSENSUS: C-x(56)-C-x(10)-C-x(13)-C-x(17,18)-C-x(13)-C-x(2)-  
 C-x(58)-C-x(10,11)-  
 CONSENSUS: C-x(10,12)-C-x(16,22)-C.

40

NAME: Fetuin family signature 2.  
 CONSENSUS: L-E-T-x-C-H-x-L-D-P-T-P.

NAME: Legume lectins beta-chain signature.  
 45 CONSENSUS: [LIV]-[STAG]-V-[DEQV]-[FLI]-D-[ST].

NAME: Legume lectins alpha-chain signature.  
 CONSENSUS: [LIV]-x-[EDQ]-[FYWKR]-V-x-[LIV]-G-[LF]-[ST].

50 NAME: Vertebrate galactoside-binding lectin signature.  
 CONSENSUS: W-[GEK]-x-[EQ]-x-[KRE]-x(3,6)-[PCTF]-[LIVMF]-  
 [NQE GSKV]-x-[GH]-x(3)-  
 CONSENSUS: [DENKHS]-[LIVMFC].

55 NAME: Lysosome-associated membrane glycoproteins duplicated  
 domain signature.  
 CONSENSUS: [STA]-C-[LIVM]-[LIVMFYW]-A-x-[LIVMFYW]-x(3)-  
 [LIVMFYW]-x(3)-Y.



- NAME: LAMP glycoproteins transmembrane and cytoplasmic domain signature.  
 5 CONSENSUS: C-x(2)-D-x(3,4)-[LIVM](2)-P-[LIVM]-x-[LIVM]-G-x(2)-[LIVM]-x-G-[LIVM](2)-  
 CONSENSUS: x-[LIVM](4)-A-[FY]-x-[LIVM]-x(2)-[KR]-[RH]-x(1,2)-[STAG](2)-Y-[EQ].
- 10 NAME: Glycophorin A signature.  
 CONSENSUS: I-I-x-[GAC]-V-M-A-G-[LIVM](2).
- NAME: PMP-22 / EMP / MP20 family signature 1.  
 15 CONSENSUS: [LIVMF](4)-[SA]-T-x(2)-[DNKS]-x-W-x(9,13)-[LIV]-W-x(2)-C.
- NAME: PMP-22 / EMP / MP20 family signature 2.  
 CONSENSUS: [RQ]-[AV]-x-M-[IV]-L-S-x-[LI]-x(4)-[GSA]-[LIVMF](3).
- 20 NAME: Oxysterol-binding protein family signature.  
 CONSENSUS: E-[KQ]-x-S-H-[HR]-P-P-x-[STACF]-A.
- NAME: Yeast PIR proteins repeats signature.  
 25 CONSENSUS: S-Q-[IV]-[STGNH]-D-G-Q-[LIV]-Q-[AIV]-[STA].
- NAME: Seminal vesicle protein I repeats signature.  
 CONSENSUS: [IVM]-x-G-Q-D-x-V-K-x(5)-[KN]-G-x(3)-[STLV].
- 30 NAME: Seminal vesicle protein II repeats signature.  
 CONSENSUS: [GSA]-Q-x-K-S-[FY]-x-Q-x-K-[SA].
- NAME: Serum amyloid A proteins signature.  
 CONSENSUS: A-R-G-N-Y-[ED]-A-x-[QKR]-R-G-x-G-G-x-W-A.
- 35 NAME: Spermadhesins family signature 1.  
 CONSENSUS: C-G-x(2)-[LI]-x(4)-G-x-I-x(9)-C-x-W-T.
- NAME: Spermadhesins family signature 2.  
 40 CONSENSUS: C-x-K-E-x-[LIVM]-E-[LIVM]-x-[DE]-x(3)-[GS]-x(5)-K-x-C.
- NAME: Stress-induced proteins SRP1/TIP1 family signature.  
 CONSENSUS: P-W-Y-[ST](2)-R-L.
- 45 NAME: Glypicans signature.  
 CONSENSUS: C-x(2)-C-x-G-[LIVM]-x(4)-P-C-x(2)-[FY]-C-x(2)-[LIVM]-x(2)-G-C.
- NAME: Syndecans signature.  
 50 CONSENSUS: [FY]-R-[IM]-[KR]-K(2)-D-E-G-S-Y.
- NAME: Tissue factor signature.  
 CONSENSUS: W-K-x-K-C-x(2)-T-x-[DEN]-T-E-C-D-[LIVM]-T-D-E.
- 55 NAME: Translationally controlled tumor protein signature 1.  
 CONSENSUS: [IA]-G-[GAS]-N-[PA]-S-A-E-[GDE]-[PAGE]-x(0,1)-[DEG]-x-[DEN]-x(2)-[DE].

- NAME: Translationally controlled tumor protein signature 2.  
 5 CONSENSUS: [FL]-[FY]-[IVT]-G-E-x-[MA]-x(2,5)-[DEN]-[GAS]-x-  
 [LV]-[AV]-x(3)-[FY]-[KR]-  
 CONSENSUS: [DE].
- NAME: Tub family signature 1.  
 CONSENSUS: F-[KHQ]-G-R-V-[ST]-x-A-S-V-K-N-F-Q.
- 10 NAME: Tub family signature 2.  
 CONSENSUS: A-F-[AG]-I-[SAC]-[LIVM]-[ST]-S-F-x-[GST]-K-x-A-C-E.
- NAME: HCP repeats signature.  
 15 CONSENSUS: H-R-H-R-G-H-x(2)-[DE](?).
- NAME: Bacterial ice-nucleation proteins octamer repeat.  
 CONSENSUS: A-G-Y-G-S-T-x-T.
- 20 NAME: Cell cycle proteins ftsW / rodA / spoVE signature.  
 CONSENSUS: [NV]-x(5)-[GTR]-[LIVMA]-x-P-[PTLIVM]-x-G-[LIVM]-  
 x(3)-[LIVMFW](2)-S-[YSA]-  
 CONSENSUS: G-G-[STN]-[SA].
- NAME: Enterobacterial virulence outer membrane protein  
 25 signature 1.  
 CONSENSUS: G-[LIVMFY]-N-[LIVM]-K-Y-R-Y-E.
- NAME: Enterobacterial virulence outer membrane protein  
 signature 2.  
 30 CONSENSUS: [FYW]-x(2)-G-x-G-Y-[KR]-F>.
- NAME: Hydrogenases expression/synthesis hypA family  
 signature.  
 35 CONSENSUS: F-[CSA]-[FY]-[DE]-[LIVA](2)-x(3)-[ST]-[LIVM]-  
 x(1b)-C-x(2)-C-x(12,15)-  
 CONSENSUS: C-P-x-C.
- NAME: Hydrogenases expression/synthesis hupF/hupC family  
 signature.  
 40 CONSENSUS: <M-C-[LIV]-[GA]-[LIV]-P-x-[QKR]-[LIV].
- NAME: Staphylocoagulase repeat signature.  
 45 CONSENSUS: A-R-P-x(3)-K-x-S-x-T-N-A-Y-N-V-T-T-x(2)-[DN]-G-  
 x(3)-Y-G.
- NAME: 11-S plant seed storage proteins signature.  
 CONSENSUS: N-G-x-[DE](2)-x-[LIVMF]-C-[ST]-x(11,12)-[PAG]-D.
- NAME: Dehydrins signature 1.  
 50 CONSENSUS: S(5)-[DE]-x-[DE]-G-x(1,2)-G-x(0,1)-[KR](4).
- NAME: Dehydrins signature 2.  
 CONSENSUS: [KR]-[LIM]-K-[DE]-K-[LIM]-P-G.
- 55 NAME: Germin family signature.  
 CONSENSUS: G-x(4)-H-x-H-P-x-A-x-E-[LIVM].
- NAME: Oleosins signature.

CONSENSUS: [AG]-[ET]-x(2)-[AG]-x(2)-[LIVM]-[SAD]-T-P-  
[LIVMF](4)-F-S-P-[LIVM](3)-  
CONSENSUS: P-A.

5 NAME: Small hydrophilic plant seed proteins signature.  
CONSENSUS: G-[EQ]-T-V-V-P-G-G-T.

NAME: Pathogenesis-related proteins BetvI family signature.  
CONSENSUS: G-x(2)-[LIVMF]-x(4)-E-x(2)-[CSTAEN]-x(8,9)-[GND]-  
10 G-[GS]-[CS]-x(2)-K-x(4)-  
CONSENSUS: [FY].

NAME: Pollen proteins Ole e I family signature.  
CONSENSUS: [EQ]-G-x-V-Y-C-D-T-C-R.

15 NAME: Thaumatin family signature.  
CONSENSUS: G-x-[GF]-x-C-x-T-[GA]-D-C-x(1,2)-G-x(2,3)-C.

NAME: Mrp family signature.  
20 CONSENSUS: W-x(2)-[LIVM]-D-[LIVMY](4)-D-x-P-P-G-T-[GS]-D.

NAME: Glucose inhibited division protein A family signature  
1.  
CONSENSUS: [GS]-P-x-Y-C-P-S-[LIVM]-E-x-K-[LIVM]-x-[KR]-F.

25 NAME: Glucose inhibited division protein A family signature  
2.  
CONSENSUS: A-G-Q-x-[NT]-G-x(2)-G-Y-x-E-[SAG](3)-[QS]-G-  
[LIVM](2)-A-G-[LIVMT]-N-A.

30 NAME: NOL1/NOP2/sun family signature.  
CONSENSUS: [FV]-D-[KRA]-[LIVMA]-L-x-D-[AV]-P-C-[ET]-[GA].

NAME: PET112 family signature.  
35 CONSENSUS: [DN]-x-[DN]-R-x(3)-P-L-[LIV]-E-[LIV]-x-[ET]-x-P.

NAME: Protein smpB signature.  
CONSENSUS: [TA]-G-[LIVM]-x-L-x-G-x-E-[LIVM]-[KQ]-[SA]-[LIVM].

40 NAME: Hypothetical cof family signature 1.  
CONSENSUS: [LIVFYAN]-[LIVMFA]-x(2)-D-[LIVMF]-[ND]-G-T-[LIV]-  
[LVY]-[STANLM].

NAME: Hypothetical cof family signature 2.  
45 CONSENSUS: [LIVMFC]-G-D-[GSANQ]-x-N-D-x(3)-[LIMFY]-x(2)-[AV]-  
x(2)-[GSCP]-x(2)-  
CONSENSUS: [LMP]-x(2)-[GAS].

NAME: RI01/ZK632.3/MJ0444 family signature.  
50 CONSENSUS: [LIVM]-V-H-[GA]-D-L-S-E-[FY]-N-x-[LIVM].

NAME: SUA5/yci0/yrdC family signature.  
CONSENSUS: [LIVMTA](3)-[LIVMFYC]-[PG]-T-[DE]-[STA]-x-[FY]-  
[GA]-[LIVM]-[GS].

55 NAME: Uncharacterized protein family UPF0001 signature.  
CONSENSUS: [FW]-H-[FM]-[IV]-G-x-[LIV]-Q-x-[NKR]-K-x(3)-[LIV].

- NAME: Uncharacterized protein family UPF0003 signature.  
 CONSENSUS: G-x-V-x(2)-[LIV]-x(3)-[SA]-x(6)-D-x(3)-[LIVT](3)-  
 P-N-x(2)-[LIVMF](2)-  
 CONSENSUS: x(5)-N.
- 5 NAME: Uncharacterized protein family UPF0004 signature.  
 CONSENSUS: [LIVM]-x-[LIVMT]-x(2)-G-C-x(3)-C-[STAN]-[FY]-C-x-  
 [LIVM]-x(4)-G.
- 10 NAME: Uncharacterized protein family UPF0005 signature.  
 CONSENSUS: G-[LIVM](2)-[SA]-x(5,8)-G-x(2)-[LIVM]-G-P-x-L-  
 x(4)-[SAG]-x(4,6)-  
 CONSENSUS: [LIVM](2)-x(2)-A-x(3)-T-A-[LIVM](2)-F.
- 15 NAME: Uncharacterized protein family UPF0006 signature 1.  
 CONSENSUS: [LIVMFY](2)-D-[STA]-H-x-H-[LIVMF]-[DN].
- NAME: Uncharacterized protein family UPF0006 signature 2.  
 CONSENSUS: P-[LIVM]-x-[LIVM]-H-x-R-x-[TA]-x-[DE].
- 20 NAME: Uncharacterized protein family UPF0006 signature 3.  
 CONSENSUS: [LVSA]-[LIVA]-x(2)-[LIVM]-[PS]-x(3)-L-[LIVM]-  
 [LIVMS]-E-T-D-x-P.
- 25 NAME: Uncharacterized protein family UPF0007 signature.  
 CONSENSUS: V-L-[IV]-H-D-[GA]-A-R.
- NAME: Uncharacterized protein family UPF0011 signature.  
 CONSENSUS: S-D-A-G-x-P-x-[LIV]-[SN]-D-P-G.
- 30 NAME: Uncharacterized protein family UPF0012 signature.  
 CONSENSUS: [GTA]-x(2)-[IVT]-C-Y-D-[LIVM]-x-F-P-x(9)-G.
- NAME: Uncharacterized protein family UPF0015 signature.  
 CONSENSUS: [DE]-[LIVMF](3)-R-T-[SG]-G-x(2)-R-x-S-x-[FY]-  
 [LIVM](2)-W-Q.
- 35 NAME: Uncharacterized protein family UPF0016 signature.  
 CONSENSUS: E-[LIVM]-G-D-K-T-F-[LIVMF](2)-A.
- 40 NAME: Uncharacterized protein family UPF0017 signature.  
 CONSENSUS: D-x(8)-[GN]-[LFY]-x(4)-[DET]-[LY]-Y-x(3)-[ST]-  
 x(7)-[IV]-x(2)-[PS]-x-  
 CONSENSUS: [LIVM]-x-[LIVM]-x(3)-[DN]-D.
- 45 NAME: Uncharacterized protein family UPF0019 signature.  
 CONSENSUS: L-P-V-[VT]-[NQL]-F-[AT]-A-G-G-[LIV]-A-T-P-A-D-A-A-  
 [LM].
- 50 NAME: Uncharacterized protein family UPF0020 signature.  
 CONSENSUS: D-P-[LIVMF]-C-G-[ST]-G-x(3)-[LI]-E.
- NAME: Uncharacterized protein family UPF0021 signature.  
 CONSENSUS: C-K-x(2)-F-x(4)-E-x(22,23)-S-G-G-K-D.
- 55 NAME: Uncharacterized protein family UPF0023 signature.  
 CONSENSUS: D-x-D-E-[LIV]-L-x(4)-V-F-x(3)-S-K-G.

- NAME: Uncharacterized protein family UPF0024 signature.  
 5 CONSENSUS: G-x-K-D-[KR]-x-A-[LV]-T-x-Q-x-[LIVF]-[SGC].
- NAME: Uncharacterized protein family UPF0025 signature.  
 CONSENSUS: D-V-[LIV]-x(2)-G-H-[ST]-H-x(12)-[LIVMF]-N-P-G.
- NAME: Uncharacterized protein family UPF0027 signature.  
 10 CONSENSUS: Q-[LIVM]-x-N-x-A-x-[LIVM]-P-x-I-x(6)-[LIVM]-P-D-x-H-x-G-x-G-x(2)-[IV]-G.
- NAME: Uncharacterized protein family UPF0028 signature.  
 CONSENSUS: [GA]-[GS]-G-[GA]-A-R-G-x-[SA]-H-x-G-x(7)-[IV]-x-[IV]-D-x(2)-[GA]-G-x-S-  
 15 CONSENSUS: x-G.
- NAME: Uncharacterized protein family UPF0029 signature.  
 CONSENSUS: G-x(2)-[LIVM](2)-x(2)-[LIVM]-x(4)-[LIVM]-x(5)-  
 [LIVM](2)-x-R-[FYW](2)-G-  
 20 CONSENSUS: G-x(2)-[LIVM]-G.
- NAME: Uncharacterized protein family UPF0030 signature.  
 CONSENSUS: [GA]-L-I-[LIV]-P-G-G-E-S-T-[STA].
- NAME: Uncharacterized protein family UPF0031 signature 1.  
 25 CONSENSUS: [SAV]-[IVW]-[LVA]-[LIV]-G-[PNS]-G-L-[GP]-x-[DENQT].
- NAME: Uncharacterized protein family UPF0031 signature 2.  
 CONSENSUS: [GA]-G-x-G-D-[TV]-[LT]-[STA]-G-x-[LIVM].
- NAME: Uncharacterized protein family UPF0032 signature.  
 30 CONSENSUS: Y-x(2)-F-[LIVMA](2)-x-L-x(4)-G-x(2)-F-[EQ]-[LIVMF]-P-[LIVM].
- NAME: Uncharacterized protein family UPF0033 signature.  
 35 CONSENSUS: L-[DN]-x(2)-[TAG]-x(2)-C-P-x-P-x-[LIVM].
- NAME: Uncharacterized protein family UPF0034 signature.  
 CONSENSUS: [LIVM]-[DNG]-[LIVM]-N-x-G-C-P-x(3)-[LIVMASQ]-x(5)-  
 40 G-[SAC].
- NAME: Uncharacterized protein family UPF0035 signature.  
 CONSENSUS: L-L-T-x-R-[SA]-x(3)-R-x(3)-G-x(3)-F-P-G-G.
- NAME: Uncharacterized protein family UPF0036 signature.  
 45 CONSENSUS: H-x-S-G-H-[GA]-x(3)-[DE]-x(3)-[LM]-x(5)-P-x(3)-[LIVM]-P-x-H-G-[DE].
- NAME: Uncharacterized protein family UPF0038 signature.  
 50 CONSENSUS: G-x-[LI]-x-R-x(2)-L-x(4)-F-x(8)-[LIV]-x(5)-P-x-[LIV].
- NAME: Uncharacterized protein family UPF0044 signature.  
 CONSENSUS: L-[ST]-x(3)-K-x(3)-[KR]-[SGA]-x-[GA]-H-x-L-x-P-  
 55 [LIV]-x(2)-[LIV]-[GA]-  
 CONSENSUS: x(2)-G.
- NAME: Uncharacterized protein family UPF0047 signature.

CONSENSUS: S-X(2)-[LIV]-x-[LIV]-x(2)-G-x(4)-G-T-W-Q-x-[LIV].

NAME: Uncharacterized protein family UPF0054 signature.

CONSENSUS: H-[GS]-x-L-H-L-[LI]-G-[FYW]-D-H.

5

NAME: Uncharacterized protein family UPF0057 signature.

CONSENSUS: [LIV]-x-[STA]-[LIVF](3)-P-P-[LIVA]-[GA]-[IV]-x(4)-[GKN].

10

NAME: Hypothetical YER057c/yjjV family signature.

CONSENSUS: P-[AT]-R-[SA]-x-[LIVMY]-x(2)-[AK]-x-L-P-x(4)-[LIVM]-E.

15

NAME: Hypothetical hesB/yadR/yfhF family signature.

CONSENSUS: F-x-[LIVMFY]-x-N-[PG]-[NSK]-x(4)-C-x-C-[GS]-x-S-F.

NAME: Hypothetical yab0/yceC/sfhB family signature.

CONSENSUS: [NHY]-R-[LI]-D-x(2)-T-[ST]-G-[LIVMA]-[LIVMF](2)-[LIVMFG]-[SGAC].

20

#### Deposit of Clones

25

Each clone has been transfected into separate bacterial cells (*E. coli*) in the composite deposit.

30

The clones are located and publically available from the Resource Center of the German Human Genome Project (Heubner Weg 6, 14059 Berlin, GERMANY), from which each clone comprising a particular polynucleotide is obtainable. The Resource Center library numbers are slightly different than those presented here, but may be readily obtained by the following key or with the assistance of Resource Center personnel.

35

The library name becomes a number: brain (hfbr2) becomes 5b4; kidney (hfk2) becomes 5bb; mammary carcinoma (hmcfl) becomes 727; testis (htes3) becomes 434; amygdala (hamy2) becomes 7b1, melanoma (hmel2) becomes 7b2 and uterus (hutel) becomes 5bb. Next, the plate number is converted to two digits (e.g., "2" becomes "02") and is moved behind the plate coordinate, and the underscore is dropped. The following examples are helpful:

40

<u>Listed Number</u>	<u>Resource Center Number</u>
DKFZphamy2_10h17	DKFZp7b1H1710
DKFZphfbr2_78i21	DKFZp5b4I2178
DKFZphfkd2_3k1	DKFZp5bbK013
DKFZphmcf1_1c23	DKFZp727C231
DKFZhmel2_12j1	DKFZp7b2J0112
DKFZphtes3_1bb5	DKFZp434B051b
DKFZphutel_17k7	DKFZp5bbK0717

45

The libraries were constructed using two commercially available vectors. The brain (hfbr2 designations) and kidney (hfkd2 designations) libraries utilize pAMP 1 from Life Technologies and are maintained in XL-2Blue (Stratagene); the amygdala (hamy2), testes (htes3) and melanoma (hmel2) libraries are constructed in pSPORT1, also from Life Technologies, and are maintained in DH10B (Life Technologies). In addition to the following techniques, consultation with the commercial literature available on these clones will make evident all of the housekeeping techniques needed to propagate and isolate the individual constructs. All inserts may be excised with a NotI/SalI digestion. Alternatively, universal primers, flanking the cloning region, may be used to amplify the inserts using PCR methods.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. Methods of probe design are presented below.

Oligonucleotide probes may be labeled with  $^{-32}\text{P}$  ATP (specific activity 6000 Ci/mole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other, non-radioactive labeling techniques can also be used. Unincorporated label typically is removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe can be quantified by measurement in a scintillation counter. Preferably, specific activity of the resulting probe generally should be approximately  $4 \times 10^5$  dmp/pmole.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100  $\mu$ l of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 50 - 100  $\mu$ g/ml (for XL-2Blue strains 25  $\mu$ g/ml tetracycline should also be used). The culture should preferably be grown to saturation at 37°C., and the saturated culture should preferably be diluted in fresh L-broth.

Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 g/ml (for XL-2Blue strains 25 g/ml tetracycline should also be used) and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them. The filter is then preferably incubated at 65°C. for 1 hour with gentle agitation in 6 x SSC (20 x stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 g/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to  $1 \times 10^6$  dpm/mL. The filter is then preferably incubated at 65°C. with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2 x SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2 x SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1 x SSC/0.5% SDS at 65°C. for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Alternatively, clones may be grown as described above, and PCR used to isolate the insert DNAs. Methods of PCR are described below and are otherwise well known.

#### ERROR SCREENING

The DNA sequences found herein derive from individual clones, which are publicly available, as noted above. Thus, the skilled artisan will recognize that any specific sequence disclosed herein



readily can be screened for errors by resequencing a particular fragment, in both directions (i.e., by sequencing both strands). Alternatively, error screening can be performed by amplifying and/or cloning any of the inventive DNAs, using for example RT-PCR, and sequencing the resulting amplified product. In the event that there is a sequencing error, reference should be made to the deposited clone as the correct sequence.

#### USES AND BIOLOGICAL ACTIVITIES OF THE INVENTIVE MOLECULES

The inventive molecules and their derivatives are susceptible to a wide variety of uses, based on functional and/or structural properties. The skilled worker will appreciate, based on the biological activities detailed below, and discussed with regard to the individual sequences herein, that the inventive molecules will find usefulness in numerous therapeutic and diagnostic applications.

The DNA molecules, especially the potassium salts thereof, can be used as fertilizer supplements due to their high nitrogen and phosphorus contents. Since the DNAs are of defined length, they are also useful in gel electrophoresis as molecular weight markers. Due to their similarity with known molecules, certain of the DNA molecules and their variants and derivatives may be used in any number of different diagnostic procedures and therapeutic applications. They may also be used to make the encoded proteins.

The proteins themselves have many possible uses. They may be used as a nutritional supplement for humans, animals and even for laboratory use as, for example, medium for bacterial cultures. Moreover, since the proteins are of defined, known sizes, they may be used as molecular weight markers for gel electrophoresis and gel filtration. Because they are of defined sequences, they also have use in microsequencing and protein fingerprinting applications.

#### Expression Profiling Applications

Given their known tissue expression and functional associations, assemblages of the inventive proteins (or corresponding antibodies) and nucleic acids are particularly suited to expression profiling applications. Expression profiling generally entails constructing an array of indicators that signal

the presence of a particular RNA or protein expression product. Such arrays can be used to evaluate, for example, pharmacological effectiveness and toxicity. In particular, expression profiles from such arrays can be generated from cells treated with known compounds, having known properties, and these profiles can be compared to profiles of unknowns to evaluate similarities and differences, which can be correlated with efficacy or toxicity.

Additional uses of profiling include diagnosis, tracking development, and ascertaining signaling and metabolic pathways.

For examples of references describing profiling and its uses, see Farr et al., U.S. Patent 5,811,231 (1998); Seilhamer et al., U.S. Patent 5,840,484 (1998); Rine et al., U.S. Patent No. 5,777,888 (1998); WO 97/27317; WO 99/05323; WO 99/09218; and WO 99/14369. For a device for implementing such techniques, see Lipshutz et al., U.S. Patent No. 5,856,174 (1999) and Anderson et al., U.S. Patent No. 5,922,591 (1999).

In one embodiment, a subset of the inventive DNAs will be arrayed on a substrate, like a gene chip, a filter or a 96-well plate. Test samples containing cells are maintained in the presence of a label capable of incorporation into nascent mRNA. Samples are treated with test and control compounds, which will induce mRNA expression in the sample, resulting in incorporation of label. Whole mRNA is isolated and applied to the array such that it hybridizes with the DNAs contained therein. After washing, the amount of hybridization is quantified and a profile is generated. These steps are repeated with various control and test compounds, thereby generating a library of profiles, which can be used to ascertain the relationships relevant to pharmacological efficacy or toxicity.

The matrices used in such profiling, however, need not be limited to those utilizing DNAs. Rather, other nucleic acids, like RNAs and protein nucleic acids (PNAs), as well as the inventive proteins and antibodies corresponding to the inventive proteins may also be employed. Hence, for example, antibodies could form the array and the samples could be treated in order to label nascent proteins. Whole proteins then would be isolated and applied to the antibody matrix. Developing the resulting signal would result in a protein expression profile, which is useful in

essentially the same manner as the nucleic acid profile. A protein matrix could be used, for example, in evaluating antibody responses to pharmaceutical agents in order to eliminate possible cross-reactivity.

5        Moreover, where nucleic acids are used in the matrix, it is often beneficial to use variants (as defined below) of the molecules described hereinin. This can be used to account for genetic variations that are of little or no consequence to the function of the resultant gene product. Hence, they can account  
10    for wobble or conservative amino acid variations that do not perturb function, like variations in some of the protein motifs elucidated below. Thus, each position in the matrix can employ multiple nucleic acid probes that account for a series of variants.

15        Expression profiling may also be done, in another embodiment, using two-dimensional protein gels in which the inventive proteins are detected. The resultant profiles can be used in the same way as described.

20        Matrices useful for profiling may be constructed based on different criteria. Of course, the more relevant profiles will take into account expression of most human genes, preferably all of them. In certain situations, however, it is advantageous to look at a smaller subset. For example, if one were concerned about fetal neural toxicity, a fetal brain-specific matrix might  
25    be chosen. On the other hand, if one were interested in targeting mammary carcinoma tissue, a corresponding matrix could be used. Thus, matrices may be constructed using all of the sequences available from a tissue-specific library.

\* \* \*

30        The following discussion relates to some of the various functional and structural groupings that would be of interest to the artisan wishing to construct profiling matrices. Of course, the artisan will also recognized that these functional descriptions may find additional applicability in the therapeutic  
35    and diagnostic applications discussed below.

#### Cell Cycle

A proliferating cell must coordinate replication and chromosomal separation to ensure that the genome is replicated

completely, and that a single copy is correctly inherited by each daughter cell. The cell cycle is the coordinated series of events that achieves these aims. Many of the key events are initiated by a family of conserved Seiren/threonine protein kinases, the cyclin-dependent kinases (CDKs), that are activated by the cyclin family of proteins (cyclins A-H). In turn, the cyclin-CDK complexes are modulated by other protein kinases or phosphatases, and by binding specific inhibitor proteins. The enormous variety of ways in which CDK activity can be regulated allows the cell to respond to internal signals generated by preceding events in the cell cycle and to external growth signals.

The somatic cell cycle is divided into four phases: DNA replication (S phase) and chromosome separation (M phase) are separated by gap phases (G1 and G2). At specific control points the decision to begin the next stage (DNA synthesis or mitosis) is carefully regulated.

Cdc2, the primary kinase, is especially required for the G1-S transition and S phase. Cdc4 and Cdc6 are involved at the restriction point, where the cell can decide to proliferate or arrest (G1 $\leftrightarrow$ G0) and Cdc7 is a CDK activating kinase (CAK) as well as a subunit of TFIIH.

The Cyclin-CDK complexes are regulated in various ways. One is through phosphorylation by CDK activating kinases (CAK), like the Y15 kinase (Wee1) and dephosphorylation by CDK associated phosphatases (CAP), like Cdc25A a member of the Cdc25 family (Cdc25A, B and C).

An other way of regulation occurs through two classes of CDK inhibitors (CKI), the INK4 proteins p15, p16, p18, and p19, who negatively regulates the cyclin D CDK complexes and second the p21 family with p21, p27, and p57.

The cell cycle is also regulated through ubiquitin-mediated proteolysis involving the destruction of both cyclins and CDK inhibitors by the 26S proteasome, that requires an ubiquitin conjugating enzyme (UBC) and an ubiquitin ligase. The instability is conferred by PEST regions (cyclin D and E) or a ten amino acid

region in the amino terminus (degradation box) in the A- and B-type cyclins.

All these modifications play an important role for the cellular localization, because only the nuclear CDK-cyclin complexes are functional for cell cycle. During G<sub>1</sub> phase of the cell cycle, cyclins A, E and D are synthesized and bind to their cyclin-dependent kinase (CDK) partners. CDK complexes containing cyclins A, E and D<sub>1</sub> are then imported into and concentrated within nuclei. Cdk<sub>6</sub>-cyclin D<sub>3</sub> has been localized to both cytoplasmic and nuclear compartments, although only the nuclear complex is active. As cells enter S phase, cyclin A and cyclin E complexes remain within the nucleus, whereas cyclin D<sub>1</sub> relocates to the cytoplasm for proteolysis at the onset of S phase. Like Cdk<sub>2</sub>-cyclin A, Cdc<sub>2</sub>-cyclin A is nuclear and remains so until it is degraded during mitosis. By contrast, as a result of ongoing nuclear import and more rapid re-export, cyclin B<sub>1</sub>, which binds to Cdc<sub>2</sub> upon synthesis during S phase, is predominantly cytoplasmic. Cdc<sub>2</sub>-cyclin B<sub>2</sub> is also cytoplasmic, although this might occur through anchoring of the complex to some cytoplasmic constituent. At prophase, phosphorylation of cyclin B<sub>1</sub> promotes accumulation of Cdc<sub>2</sub>-cyclin B<sub>1</sub> in the nucleus, whereas cyclin B<sub>2</sub> remains in the cytoplasm until nuclear envelope breakdown.

Two crucial regulators of Cdc<sub>2</sub>-cyclin B-Wee<sub>1</sub> and Cdc<sub>25C</sub> exist and are responsible for the G<sub>2</sub> to M control point. Wee<sub>1</sub> is a nuclear protein throughout the cell cycle, whereas Cdc<sub>25C</sub> binds to 14-3-3 proteins during interphase and remains predominantly cytoplasmic. In some systems Cdc<sub>25C</sub>, like cyclin B<sub>1</sub>, rushes precipitously into the nucleus just before entry into mitosis.

The 110-kDa retinoblastoma (tumor suppressor) protein (RB), a pRB-family member is an important regulator of cell-cycle progression and differentiation. Like the E2F family (E2F<sub>1-5</sub>) or DP family (DP<sub>1-3</sub>) of transcription activators, RB suppresses inappropriate proliferation by arresting cells in G<sub>1</sub> by repressing the transcription of genes required for the transition into S phase. Before the cell proceeds into S phase, RB becomes phosphorylated at multiple sites by the cyclin dependent protein

kinases (CDKs) and loses its transcriptional repressing activity. Phosphorylation of RB during late G1 phase results in the dissociation of the E2F-RB repressor complex which allows S-phase specific genes to be transcribed. Cyclin E is the evolutionary  
5 conserved target for E2F and interacts together with CDC2 in late G1.

For a proliferating cell it is vital that only undamaged DNA is replicated because if DNA damage is substantial, its replication can lead to chromosome loss or rearrangement. Thus,  
10 we find a G1<->S checkpoint in late G1 that requires tumor suppressor p53. A p53-dependent G1 arrest is effected by the cyclin dependent kinase inhibitor p21 through higher expression levels that inhibits almost all cyclin CDK complexes.

The kinase responsible for phosphorylating the unidentified  
15 kinetochore component in metaphase may be a member of the MAP kinase family and appears to be the proto oncogene c-MOS, a cytostatic factor (CSF) in meiosis.

Several categories of proteins are coded for by clones of the invention within the overall group of "Cell cycle" and  
20 include, among others, the following:

PA26-T2 protein: PA26-T2 is a p53 responsive gene. The protein is predominantly expressed in brain, breast and kidney and represents a novel regulator of cellular growth. Isoforms are  
25 differentially induced by genotoxic stress (UV, gamma-irradiation and cytotoxic drugs) in a p53-dependent manner. The p53 tumor antigen is found in increased amounts in a wide variety of transformed cells. The protein is also detectable in many actively proliferating, nontransformed cells, but it is  
30 undetectable or present at low levels in resting cells. P53 is postulated to bind as a tetramer to a p53-binding site (PBS) and to activate the expression of adjacent genes that inhibit growth and/or invasion. Deletion or inactivation of one or both p53 alleles reduces the expression of tetramers, resulting in  
35 decreased expression of the growth inhibitory genes. This mechanism is found in tumors of several types. (OMIN \*191170)  
Clones in this category include: amy2\_121m2

Cell structure and motility

One of the major differences between prokaryotes and eukaryotes is the ability of the eukaryotic cell to adopt very different shapes dependent on its function during the differentiation process. Animal cells vary from being round to extended cylindric forms like motorneurons or muscle cells. In humans, more than 100 different cell types can be distinguished, each having a characteristic shape. The form of a cell often is closely related to its capacity to move. Some completely differentiated cells like fibroblasts can still change their form actively, thereby migrating. Other cell types serve as motor elements - "macroscopically" like muscle cells or "microscopically" like ciliated epithelia. Such tasks are fulfilled by a big class of proteins; on the one hand responsible for maintenance of cell structure and contacting neighbor cells or the intercellular matrix and on the other hand for cell motility. These topics cannot be regarded separately: The motility apparatus e.g. must be fixed in the cytoskeleton. Three different types of filaments can be distinguished: Actin filaments, tubulin filaments and intermediate filaments, each present in almost all types of cells.

Actin filaments (F-actin) are built up of monomers (G-Actin). In muscle cells, actin, myosin, for both of which several paralogous genes are known, as well as many more proteins are constituents of the contractile apparatus.

The "thin" and "thick filaments" in a muscle cell consist mainly of actin and myosin, respectively.

Several different proteins are responsible for the anchoring of the actin filaments in the Z-disks (e.g. alpha-actinin and desmin) or at the end of the myofibers in the cell membrane.

Troponin I, -C, -T and Tropomyosin - associated with actin - confer the  $Ca^{++}$ - dependent triggering of contraction.

Length of the sarcomere is controlled by the giant protein titin.

In smooth muscle, there is no troponin. Contraction activity is controlled by phosphorylation / dephosphorylation of myosin by a specialized kinase instead. Contractile fibers are not organized in sarcomeres.

Apart from contributing to muscle contraction, the actomyosin system is responsible for many other motions at cellular level, e.g. the amoeboid movement of pseudopodia or the fission of cells at the end of mitosis by a contractile ring.

Besides this, actin fibers fulfill structural tasks like maintenance of the shape of stereocilia or microvilli. Here, actin filaments are connected by proteins like fimbrin. But not only specialized structures like the mentioned ones contain actin fibers. There is a network covering the complete cell volume with F-actin as a major constituent. Whereas the actin filaments in the structures mentioned above are relatively stable, this F-actin is highly dynamic. Management of the network structure and turnover is achieved by connecting proteins like alpha-actinin, fimbrin or fil-1; turnover is regulated by gelsolin, villin, and different capping- and fragmentation-proteins.

Microtubules are built up of alpha-beta tubulin heterodimers. Turnover of filaments is achieved by building-in and releasing of monomers with different time constant rates at both ends. The resulting cycle is called "treadmilling". Thirteen strings of tubulin duplets build up one subfiber, whereas one fiber contains two or three of those. A complete axoneme consists of 9 radial and 2 central fibers. This "9+2" - structure is the basis both of flagella, their basal bodies and centrioles. In flagella, several additional structures like radial elements exist. Nexin connects the fibers and dyneine is the motor ATPase which shifts the fibers relative to each other. Several genetic diseases like the Kartagener syndrome are caused by deficiencies of distinct proteins in cilia.

Besides this, microtubules are abundant in all types of cells. They are part of a delivery system for organelles, e.g. in



the golgi apparatus. A further very important system based on microtubules is the mitotic spindle, it is organized by the centrosomes. Besides many other components, the major part of a centrosome are two centrioles which are built up of nine  
5 microtubule-triplets. Most remarkably, new centrioles are not synthesized de novo but generated by duplication of old ones.

Cytoplasmic microtubules are associated with many different proteins. Two major classes are known: The MAPs ("microtubule-associated proteins", with molecular masses between 200 and 300  
10 kD) and the much smaller tau-Proteins with a MW between 60 and 70 kD. These proteins regulate the treadmill-process and the interaction with other structures in the cell.

Besides actin and myosin the so-called intermediate filaments constitute a third class of filaments. In contrast to  
15 the former two groups, they do not participate in motility, nor are they dynamic structures subject to a vivid turnover. The most important ones are neurofilaments (in neurons), keratin filaments (mainly in epithelial cells), and vimentin filaments (in many sorts different cell types).

The biological function of both the cytoskeleton as well as contractile apparatus of a cell does not end at the cell  
20 membrane. Cells must be embedded in the extracellular matrix, all cells of a muscle must act as one single mechanical unit and epithelia must resist macroscopic mechanical forces. Hence, cell adhesion and the extracellular matrix are closely connected to  
25 the cytoskeleton. Vincullin is one of the proteins which serve as an anchor for intracellular fibers (actin). Different types of desmosomes and tight junctions connect neighbor cells with intercellular fibers. On the inside, cytoplasmic plaques connect  
30 them to the cytoskeleton. These structures, on the one hand, serve as mechanical elements whereas gap junctions, on the other hand, connect cells metabolically.

The extracellular matrix consists of a network of proteins, glycoproteins and polysaccharides. Different proteins are present  
35 in relation to different mechanical demands: Elastin is found in tissues with high elasticity (lungs, heart) whereas collagen,

a more hard-wearing protein, is found in tendons and ligaments. Fibronectin is an extracellular protein highly important for cell adhesion.

Reference: Murray J et al (1992): Cell Motil Cytoskeleton  
5 22: 211-223.

Within the overall group of Cell Structure and Motility several categories of proteins are coded for by clones of the invention:

Ankyrins: Ankyrins are peripheral membrane proteins which  
10 interconnect integral proteins with the spectrin-based membrane skeleton. Thus these proteins are involved in coupling of cyto skeleton and cell membrane. OMIM reports that Ankyrins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) Hereditary  
15 Spherocytosis (OMIM \*182900); 2) Hemolytic Poikilocytic Anemia due to reduced ankyrin binding sites (OMIM 141700); 3) Atypical Elliptocytosis (OMIM 225450); 4) Autosomal recessive spherocytosis (OMIM #270970); 5) Werner Syndrome (OMIM \*277700); and 6) Rhesus-unlinked type Elliptocytosis (OMIM #130600).  
20 Ankyrin binding glycoprotein proteins mediate Ankyrin effects, especially in neuronal adhesion and prostate tumour cell transformation: Clones in this category include: amy2\_121f19.

Tropomyosins are ubiquitous proteins of 35 to 45 kD associated with the actin filaments of myofibrils and stress  
25 fibers. They are involved in cardiomyopathies (OMIM \*191030, \*191010, \*190990, \*600317). Clones in this category include: tes3\_16b5.

### Differentiation/Development

30 Almost every multicellular organism originates from meiotic cell divisions and the recombination of a paternal and a maternal set of chromosomes. After fertilization of the egg, all cells of a body originate from this one cell. Thus the cells of the developing body are initially genetically alike. But  
35 phenotypically they become very different. They are specialized to a certain cell type and arranged in an organized pattern to a certain type of tissue and the whole structure has the well-

defined shape of an organ. All these features are determined by the DNA sequence of the genome, which is reproduced in every cell. Each cell acts on the genetic instructions given to a certain time and at a certain place of development and plays its individual part in the multicellular organism. Cell differentiation may be divided into three general steps: cell cycle exit, apoptosis protection and tissue specific gene expression. These processes are coordinated to provide the final and unique tissue characteristics.

10       An animal cell that has achieved a certain level of development is said to be determined. This differentiation of a cell may be irreversible and in that case the cell may be renewed only by simple duplication. Other cells are renewed by means of stem cells which are immortal ( e.g. stem cells of the bone marrow, epidermal stem cells). The genetic control of development is extensively studied in non-vertebrates and vertebrates. The classical animal model is the fruit fly *Drosophila* and the modern model is the transgenic mouse. Animal transgenesis has proven to be useful for physiological as well as

20       physiopathological studies. Besides the approach based on the random integration of a DNA construct in the mouse genome, gene targeting can be achieved using totipotent embryonic stem cells for targeted transgenesis. Transgenic mice are then derived from the embryonic stem cells. This allows the introduction of null mutations in the genome (so-called knock-out) or the control of the transgene expression by the endogenous regulatory sequence of the gene of interest (so-called knock-in). Mice can be created that express wild-type genes, mutant genes, marker genes or cell lethal genes in a tissue specific manner. These animal

30       models allow to follow changes in tissue and organ development and lead to a better understanding of the cellular function of many genes or to the generation of animal models for human diseases. Fundamental problems in immunology, onset and development of cancer, regulation in fatty acid metabolism, aspects of cardiovascular function, control of the central

35       nervous system development, analysis of reproductive development and function are only some examples of research interests.

The final stage of cell differentiation is growth arrest. In animal tissues with rapid cell turnover terminally differentiated cells undergo programmed cell death. The cells have the ability to kill themselves by activating an intrinsic  
5 cell suicide program when they are no longer needed or have become seriously damaged. The execution of this program is termed apoptosis. Apoptosis is of importance for development and homeostasis of animals. The key components of this program have been conserved in evolution from worms (*C. elegans*) to insects  
10 (*Drosophila*) to humans. The roles of apoptosis include the sculpting of structures during development, deletion of unneeded cells and tissues, regulation of growth and cell number, and the elimination of abnormal and potentially dangerous cells. In this way apoptosis provides "quality control mechanism" that limits  
15 the accumulation of harmful cells, such as virus-infected cells and tumor cells. On the other hand inappropriate apoptosis is associated with a wide variety of diseases, including AIDS, neuro-degenerative disorders and ischemic stroke. Because it is now clear that apoptosis is a result of an active, gene-directed  
20 process, it should be eventually possible to manipulate this form of cell death by developing drugs that interact with its recently identified mechanisms of action. Inducers of cell differentiation, cell cycle arrest and apoptosis might be the novel molecular targets for new anticancer agents in addition to  
25 the signaling pathways for growth factors and cytokines.

Proteins, factors, receptors and genes of importance in apoptosis:

Proteases:

- 30 - Calpain, an intracellular cysteine protease, exact role unknown.
- Caspase-1 to Caspase-11, a family of proteases synthesized as an inactive proenzyme. Targets of the activated enzymes include: poly(ADP-ribose) polymerase, DNA-dependent protein kinase, U1 ribonucleoprotein, nuclear laminins and cytoskeleton  
35 components (actin).

- Granzyme B, a serine protease released by cytotoxic T-cells.

Receptors:

5 - CD 95 (synonyms: Fas, AP0-1), a receptor protein of the TNF-receptor family which includes TNF-R1 and TNF-R2 with the common characteristic of a 70 amino acid cytoplasmic domain.

- FADD (synonym: MORT-1), a cytoplasmic protein

- DR-3 (synonym: AP0-3) a member of the TNF-receptor-family

- DR-4 and DR-5

10 Genes:

- ced-3, ced-4 and ced-9 encode the general apoptotic and antiapoptotic program in *Caenorhabditis elegans*. Apaf-3 is the mammalian homologue of ced-3.

15 - Bcl-2 / Bcl-xL / Bax / Bcl-xS / Bak: a large gene family that can either inhibit or promote apoptosis.

- Cytokine response modifier A, a cowpox virus gene whose gene product inhibits caspases.

Others:

20 - Caspase-activated DNase (CAD) and its inhibitor (ICAD), causes DNA fragmentation in the nucleus

- Ceramide, a complex lipid that acts as a second messenger.

- c-Jun N-terminal kinase (JNK) is a proline-directed kinase

- p53 protein, is essential for the induction of apoptosis as a response to chromosomal damage.

25 - RAIDD, a death signal-transducing protein.

- Receptor interacting protein (RIP) is an accessory protein with a death domain and a serine/threonine kinase activity.

- Sphingomyelinase, an enzyme that hydrolyzes the complex lipid sphingomyelin to ceramide.

- Tumor necrosis factor (TNF) is a type -II membrane protein

- TNF-receptor associated factor (TRAF2), is an accessory  
5 protein that can bind to both TNF-R1 and TNF-R2.

Within the overall group of Differentiation/Development, several categories of proteins are coded for by clones of the invention:

10     Notch family proteins: Notch family molecules are negative regulators of neuronal differentiation in early brain development. Clones in this category include: amy2\_1i24.

15     Testis-specific Y-encoded proteins: The TSPY genes are arranged in clusters on the Y chromosome of many mammalian species. TSPY is believed to function in early spermatogenesis and is a candidate for GBY, the putative gonadoblastoma-inducing gene on the Y. These proteins are involved in early spermatogenesis. Clones in this category include: amy2\_7j5.

20     Inflammation-mediating proteins: Inflammation is a basic mechanism responsible for recruiting and activation of immun-competent cells. By various mediators, cells are activated and triggered to differentiate. Hyperactivation of these pathways leads to various disease states: In neuronal tissues, in  
25 inflammatory diseases such as experimental autoimmune encephalomyelitis (EAE), neuritis(EAN) and uveitis (EAU) allograft inflammatory factor-1 is produced by macrophages and microglia cells. Clones in this category include: amy2\_2b19.

#### Intracellular transport and trafficking

30     Eukaryotic cells rely for their viability on the partitioning of many basic cellular processes into membrane-bounded organelles. These are the nucleus, endoplasmic reticulum (ER), Golgi apparatus, endosomes, lysosomal compartments, mitochondria and peroxisomes. Most molecules destined for the  
35 lysosome, cell surface and outside the cell are routed through

the ER and Golgi, which together with the vesicular intermediates between them, comprise the secretory pathway (Palade 1975). In the ER and Golgi compartments proteins are sorted, modified and often assembled into complexes *en route* to their final

5 destination. Incorrectly assembled proteins are retained in the ER until they fold correctly or are targeted for degradation. Additional proteins are translocated into and function within the luminal spaces of organelles or are secreted. Thus a large proportion of proteins synthesized require targeting to membranes  
10 either for insertion into or transport across them. A major purpose of this is growth. The secretory pathway is dependent on an intact cytoskeleton and also closely linked to general metabolism by affecting ribosome biogenesis (Mizuta and Warner, 1994). A huge number of proteins is required for targeting,  
15 translocation and sorting of newly synthesized proteins.

The first step in sorting is the recognition of *cis*-acting targeting or signal sequences that organelle-targeted proteins contain. This is carried out by cytosolic targeting factors and/or receptors on the membrane to which the protein is  
20 targeted. In some cases the primary sequences are extremely degenerate, with only the overall character being conserved (hydrophobicity for an ER signal sequence, helical amphiphilicity for mitochondrial targeting sequence (Kaiser et al., 1987; Lemire et al., 1989). Following the targeting step, proteins are either  
25 inserted into or transported across the membrane (translocated) through a proteinaceous apparatus (termed the translocon). The translocon include or recruit motors to drive the translocation process in the correct direction (Schatz and Dobberstein, 1996).

Defined intracellular protein transport steps:

- 30     ▪ ER
- targeting to the ER
  - translocation into the lumen of the ER, and,
- depending on the presence of certain signals in the peptide sequence transport through the golgi complex
- 35     ▪ Mitochondria
- targeting
  - translocation
- Peroxisomes

- The general secretory pathway
  - protein modification, assembly and quality control in the ER
  - vesicle-mediated trafficking
  - vesicle docking and fusion
  - transport through the golgi apparatus and sorting at the trans-golgi
  - transport to the cell surface
  - transport routes to the lysosome

- Endocytosis
- Specialized protein transport routes
- Protein export from the cytoplasm

References: Palade, G (1975) Science 189:347-358; Mizuta et al. (1994) Mol Cell Biol 14: 2493-2502; Kaiser et al. (1987) Science 235: 312-317; Lemire et al. (1989) J Biol Chem 264: 20206-20215; Schatz et al. (1996) Science 271: 1519-1526.

#### Rab proteins

In eukaryotic cells the compartmentalisation of processes is a prerequisite for a tight regulation of processes and activities. The cells contain a highly dynamic set of membrane compartments that are responsible for packaging, sorting, secreting, and recycling proteins and other molecules. Trafficking between organelles within the secretory pathway occurs as vesicles derived from a donor compartment fuse with specific acceptor membranes, resulting in the directional transfer of cargo molecules. This process is tightly controlled by the Rab/Ypt family of proteins (reviewed by Novick and Zerial, 1997), a branch of the superfamily of small GTPases. Rab proteins regulate a variety of functions, including vesicle translocation and docking at specific fusion sites. Rabs may also play critical roles in higher order processes such as modulating the levels of neurotransmitter release in neurons, a likely mechanism in synaptic plasticity that underlies learning and memory (Geppert and Südhof, 1998).

Small GTPases share a common three-dimensional fold that, in the GTP bound state, can bind a variety of downstream effector proteins. GTP hydrolysis leads to a conformational change in the "switch" regions that renders the GTPase unrecognizable to its



effectors. In this way, by localizing and activating a select set of effectors, a common structural motif is used to control a wide array of distinct cellular processes.

5 The final steps in membrane fusion are likely to be driven by a set of proteins known as SNAREs. After a vesicle becomes docked, the cytoplasmic domains of VAMP (also termed synaptobrevin) and syntaxin on opposing membranes, in combination with a SNAP-25 molecule, coalesce into an elongated  $\alpha$ -helical bundle (Poirier et al., 1998; Sutton et al., 1998), which may  
10 lead to fusion. Because numerous SNARE isoforms have been identified that localize to distinct membrane compartments, it was originally proposed that the specificity of interaction between the SNARE proteins accounted for the specificity in membrane trafficking. Recent results, however, suggest that  
15 SNAREs are not specific in their ability to form complexes in vitro, suggesting that trafficking specificity requires additional factors (Yang et al., 1999). In this regard, Rab proteins are strong candidates for governing the specificity of vesicle trafficking. Like the SNAREs, many isoforms (40) of the  
20 Rab family have been identified that localize to specific membrane compartments (reviewed by Novick and Zerial, 1997).

Concomitant with the SNARE cycle, Rab proteins undergo a intricate cycle of membrane and protein interactions. Rabs are posttranslationally modified at C-terminal cysteines by the  
25 addition of two geranylgeranyl groups, which mediate membrane association when the Rab is in the GTP-bound state. After guanine nucleotide hydrolysis occurs, the Rab is extracted from the membrane upon forming a complex with a cytosolic GDP-dissociation inhibitor (GDI). This cytosolic intermediate is then recycled  
30 onto a newly forming vesicle, most likely through a secondary factor termed a GDI dissociation factor (GDF), which displaces GDI. After the Rab becomes membrane bound, a guanidine nucleotide exchange factor (GEF) promotes release of GDP and the subsequent loading of GTP. In its GTP-bound conformation, the Rab is then  
35 free to associate with its specific set of effectors, which can in turn trigger events leading to the eventual fusion of the vesicle with a target membrane. To complete the cycle, perhaps after or concurrent with membrane fusion, a GTPase activating protein (GAP) accelerates nucleotide hydrolysis, switching off

the GTPase. The remaining GDP-bound Rab can then participate in a new round of fusion.

Rab interactions with effectors are likely to regulate vesicle targeting and membrane fusion in three ways. First, a Rab may specifically facilitate vectorial vesicle transport. Vesicles are transported from their site of origin to acceptor compartments likely through associations with cytoskeletal elements and transport motors. A protein has been identified with a domain structure that suggests a connection between the cytoskeleton and the Rabs. This protein, called Rabkinesin-b, contains a kinesin-like ATPase motor domain followed by a coiled-coil stalk region and a RBD that specifically binds Rab6 (Echard et al., 1998 ). An additional link with the cytoskeleton is provided by the Rab effector, Rabphilin-3A. Rabphilin-3A has been shown in vitro to interact with -actinin, an actin-bundling protein, but only when not bound to Rab3A (Kato et al., 1996 ). These results raise the intriguing possibility that Rab proteins regulate vesicle interactions with the cytoskeleton and thereby play an active role in targeting vesicles to their appropriate destinations.

Second, Rab proteins may regulate membrane trafficking at the vesicle docking step. A number of Rab effectors, including Rabaptin-5, EEA1, Rabphilin-3A, and Rim, may serve as molecular tethers. Each effector protein contains a RBD, followed by a linker region (some having the potential to form elongated coiled-coil structures), and a domain capable of interacting with a second Rab or the target membrane. Rabaptin-5, for example, contains two RBDs, one near the N terminus that specifically recognizes Rab4 and a second near the C terminus that binds Rab5 (Vitale et al., 1998 ). Both Rim, which is localized to the target membrane, and Rabphilin-3A, which is localized to the vesicle, contain N-terminal RBDs and C-terminal Ca<sup>2+</sup>-binding C2 domains, implicating these effectors in synaptic vesicle localization or docking in response to Ca<sup>2+</sup> influx (Wang et al., 1997 ). Tethering effectors may also recognize protein complexes on the acceptor membrane. Sec4p, a yeast Rab3A homolog, interacts with the exocyst (Guo et al., 1999 ), a complex of seven or more subunits that is assembled at sites of vesicle fusion along the

plasma membrane. The exocyst complex may therefore function as a landmark for Rab/effector-mediated vesicle docking.

Third, once a vesicle has become tethered to its fusion site, Rab proteins may selectively activate the SNARE fusion machinery. The mechanism of this activation is unknown but may involve direct interactions of Rabs or, more likely, their effectors with SNAREs. For example, Hrs-2 is a protein that binds to SNAP-25 and contains a Zn<sup>2+</sup>-finger motif characteristic of Rab-binding proteins such as Rabphilin-3A, Rim, EEA1, and Noc2, suggesting that Hrs-2 may form a physical link between Rabs and SNAREs (Bean et al., 1997). In addition, certain mutations in the syntaxin-binding protein Sly1p, the Sec1p homolog utilized in ER to Golgi trafficking, eliminate the requirement for Ypt1p, a Rab protein that functions at this trafficking step (Dascher et al., 1991). Rabs may therefore regulate SNARE associations through Sec1 family members. In support of this idea, a Rab effector was recently found to interact with a vacuole Rab, a Sec1p homolog, and a SNARE protein (Peterson et al., 1999), which suggests that this effector serves to connect Rab and SNARE function. In this way, Rabs and their effectors may facilitate the correct pairing of SNAREs.

References: Dascher et al. (1991) Mol. Cell. Biol. 11, 872-885; Echard et al. (1998). Science. 279, 580-585; Geppert et al. (1998) Annu. Rev. Neurosci. 21, 75-95; Guo et al. (1999). EMBO J. 18, 1071-1080; Kato et al. (1996) J. Biol. Chem. 271, 31775-31778; Novick et al. (1997) Curr. Opin. Cell Biol. 9, 496-504; Peterson (1999) Curr. Biol. 9, 159-162; Poirier et al. (1998) Nat. Struct. Biol. 5, 765-769; Vitale et al. (1998) EMBO J. 17, 1941-1951; Wang et al. (1997) Nature. 388, 593-598; Yang et al. (1999) J. Biol. Chem. 274, 5649-5653.

Within the overall group of Intracellular Transport and Trafficking several categories of proteins are coded for by clones of the invention.

Vesicular trafficking: Various proteins are involved in trafficking of vesicles inside the cell and for the exocytotic pathway. For example, Sec7 of *Saccharomyces cerevisiae* takes function in vesicular trafficking. Synaptotagmins are essential for Ca<sup>2+</sup>-regulated exocytosis of neurosecretory vesicles. Other proteins such as Dynamin are microtubule-associated force-

producing proteins, which are involved in the production of microtubule bundles. By binding and subsequent hydrolysis of GTP such proteins provide the motor for vesicular transport during endocytosis. Clones in this category include: amy2\_14b5,  
5 amy\_2013 and fkd2\_3k1.

Protein sorting: Protein sorting is a process essential for the maintenance of a cell's functionality and structural integrity. Most proteins perform their biological function in special compartments in the cell. The process of sorting is  
10 complex and highly regulated. Clones in this category include: mel2\_7g14.

### Metabolism

This group includes proteins which are involved in the  
15 uptake and consumption of nutrients, and enzymes which are part of the biochemical pathways for energy metabolism or which are involved in the supply of building blocks of nucleic acids, proteins (NTPs, dNTPs, amino acids) for DNA/RNA and protein  
20 synthesis, and fatty acids (membranes), to allow for the generation of higher order structures. This group constitutes the most important and largest group in prokaryotes and lower eukaryotes. The higher the evolutionary level of an organism is, however, the more other protein classes like 'signal  
transduction', 'cell cycle' and 'differentiation and development'  
25 increase in importance and number of representatives.

Proteins involved in the metabolism of energy and compounds (here: other than nucleic acids or proteins) are usually the products of house keeping genes, they are often constitutively and/or ubiquitously expressed.

30 Several categories of proteins are coded for by clones of the invention within the overall group of Metabolism:

Fatty acid metabolism: OMIM lists more than 50 diseases caused by pathologic altered fatty acid metabolism. 1-acyl-  
35 glycerol-3-phosphate acyltransferase is involved in fatty acid metabolism and is ubiquitously expressed, with a slight predominance in uterus, placenta and foreskin. Clones in this category include: amy2\_2c22

Repair and surveillance of protein damage: Several classes of protein are involved in repair and surveillance of protein damage. L-isoaspartyl methyltransferase (Pimt), as an example, is a highly conserved enzyme utilising S-adenosylmethionine (AdoMet) to methylate aspartate residues of proteins damaged by age-related isomerisation and deamidation. Clones in this category include: fbr2\_7&i21.

### Nucleic acid management

The genetic information is stored in the form of nucleic acids in all organisms. Two kinds of nucleic acids exist, DNA and RNA. Whereas the more stable DNA in most organisms constitutes the storage form of the genetic information, the labile RNA and in particular mRNA is an intermediate used for the temporal expression of specific genes.

In eukaryotes, DNA is usually a double stranded linear molecule consisting of two antiparallel strands and made up of a deoxyribose, a phosphorus backbone and the four bases A, C, G, and T. The DNA of some organisms has a ring structure. The structure of DNA was unraveled years ago by Watson and Crick. DNA is directional molecule determined by the C-atoms of the sugar.

The most important processes dealing with nucleic acids are:

- replication (e.g. DNA polymerases, Telomerase)
- transcription (RNA polymerases)
- RNA processing (maturation - splicing and degradation)
- in addition, enzymes and proteins exist which require a nucleic acid (mostly RNA) in the active center to be functional (ribozymes - e.g. RNase, Ribosomal proteins)

The DNA of a cell is replicated in the S-phase of the cell cycle. Several enzymes carry out the task of doubling this nucleic acid. As all steps of the cell cycle, also the process of replication is tightly regulated. The enzyme DNA polymerase and several other proteins are involved in this process. Whereas many prokaryotes do have only one origin of replication (i.e., the starting point of the replication cycle), in eukaryotic DNAs (chromosomes) multiple such start points exist. The switch from the synthesis (S) phase to the subsequent G2 or M phases of the cell cycle are dependent on the completion of the replication.

This makes clear, that a number of proteins are involved in the replication itself as well as in the control of the process.

Since most eukaryotic chromosomes are linear structures,

additional proteins and enzymes are necessary to make sure that

5 the structure is maintained through successive generations. This includes those proteins necessary to build the three dimensional structure of chromosomes (e.g. histones) and the structural network of the nucleus and nucleolus (including the defined localization of transcriptionally active genes in the vicinity of  
10 nucleoli) but also such enzymes as telomerase which guarantees the integrity of the chromosomal ends.

The expression of genes is usually performed in two steps.

First a messenger RNA (mRNA) is produced (transcribed) in one to many copies and second this mRNA is translated into the protein

15 product. The regulation of transcription is discussed under the separate heading 'transcription factors', but also the classes 'signal transduction', 'development', 'cell cycle' and others are affected as the expression of certain genes determines the fate of a cell or organism.

20 The primary transcript (hnRNA - heterogeneous nuclear RNA) is a single stranded one-to-one copy of the gene as it is located on the chromosome. Before a protein can be translated, already during transcription the process of maturation is initiated.

Firstly, a 5' cap structure is enzymatically and covalently added  
25 to the RNA, blocking the 5' end of the RNA. Second, when the RNA polymerase has terminated polymerization, the enzyme poly A polymerase adds varying numbers of adenine residues to the 3' end of the transcript. This enzyme recognizes the sequence AAUAAA or AUUAAA (+ some minor variations), cuts the RNA 10 - 30

30 nucleotides downstream and adds the A residues. The size of the poly A sequence affects the stability of the RNA. Finally, in the process of splicing, the introns present on the genomic level and also present in the hnRNA are spliced out by a multi-protein complex consisting of several proteins and RNAs. The finally  
35 matured mRNA is exported to the cytoplasm where it is translated with help of the ribozymes.

The half life of RNA is usually much shorter than that of DNA. Usually, the mRNA is degraded shortly after synthesis, to guarantee a very defined window of expression of a given gene.

This regulation is necessary to specifically maintain or change the set of proteins present at any time in a cell. Specific regions in the 3'UTR (untranslated region) determine the stability of the mRNA in the cytoplasm before it is degraded by RNases, enzymes consisting both of protein and RNA.

References: Watson and Crick (1953) Nature 171: 737-738.

Several categories of proteins are coded for by clones of the invention within the overall group of "Nucleic acid management" and include, among others, the following:

Proteins induced by DNA-Damage: There are several distinct pathways responsible for repair of DNA. Nucleotide excision repair is the most versatile DNA repair pathway and is the main defense of mammalian cells against UV-induced DNA damage. Defects in proteins involved in this pathway can lead to inherited disorders (such as xeroderma pigmentosum OMIM #278700, #278720, #278740 and #194400; Cockayne's syndrome OMIM #216400 and trichothiodystrophy OMIM #601675). Study of UV-sensitive yeast RAD mutants has greatly aided this process and has revealed strong conservation of the components of nucleotide excision repair in eukaryotes. Clones in this category include: amy2\_11n4 and tes3\_10i1b.

Proteins involved in Loading of transferRNAs: transfer RNAs must be coupled to an amino acid, which then is transported to the peptideyl-transferase centre of the ribosome. Clones in this category include: fbr2\_78c12.

Cytosolic ribosomal proteins: Several proteins are part of the eukaryotic ribosomal peptidyl transferase center or modulate the activity of this centre. Such proteins can find application in modulation of ribosome assembly, maintenance and activity. Clones in this category include: amy21i1

Histones: Histones are DNA-binding proteins responsible not only for DNA structure and folding and packing, but also are discussed to be involved in activation and silencing of large chromosomal regions. Clones in this category include: tes3\_31a10.

mRNA-binding proteins: mRNA-binding proteins are involved in regulation of mRNA folding, translation and stability. For example, the VILIP protein binds specifically to the

3'untranslated region of the neurotrophin receptor mRNA. Clones in this group include amy2\_2g12.

### Signal transduction

Cells in higher order organisms need to continuously communicate with its environment especially with other cells of the same organism in order to maintain the function and specialization of the whole system these cells are part of. This important task of communication is performed with help of cell-surface receptors which receive and transmit signals from outside into the cell.

#### G-proteins

The largest known family of cell-surface receptors is that of the G-protein-coupled receptors, which mediate the transmission of diverse stimuli such as neurotransmitters, glycopeptides, hormones, peptides, odorant molecules, and photons. The functional unit of these receptors is composed of the receptor molecule itself (GPCR) which is anchored in the cytoplasmic membrane with seven membrane spanning domains, the heterotrimeric G-protein which is composed of  $\alpha$  and  $\beta$ -subunits (G and G $\beta$ ), and the effectors that interact with G $\alpha$  and / or G $\beta$ . In particular, the dissociated G $\alpha$  and G $\beta$  can regulate the activities of a number of effector molecules such as adenylate cyclases, phospholipase C isoforms, ion channels, and tyrosine kinases, resulting in a variety of cellular functions. The process of signal transduction must be tightly regulated and reversible in order to avoid overstimulation, to achieve signal termination, and render the receptor responsive to subsequent stimuli [Iacovelly L. et al., (1999) *FASEB J.* 13, 1-8, Hamm, H.E. (1998) *J. Biol. Chem.* 273, 669-672].

G-proteins are GTPases that, upon binding of GTP change their conformation which in return unmasks structural motives, in particular the so called effector loop, which can mediate the interactions to target proteins, or effectors, for the GTPases. This ability enables the GTPases to cycle between active, GTP-bound and inactive, GDP bound conformations and in the process to function as molecular traffic lights in a multitude of signal transduction pathways. The most important of these signal transduction pathways that are regulated with help of G-proteins



are that of the phospholipase C / protein kinase C and that of the adenylate cyclase / protein kinase A.

The cycling of GTPases is tightly regulated by three main classes of proteins: The exchange of hydrolyzed GDP for a fresh GTP is facilitated by guanosine nucleotide exchange factors (GEFs), the hydrolysis of GTP to GDP is sped up by GTPase-activating proteins (GAPs), and the dissociation of GDP from the GTPases is inhibited by GDP dissociation inhibitors (GDIs) [Tapon and Hall (1997) *Curr.Opin. Cell. Biol.* 9, 86-92, Van Aelst and D-Souza-Schorey (1997) *Genes Dev.* 11, 2295-2322].

#### S0CS-family

A conserved motif that was originally identified in proteins that negatively regulate the signaling action of cytokines was termed S0CS box, the Suppressor Of Cytokine Signaling. Based on homology, five distinct structural protein classes have been identified since that carry this motif. The function of most of these proteins is presently not known. Common to the proteins is only the S0CS box which is located near the C-terminus of the respective peptides. Recently, the S0CS box has been demonstrated to induce binding of proteins to elongins B and C which could target the proteins (and bound substrates) to the proteasomal protein degradation pathway (Kamura, T. et al. (1998) *Genes Dev.* 12, 3872-3881; Zhang, J.-G. et al. (1999) *Proc. Natl. Acad. Sci. USA* 96, 2071-2076).

The class where the S0CS box was originally described contains several members (S0CS-1-S0CS-7 and CIS). In addition to the S0CS box, these proteins also contain a SH2 (Src-homology 2) domain and a variable N-terminus. These S0CS proteins appear to form part of a classical negative feedback loop that regulates cytokine signal transduction. Upon cytokine stimulation, expression of S0CS proteins is rapidly induced and the proteins inhibit further cytokine action. The mode of action of the S0CS proteins is variable. While S0CS-1 binds and inhibits the JAK (Janus kinases) family of cytoplasmic protein kinases [Narazaki M. et al. (1998) *Proc. Natl. Acad. Sci. USA* 95, 13130-13134, Nicholson, S.E. et al. (1999) *EMBO. J.* 18, 375-385], CIS appears to act by competing with signaling molecules such as the STATs (Transducers and Activators of Transcription) family for binding

to phosphorylated receptor cytoplasmic domains [Yoshimura, A. et al. (1995) *EMBO J.* 14, 2816-2826; Matsumoto, A. et al. (1997) *Blood* 89, 3148-3154].

A second class of SOCS box protein contains additionally WD-40 repeats which were initially identified in the mouse WSB-1 and -2 proteins. The functions of WD-40 proteins are not completely understood but seem to be rather divergent. In Cdc4p the WD-40 repeats probably are necessary for binding the substrate for Cdc34p [Mathias, N. et al. (1999) *Mol. Cell Biol.* 19, 1759-1767].

Cdc4p is a component of a ubiquitin ligase that tethers the ubiquitin-conjugating enzyme Cdc34p to its substrates. The posttranslational modification of a protein by ubiquitin usually results in rapid degradation of the ubiquitinated protein by the proteasome. The transfer of ubiquitin to substrate is a multistep process where WD-40 repeats might play an important function.

Other WD-40 containing proteins (e.g. the retino blastoma binding protein RbAp48) have been shown to bind metal ions (Zinc) and that this metal binding might mediate and/or regulate protein-protein interactions which are functionally important in chromatin metabolism [Kenzior, A.L. and Folk, W.R. (1998) *FEBS Lett.* 440, 425-429]. These proteins are involved in the RAS-cAMP pathway that regulates cellular growth [Ach R.A. et al. (1997) *Plant Cell* 9, 1595-1606].

The SPRY domain has been identified in pyrin or marenostrin, a protein which is mutated in patients with Mediterranean fever and which is similar to the butyrophilin family. While butyrophilins seem to be involved in the lactation process in mammals, the function pyrin is unknown. Three proteins (SSB-1 to -3) have been identified to contain both SPRY and SOCS box motifs. The function of these proteins is also not known.

Ankyrin repeat containing proteins share a 33-residue repeating motif, an L-shaped structure with protruding -hairpin tips which mediate specific macromolecular interactions with cytoskeletal, membrane, and regulatory proteins. These proteins play fundamental roles in diverse biological activities including growth and development, intracellular protein trafficking, the establishment and maintenance of cellular polarity, cell adhesion signal transduction, and mRNA transcription. Three proteins that

contain ankyrin repeats (ASB-1 to -3) have been identified to contain a C-terminal SOCS box additionally to the ankyrin repeats. The function of these proteins or the individual domains remains to be discovered [Hilton, D.J. et al. (1998) *Proc. Natl.*

5 *Acad. Sci. USA* 95, 114-119].

A few small GTPases (RAR and RAR like) do also contain a SOCS box. GTPases are involved in signal transduction during cellular communication. The function of the SOCS box in this type of proteins is currently unclear [Hilton, D.J. et al. (1998)

10 *Proc. Natl. Acad. Sci. USA* 95, 114-119].

#### Ca<sup>2+</sup> as second messenger

The bivalent cation Ca<sup>2+</sup> is, besides cAMP, one of the two major second messengers in eukaryotic cells. Its intracellular concentration is tightly regulated and usually kept very low compared to the cell's environment. Ca<sup>2+</sup> binding proteins and transporters (Gap junction, Voltage-gated, second messenger-gated) help to sequester huge amounts of the ion in various organelles from where Ca<sup>2+</sup> can be released upon extracellular stimuli. E.g. the contraction of the muscle is dependent on the presence of Ca<sup>2+</sup> ions which are readily transported back into the organelles in order for the muscle to relax. In signal transduction, Ca<sup>2+</sup> functions as a second messenger that activates Ca<sup>2+</sup> dependent processes through the activation of Ca<sup>2+</sup>/calmodulin dependent protein kinases (CaM kinases) which are the major effector molecules of Ca<sup>2+</sup>. In the signaling cascades, the CaM dependent kinases activate phospholipases (e.g. phospholipase C) that in return activate other protein kinases such as protein kinase C.

#### cAMP

30 The cyclic AMP is produced by the enzyme adenylate cyclase in response to extracellular signals. Certain G-proteins stimulate the activity of adenylate cyclase which converts ATP to cAMP and PPi. Two molecules of cAMP bind to each of two regulatory subunits of cAMP dependent protein kinase which in turn dissociate from the two catalytic subunits of the heterotetramer R<sub>2</sub>C<sub>2</sub>. Upon release of the C-subunits, they become active and phosphorylate substrate proteins at Ser and Thr residues. The process leading from binding of extracellular

molecules to their receptors, the transmission of the stimuli into the cell, the activation of adenylate cyclase and the subsequent activation of cAMP dependent protein kinase is one of two major signal transduction pathways in eukaryotic cells. Since the phosphorylation of proteins is a posttranslational modification of proteins, the kinases are described in the class "signal transduction."

#### SARA

Members of the transforming growth factor  $\beta$  (TGF $\beta$ ) superfamily signal through a family of cell-surface transmembrane serine/threonine kinases, known as type I and type II receptors (Heldin et al., 1997 ; Attisano and Wrana, 1998 ; Kretzschmar and Massagué, 1998). Ligand induces formation of heteromeric complexes of these receptors, and signaling is initiated when receptor I is phosphorylated and activated by the constitutively active kinase of receptor II (Wrana et al., 1994 ). The activated type I receptor kinase then propagates the signal to a family of intracellular signaling mediators known as Smads (contraction of the C.elegans Sma and Drosophila Mad genes which were the first identified members of this class of signaling effectors).

Three classes of Smads with distinct functions have been defined: the receptor-regulated Smads, which include Smad1, 2, 3, 5, and 8; the common mediator Smad, Smad4; and the antagonistic Smads, which include Smad6 and 7 (Heldin et al., 1997; Attisano and Wrana, 1998 ; Kretzschmar and Massagué, 1998 ). Receptor-regulated Smads (R-Smads) act as direct substrates of specific type I receptors, and the proteins are phosphorylated on the last two serines at the carboxyl terminus within a highly conserved SSXS motif (Macías-Silva et al., 1996 ; Abdollah et al., 1997 ; Kretzschmar et al., 1997 ; Liu et al., 1997b ; Souchelnytskyi et al., 1997 ). Regulation of R-Smads by the receptor kinase provides an important level of specificity in this system. Thus, Smad2 and Smad3 are substrates of TGF $\beta$  or activin receptors and mediate signaling by these ligands (Macías-Silva et al., 1996 ; Liu et al., 1997b ; Nakao et al., 1997 ), whereas Smad1, 5, and 8 are targets of BMP receptors and propagate BMP signals (Hoodless et al., 1996 ; Chen et al., 1997b ; Kretzschmar et al., 1997 ; Nishimura et al., 1998 ). Once phosphorylated, R-Smads associate with the common Smad, Smad4 (Lagna et al., 1996 ; Zhang et al.,

1997 ), and mediate nuclear translocation of the heteromeric complex. In the nucleus, Smad complexes then activate specific genes through cooperative interactions with DNA and other DNA-binding proteins such as FAST1, FAST2, and Fos/Jun (Chen et al., 1996 ; Chen et al., 1997a ; Liu et al., 1997a ; Labbé et al., 1998 ; Zhang et al., 1998 ; Zhou et al., 1998 ). In contrast to R-Smads and Smad4, the antagonistic Smads, Smad6 and 7, appear to function by blocking ligand-dependent signaling (reviewed in Heldin et al., 1997 ).

Phosphorylation of R-Smads by the type I receptor is essential for activating the TGF $\beta$  signaling pathway (Heldin et al., 1997 ; Attisano and Wrana, 1998 ; Kretzschmar and Massagué, 1998 ). However, little is known of how Smad interaction with receptors is controlled. A novel Smad2/Smad3 interacting protein has been described (Tsukazaki T. et al., 1998 ) that contains a double zinc finger, or FYVE domain, and which has been called SARA (Smad anchor for receptor activation). The SARA motif recruits Smad2 into distinct subcellular domains and co-localizes and interacts with TGF $\beta$  receptors. TGF $\beta$  signaling induces dissociation of Smad2 from SARA with concomitant formation of Smad2/Smad4 complexes and nuclear translocation. Moreover, deletion of the FYVE domain in SARA causes mislocalization of Smad2 and inhibits TGF $\beta$ -dependent transcriptional responses. Thus, SARA defines a component of TGF $\beta$  signaling that functions to recruit Smad2 to the receptor by controlling the subcellular localization of Smad.

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Curr. Biol. 7, 270-276; Zhang et al. (1998) Nature 394, 909-  
5 913; Zhou et al. (1998) Mol. Cell 2, 121-127.

### Calcium

The bivalent cation  $\text{Ca}^{2+}$  is, along with cAMP, one of the two  
major second messengers in eukaryotic cells. Its intracellular  
10 concentration is tightly regulated and usually kept very low  
compared to the cell's environment.  $\text{Ca}^{2+}$  binding proteins and  
transporters (Gap junction, Voltage-gated, second messenger-  
gated) help to sequester huge amounts of the ion in various  
organelles from where  $\text{Ca}^{2+}$  can be released upon extracellular  
15 stimuli. E.g. the contraction of the muscle is dependent on the  
presence of  $\text{Ca}^{2+}$  ions which are readily transported back into the  
organelles in order for the muscle to relax. In signal  
transduction,  $\text{Ca}^{2+}$  functions as a second messenger that activates  
 $\text{Ca}^{2+}$  dependent processes through the activation of  $\text{Ca}^{2+}$ /calmodulin  
20 dependent protein kinases (CaM kinases) which are the major  
effector molecules of  $\text{Ca}^{2+}$ . In the signaling cascades, the CaM  
dependent kinases activate phospholipases (e.g. phospholipase C)  
that in return activate other protein kinases such as protein  
kinase C.

### 25 Rab proteins

In eukaryotic cells the compartmentalization of processes is  
a prerequisite for a tight regulation of processes and  
activities. The cells contain a highly dynamic set of membrane  
compartments that are responsible for packaging, sorting,  
30 secreting, and recycling proteins and other molecules.  
Trafficking between organelles within the secretory pathway  
occurs as vesicles derived from a donor compartment fuse with  
specific acceptor membranes, resulting in the directional  
transfer of cargo molecules. This process is tightly controlled  
35 by the Rab/Ypt family of proteins (reviewed by Novick and Zerial,  
1997 ), a branch of the superfamily of small GTPases. Rab  
proteins regulate a variety of functions, including vesicle  
translocation and docking at specific fusion sites. Rabs may also  
play critical roles in higher order processes such as modulating

the levels of neurotransmitter release in neurons, a likely mechanism in synaptic plasticity that underlies learning and memory (Geppert and Südhof, 1998 ).

5 Small GTPases share a common three-dimensional fold that, in the GTP bound state, can bind a variety of downstream effector proteins. GTP hydrolysis leads to a conformational change in the "switch" regions that renders the GTPase unrecognizable to its effectors. In this way, by localizing and activating a select set of effectors, a common structural motif is used to control a wide  
10 array of distinct cellular processes.

The final steps in membrane fusion are likely to be driven by a set of proteins known as SNAREs. After a vesicle becomes docked, the cytoplasmic domains of VAMP (also termed synaptobrevin) and syntaxin on opposing membranes, in combination  
15 with a SNAP-25 molecule, coalesce into an elongated  $\alpha$ -helical bundle (Poirier et al., 1998 ; Sutton et al., 1998 ), which may lead to fusion. Because numerous SNARE isoforms have been identified that localize to distinct membrane compartments, it was originally proposed that the specificity of interaction  
20 between the SNARE proteins accounted for the specificity in membrane trafficking. Recent results, however, suggest that SNAREs are not specific in their ability to form complexes in vitro, suggesting that trafficking specificity requires additional factors (Yang et al., 1999 ). In this regard, Rab  
25 proteins are strong candidates for governing the specificity of vesicle trafficking. Like the SNAREs, many isoforms (40) of the Rab family have been identified that localize to specific membrane compartments (reviewed by Novick and Zerial, 1997 ).

Concomitant with the SNARE cycle, Rab proteins undergo a  
30 intricate cycle of membrane and protein interactions. Rabs are posttranslationally modified at C-terminal cysteines by the addition of two geranylgeranyl groups, which mediate membrane association when the Rab is in the GTP-bound state. After guanine nucleotide hydrolysis occurs, the Rab is extracted from the  
35 membrane upon forming a complex with a cytosolic GDP-dissociation inhibitor (GDI). This cytosolic intermediate is then recycled onto a newly forming vesicle, most likely through a secondary factor termed a GDI dissociation factor (GDF), which displaces GDI. After the Rab becomes membrane bound, a guanidine nucleotide

exchange factor (GEF) promotes release of GDP and the subsequent loading of GTP. In its GTP-bound conformation, the Rab is then free to associate with its specific set of effectors, which can in turn trigger events leading to the eventual fusion of the vesicle with a target membrane. To complete the cycle, perhaps after or concurrent with membrane fusion, a GTPase activating protein (GAP) accelerates nucleotide hydrolysis, switching off the GTPase. The remaining GDP-bound Rab can then participate in a new round of fusion.

Rab interactions with effectors are likely to regulate vesicle targeting and membrane fusion in three ways. First, a Rab may specifically facilitate vectorial vesicle transport. Vesicles are transported from their site of origin to acceptor compartments likely through associations with cytoskeletal elements and transport motors. A protein has been identified with a domain structure that suggests a connection between the cytoskeleton and the Rabs. This protein, called Rabkinesin-b, contains a kinesin-like ATPase motor domain followed by a coiled-coil stalk region and a RBD that specifically binds Rab6 (Echard et al., 1998 ). An additional link with the cytoskeleton is provided by the Rab effector, Rabphilin-3A. Rabphilin-3A has been shown in vitro to interact with -actinin, an actin-bundling protein, but only when not bound to Rab3A (Kato et al., 1996 ). These results raise the intriguing possibility that Rab proteins regulate vesicle interactions with the cytoskeleton and thereby play an active role in targeting vesicles to their appropriate destinations.

Second, Rab proteins may regulate membrane trafficking at the vesicle docking step. A number of Rab effectors, including Rabaptin-5, EEA1, Rabphilin-3A, and Rim, may serve as molecular tethers. Each effector protein contains a RBD, followed by a linker region (some having the potential to form elongated coiled-coil structures), and a domain capable of interacting with a second Rab or the target membrane. Rabaptin-5, for example, contains two RBDs, one near the N terminus that specifically recognizes Rab4 and a second near the C terminus that binds Rab5 (Vitale et al., 1998 ). Both Rim, which is localized to the target membrane, and Rabphilin-3A, which is localized to the vesicle, contain N-terminal RBDs and C-terminal  $\text{Ca}^{2+}$ -binding C2



domains, implicating these effectors in synaptic vesicle localization or docking in response to  $Ca^{2+}$  influx (Wang et al., 1997). Tethering effectors may also recognize protein complexes on the acceptor membrane. Sec4p, a yeast Rab3A homolog, interacts with the exocyst (Guo et al., 1999), a complex of seven or more subunits that is assembled at sites of vesicle fusion along the plasma membrane. The exocyst complex may therefore function as a landmark for Rab/effector-mediated vesicle docking.

Third, once a vesicle has become tethered to its fusion site, Rab proteins may selectively activate the SNARE fusion machinery. The mechanism of this activation is unknown but may involve direct interactions of Rabs or, more likely, their effectors with SNAREs. For example, Hrs-2 is a protein that binds to SNAP-25 and contains a  $Zn^{2+}$ -finger motif characteristic of Rab-binding proteins such as Rabphilin-3A, Rim, EEA1, and Noc2, suggesting that Hrs-2 may form a physical link between Rabs and SNAREs (Bean et al., 1997). In addition, certain mutations in the syntaxin-binding protein Sly1p, the Sec1p homolog utilized in ER to Golgi trafficking, eliminate the requirement for Ypt1p, a Rab protein that functions at this trafficking step (Dascher et al., 1991). Rabs may therefore regulate SNARE associations through Sec1 family members. In support of this idea, a Rab effector was recently found to interact with a vacuole Rab, a Sec1p homolog, and a SNARE protein (Peterson et al., 1999), which suggests that this effector serves to connect Rab and SNARE function. In this way, Rabs and their effectors may facilitate the correct pairing of SNAREs.

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### Kinases

Reversible posttranslational modifications of proteins are major means of regulating cellular activities. Among the various modifications that are carried out by the cells, the addition of phosphoryl groups to Ser/Thr or Tyr residues is the most

5 important and widely used. The phosphorylation of proteins is accomplished by protein kinases, while the reverse reaction, the removal of phosphoryl groups, is carried out by phosphatases. Kinases / Phosphatases regulate key positions e.g. in the processes of cell proliferation, differentiation and  
10 communication/signaling. These processes must be tightly regulated in order to maintain a steady state level of cellular fate. Mis-regulation of kinase activities (or that of phosphatases) is made responsible for a multitude of disease processes such as oncogenesis, inflammatory processes,  
15 arteriosclerosis, and psoriasis.

Protein kinases constitute the largest protein family that is currently known. Several hundred kinases have been identified already. Classically, kinases are subdivided into two classes based on the amino acid residues in their substrates that are  
20 phosphorylated by the particular enzymes. The kinases specifically add phosphoryl groups from adenosine triphosphate (ATP) or, less frequently, guanosine triphosphate (GTP), either to serine and/or threonine or to tyrosine residues of substrate proteins. An estimated 1,000 to 10,000 proteins present in a  
25 typical mammalian cell are believed to be regulated also by the action of protein kinases.

Protein kinases are frequently integral parts of signaling cascades that transmit extracellular stimuli (e.g. hormones, neurotransmitters, growth- or differentiation factors) into the  
30 cell and result in various responses by the cells. The kinases play key roles in these cascades as they constitute a sort of 'molecular switches' turning on or off the activities of other enzymes and proteins, e.g. metabolic, regulatory, channels and pumps, receptors, cytoskeletal, transcription factors.

35 The regulation of kinase activities is accomplished by various means:

The best characterized example for the regulation via regulatory subunits is the cAMP-dependent protein kinase (PKA) which is also a prototype for second messenger activated protein

kinases. This enzyme consists of a heterotetramer of two catalytic (C) and two regulatory (R) subunits. Upon binding of two molecules of second messenger (cAMP) in each R subunit, the catalytic subunits are released and active. Both of the catalytic and the regulatory subunits several isoforms exist. The combination of catalytic and regulatory subunits determines the localization of the holoenzyme and also the substrate spectrum that is available for phosphorylation. The consensus pattern necessary to be present in the substrate for PKA action is RRXS/T where X can be any amino acid.

The casein kinase II comprises another examples for holoenzymes that consist of catalytic and regulatory subunits. Other kinases that are activated by second messengers are cGMP-dependent protein kinase and Protein kinase C (PKC) which is activated by diacylglycerol, which in turn is produced by phospholipases by cleavage of phosphatidylcholine.

Receptor kinases usually consists of an extracellular domain which can bind effector molecules (e.g. growth factors and hormones) and transfer the stimulus to the intracellular domain of these proteins which usually is a protein tyrosine kinase. Other tyrosine kinases lack an extracellular domain but are associated with receptors which transfer the signal after effector binding by activating the associated protein kinase enzyme (e.g. Src kinase family; Src, Blk, Fgr, Fyn, Lck Lyn, Yes and Janus kinase family; Jak1-3, Tyk2).

Dysfunction of kinases, e.g. caused by non-functioning regulation, can be the cause of inflammatory diseases and uncontrolled proliferation. v-Src which is a truncated version of the C-Src protooncogene tyrosine kinase is a classical example for this process as v-Src does not contain the regulatory domain of the cellular gene and is thus constitutively active.

Several categories of proteins are coded for by clones of the invention within the overall group of "Signal transduction" and include, among others, the following:

Discs-large family: In *Drosophila* more than 50 genes are described in which mutation leads to loss of cell proliferation control indicating that they are tumor suppressor genes. Most of

these genes have mammalian homologs. The *Drosophila* 'discs large' tumor suppressor protein, Dlg, is the prototype of a family of proteins termed MAGUKs (membrane-associated guanylate kinase homologs). MAGUKs are localized at the membrane-cytoskeleton interface, usually at cell-cell junction, where they appear to have both structural and signaling roles. They contain several distinct domains, including a modified guanylate kinase domain, an SH3 motif, and 1 or 3 copies of the DHR (GLGF/PDZ) domain. Recessive lethal mutations in the 'discs large' tumor suppressor gene interfere with the formation of septate junctions (thought to be the arthropod equivalent of tight junctions) between epithelial cells, and they also cause neoplastic overgrowth of imaginal discs, suggesting a role for cell junctions in proliferation control. These proteins can find application in modulating/blocking the guanylate cyclase-pathway. Clones in this category include: amy2\_12d7.

Proteins with a WW Domain: Proteins that contain a WW domain which has been originally described as a short conserved region in a number of unrelated proteins, among them dystrophin, the gene responsible for Duchenne muscular dystrophy. The domain, which spans about 35 residues, is repeated up to 4 times in some proteins. It has been shown to bind proteins with particular proline-motifs, [AP]-P-P-[AP]-Y, and thus resembles somewhat SH3 domains. This domain is frequently associated with other domains typical for proteins in signal transduction processes. Examples of proteins containing the WW domain are Dystrophin, Utrophin, vertebrate YAP protein (binds the SH3 domain of the Yes oncoprotein), murine NEDD-4 (embryonic development and differentiation of the central nervous system), IQGAP (human GTPase activating protein acting on ras). Therefore these proteins should be involved in intracellular signal transduction. Diseases associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with these proteins include as reported by OMIM 1) Muscular Dystrophy, Pseudohypertrophic Progressive Duchenne and Becker Types (OMIM \*310200). Clones in this category include: tes3\_11d21.

Ion-Transporters: For signalling stringent control of ion fluxes over biological membranes is of the essence. Several trans-membrane ion-channel-proteins key elements of signal transduction pathways. Clones in this category include: amy2\_10p7  
5 and amy2\_2f18.

RING-finger proteins: A Zinc finger motif of the C3HC4 type (the so-called RING finger domain) is involved in mediating protein-protein interactions. Proteins containing a RING-finger are: mammalian V(D)J recombination activating protein (RAG1),  
10 mouse rpt-1, human rfp, human 52 Kd Ro/SS-A protein and others. The family of RING finger proteins contains a number of oncogenes. For example PML, a probable transcription factor, BRCA1, the mammalian cbl- and bmi-1 proto-oncogenes. Clones in this category include: amy2\_10h17.

15 Phosphatases: Proper targeting of PTPs is essential for many cellular signalling events including antigen induced proliferative responses of B and T cells. The physiological significance of PTPs is further unveiled through mice gene knockout studies and human genome sequencing and mapping  
20 projects. Several PTPs are shown to be critical in the pathogenesis of human diseases, as shown by over 290 entries in OMIM. Clones in this category include: tes3\_31j20.

Phosphoproteins: Some paraneoplastic syndromes affecting the nervous system are associated with antibodies that react with  
25 neuronal proteins and the causal tumor (onconeurological antigens). Several of these antibodies are markers of specific neurologic syndromes associated with distinct types of cancer. One of the antigens recognised by such antibodies is Ma-1, the neuron- and testis-specific protein 1. The expression of Mal mRNA is highly  
30 restricted to the brain and testis. Subsequent analysis suggested that Mal is likely to be a phosphoprotein (see OMIM \*604010). Clones in this category include: tes3\_5k22.

#### Transmembrane proteins

Membrane region prediction was effected using the ALOM2  
35 software (Klein et al., 1985; version 2 by K. Nakai). Similar to

many other methods, the Kyte & Doolittle (1982) amino acid hydrophobicity scale is used in ALOM2 as the primary variable for classifying sequences in terms of their localization. High prediction accuracy is achieved through the system of intelligent  
 5 decision rules and the utilization of a carefully selected training data set. The method also generates reliability estimates which makes it possible to distinguish between membrane-spanning proteins (I, intrinsic) and globular proteins with regions of high hydrophobicity buried in the core.

- 10 For a protein of length  $L$ , the block of length  $l$  with maximum hydrophobicity is found:

$$\max H = \max_{k=1, \dots, L-l+1} (1/l) \sum_{i=k}^{k+l-1} H_i$$

where  $H_i$  represents the hydrophobicity of an individual residue.

- 15 Let  $P(I/\max H)$  and  $P(E/\max H)$  be the conditional probabilities that a protein is integral or peripheral, respectively, given its value of maximal hydrophobicity  $\max H$ , and let  $P(I)$  and  $P(E)$  be the prior probabilities of intrinsic and extrinsic membrane proteins estimated from the training set. Then a sequence is  
 20 assigned to E if

$$P(E/\max H) > P(I/\max H)$$

or, after applying the Bayes rule,

$$P(E)P(\max H/E) > P(I)P(\max H/I),$$

- where the conditional probabilities  $P(\max H/E)$  and  $P(\max H/I)$   
 25 can be determined based on the estimates of probability distributions of  $\max H$  in both groups.

- Discriminant analysis allows to simplify this task by calculating the odds  $P(E/\max H):P(I/\max H)$  as  $e^b$ , where  $b$  is the left-hand side of a linear or quadratic inequality. For example,  
 30 for the window of length 17, the protein is allocated to the

peripheral category E based on the empirically derived quadratic inequality:

$$1.05(\max H)^2 + 12.30\max H + 17.49 > 0,$$

whereas the optimal inequality for assigning membrane  
5 proteins (category I) is linear:

$$-9.02\max H + 14.27 > 0$$

The odds parameter can be made more or less stringent. For example, one can require odds at least 1:10 for a protein to be classified as integral. This leads to higher selectivity but less  
10 sensitivity.

The boundaries of membrane-spanning regions in putative membrane proteins are detected by means of an iterative procedure whereby the most hydrophobic region corresponding to the value  $\max H$  is considered to be membrane and removed from the sequence.  
15 The classification procedure is then repeated again for the remaining sequence, and, if such a protein is again classified as integral, the next most hydrophobic region is considered.

Reference: Klein, P., Kanehisa, M., DeLisi, C. (1985) The detection and classification of membrane-spanning proteins.  
20 *Biochem Biophys Acta* 815: 468-476

### Transcription factors

Purified eukaryotic RNA polymerase II is unable to initiate promoter-specific transcription. A family of factors that collectively confer RNAPII promoter specificity is known as the  
25 general transcription factors (GTFs). They include the TATA-binding Protein (TBP) TFIIB, TFIIE, TFIIIF and TFI IH. These factors are conserved among all eukaryotes.

RNAPII complexes containing the entire set of GTFs or a subset of GTFs together with other proteins have been isolated  
30 from mammalian and yeast cells. Although purified RNAPII and GTFs are sufficient for promoter-specific initiation, this system fails to respond to activators. This is mediated by a further complex termed mediator complex which associates with the

carboxy-terminal heptapeptide domain (CTD) of the largest subunit of RNAPII.

Purification of human RNAPII complexes resulted in two distinct forms of human RNAPII after analysis of functional properties. One complex contained chromatin remodeling activities but was devoid of GTFs. The other complex did not contain factors that modify chromatin but contained a subset of SRB/mediator subunits and GTFs and other polypeptides that mediate transcriptional activation, a scenario similar to that reported for yeast.

A complex designated NAT (~20 SU) for negative regulator of transcription contains RNAPII, Cdk8, homologs of the yeast mediator complex as well as Rgr1 and Srb10/11 known as negative regulators of transcription.

A complex with striking similar structural and functional properties to NAT has been identified designated SMCC (~15 SU) (SRB/mediator coactivator complex), that can also mediate transcriptional activation.

The SMCC complex includes all reported NAT subunits including subunits of the TRAP complex. TRAP is a coactivator complex isolated on the basis of its interaction with the thyroid hormone receptor. Another coactivator complex DRIP, isolated on the basis of its ability to interact with the vitamin D3 receptor, contains novel subunits as well as subunits of NAT/SMCC and TRAP complexes.

The effects of each of these coactivator complexes is dependent on the TFIID complex. It is not known if the TAF subunits of TFIID are required. It is likely that new coactivator complexes will be uncovered containing both novel and previously defined components.

Beside the huge amount of transcription factors which can be part of the RNAIIP holoenzyme or the coactivator complexes there is an even larger quantity of specific transcription factors binding to promoter elements within the DNA sequences of a given gene leading to activation or repression of transcription. A



broad range of cellular responses like differentiation, proliferation, cell death and others are elicited through activating or repressing the transcription of target genes.

5 There are at least five superclasses of transcription factors:

1. Superclass contains members with characteristic basic domains:

Members are:

10 Leucine zipper factors, where the basic domain is followed by a leucine zipper of repeated leucine residues at every seventh position. The zipper mediates protein dimerization as a prerequisite for DNA-binding.

15 Helix-loop-helix factors (bHLH) contain a DNA-binding basic region followed by a motif of two potential amphipathic alpha-helices connected by a loop of variable length also mediating dimerization.

Factors with a combination of Helix-loop-helix and leucine zipper.

20 Further members of this superclass are NF-1, RF-X, and bHSH like proteins.

2. Superclass comprises factors containing zinc-coordinating DNA-binding domains.

Members are:

25 Proteins with Cys4 zinc finger of nuclear receptor type, where two such motifs differing in size, composition and function are present in each receptor molecule. Each finger comprises 4 cysteine residues coordinating one zinc ion. The second half including the second cysteine pair has alpha-helix conformation and the helix of the first finger binds to the DNA through the major groove. The sequence between the first two cysteines of the  
30 second finger mediates dimerization upon DNA-binding. This class includes the steroid hormone receptors and the thyroid hormone

receptor-like factors. Other diverse cys<sup>4</sup> zinc fingers have a motif of GATA-type.

Proteins with Cys<sup>2</sup>His<sup>2</sup> zinc finger domain(s). Each finger comprises 2 cysteine and 2 histidine residues coordinating one zinc ion, and in some cases one histidine is replaced by another cysteine. The zinc ion is essential for DNA-binding.

Proteins with Cys<sub>6</sub> cysteine-zinc cluster(s). Six cysteine residues coordinate two zinc ions, i. e. two of the thiol groups are coordinating two zinc ions each. Present in many fungal regulators.

Zinc fingers of alternating composition.

### 3. Superclass contains factors of helix-turn-helix type.

Members are:

Proteins with homeo domains. Homeo domains are three consecutive alpha-helix structures. Helix 3 contacts mainly the major groove of the DNA, some contacts at the minor groove are observed as well. Helix 2 and 3 resemble the helix-turn-helix structure of prokaryotic regulators.

Proteins with Paired box domain(s). This is a DNA-binding domain of approximately 130 amino acid residues. Its N-terminal half is basic, its C-terminal half is highly charged in general. It probably comprises 3 alpha-helices.

Proteins with Fork head / winged helix domain(s). This domain was identified by homology between HNF-3A and fkh. The domain comprises approx. 110 AA. Analysis of the crystal structure has revealed a compact structure of three alpha-helices, the third alpha-helix being exposed towards the major groove of the DNA. The domain also exerts minor groove contacts. Upon binding to DNA, it induces a bend of 13 degree.

Heat shock factors

Proteins with Tryptophan clusters. The tryptophan clusters comprise several tryptophan residues with a spacing of 12-21

amino acid residues; the subclass of myb-type DNA-binding domains typically exhibit a spacing of 19-21 amino acid residues.

Proteins with TEA domain(s). The TEA domain has been identified as a region which is conserved among the transcription factors TEF-1, TECl and abaA. This domain in TEF-1 has been shown to interact with DNA, although two additional regions may also contribute to DNA-binding. It is predicted to fold into three alpha-helices, with a randomly coiled region of 16-18 amino acid residues between helices 1 and 2, and a short stretch between helices 2 and 3 of 3-8 residues.

#### 4. Superclass contains beta-Scaffold Factors with Minor Groove Contacts

Members are:

Proteins with RHR (Rel homology) region.

The structure of the Rel-type DBD exhibits a bipartite subdomain structure, each subdomain comprising a beta-barrel with five loops that form an extensive contact surface to the major groove of the DNA. Particularly, the first loop of the N-terminal subdomain (the highly conserved recognition loop) performs contacts with the recognition element on the DNA, but other loops are involved. The fact that the main DNA-contacts are made through loops has been suggested to provide a high degree of flexibility in binding to a range of different target sequences. Augmenting interactions are achieved by two alpha-helices within the N-terminal Part that form strong minor groove contacts to the A/T-rich center of the B-element. In p53, the sequence between both alpha-helices is much shorter and even helix 2 is truncated. The second, C-terminal domain is necessary mainly for protein dimerization.

p53 proteins

MADS (MCM1-agamous-deficiens-SRF) box proteins. Proteins of this class comprise a region of homology. The DNA-binding domain also comprises the dimerization capability. In the DNA-bound dimer (shown for SRF), two antiparallel amphipathic alpha-helices

(alpha-I), form a coiled coil and are oriented approximately parallel on the minor groove. These helices make minor and major groove contacts, the N-terminal extensions form minor groove contacts. The bound DNA is bent and wrapped around the protein.  
5 It exhibits a compressed minor groove in the center and widened minor groove in the flanks.

Beta-Barrel alpha-helix transcription factors.

TATA-binding proteins

HMG proteins

10 Proteins of this class comprise a region of homology with the chromosomal non-histone HMG proteins such as HMG1. This region comprises the DNA-binding domain which in some instances such as HMG1 mediates sequence-unspecific, in other cases such  
15 LEF-1 sequence-specific binding to DNA. This domain exhibits a typical L-shaped conformation made up of 3 alpha-helices and an extended N-terminal extension of the first helix. The latter together with helix 1, which contains a kink, form the long arm of the L, whereas helices 1 and 2 form the short arm. Binding to the minor groove induces a sharp bending of the DNA by more than  
20 90 degree, away from the bound protein. The overall topology of the DNA-protein complexes resembles somewhat that of the TBP-TATA box complex.

Heteromeric CCAAT factors

Proteins with Grainyhead domain(s)

25 Cold-shock domain factors. Cold-shock domain proteins are characterized by a highly conserved region first found in prokaryotic cold-shock proteins. This domain is a single-stranded nucleic acid-binding structure interacting with DNA or RNA. It consists of an antiparallel five-stranded beta-barrel, the  
30 strands of which are connected by turns and loops. Within this structure, a three-stranded beta-strand contains a conserved RNA-binding motif, RNP1. Not all CSD proteins are transcription factors. Those which specifically bind to a certain sequence are termed Y-box proteins. Proteins of this class were previously

called protamine-like domain proteins because of having a highly positively charged domain with interspersed proline residues.

#### Proteins with Runt homology domain

The members of this transcription factor class have been identified on the basis of their homology to a defined region within the *Drosophila* protein Runt. The runt domain is part of the DNA-binding domain of these factors. It consists mainly of beta-strands, does not contain alpha-helical regions and seems to be most similar to the palm domain found in DNA polymerase beta (rat).

5. Superclass contains other transcription factors like Copper fist proteins, HMGI(Y), STAT, Pocket domain proteins and Ap2/EREBP-related factors.

The classification of transcription factors originates from TRANSFAC database:

<http://transfac.gbf.de/TRANSFAC/>

Reference: Heinemeyer

Several categories of proteins are coded for by clones of the invention within the overall group of "Transcription Factors" and include, among others, the following:

Homeobox-proteins: Homeodomain-containing transcription factors are essential for a variety of processes in vertebrate development, including organogenesis. They have been shown to regulate cell proliferation, pattern segmental identity and determine cell fate decisions during embryogenesis. For example, In zebrafish *emx2* mRNAs are found in the dorsal telencephalon, parts of the diencephalon and the otocyst. The human homologue *Emx2* appears to be already expressed in 8.5 day embryos. It is also expressed in the presumptive cerebral cortex, olfactory bulbs, in some neuroectodermal areas in embryonic head including olfactory placodes in earlier stages and olfactory epithelia later in development. Mutants of the *D. melanogaster* gene "empty spiracles" display spiracles devoid of filzkörper.

no antenna and an open head. Clones in this category include:  
amy2\_14m1b.

Proteins with myc-type, helix-loop-helix dimerization domain signature(s). This helix-loop-helix domain mediates protein  
5 dimerization has been found in various multimeric transcription factors. Clones in this category include: tes3\_18n14.

Transcriptional silencers: In addition to transcription factors, other proteins, such as YDL153c of *Saccharomyces cerevisia* are responsible for silencing of genes. Clones in this  
10 category include: amy2\_2f22.

Proteins regulating transcription factors: The activity of several transcription factor is regulated by the binding or dissociation of other proteins or by phosphorylation or dephosphorylation of the transcription factor. For example, I-  
15 kappa-B-related protein interacts with the transcription factor NF-kB. I-kappa-B-alpha mutations contribute to constitutive NF-kappaB activity in cultured and primary HRS (Hodgkin/Reed-Sternberg) cells and are therefore involved in the pathogenesis of Hodgkin's disease (HD) patients. Clones in this category  
20 include: amy2\_1c12.

Signal transducing proteins: Beta-transducin subunits of G-proteins contain WD-40 repeats. The beta subunits seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition. Due to the zinc  
25 finger the novel protein seems to be a new molecule involved in signal transduction and transcription. These proteins have been reported by OMIM to be associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) essential hypertension (OMIM \*139130). Clones in  
30 this category include: tes3\_11c22.

\* \* \*

The invention, therefore, specifically contemplates the following assemblages of materials, which track the above-identified fourteen functional groupings, that are useful in  
35 practicing the profiling aspects of the invention. One type of assemblage is nucleic acid-based and can include the following groupings of sequences and their derivatives: all sequences; human fetal brain sequences; brain derived sequences; human fetal

kidney library sequences; kidney derived sequences; human mammary carcinoma library sequences; mammary carcinoma derived sequences; human testis library sequences; testes derived sequences; cell cycle genes; cell structure and motility genes; differentiation and development genes; intracellular transport and trafficking genes; metabolism genes; nucleic acid management genes; signal transduction genes; transmembrane protein genes; and transcription factor genes. Other assemblages contain proteins or their corresponding antibodies or antibody fragments, divided along the same groupings.

#### Database Applications

Because they are human genes and gene products, the inventive molecules are useful as members of a database. Such a database may be used, for example, in drug discovery and rationale drug design or in testing the novelty and non-obviousness of newly sequenced materials. In addition, they are particularly suited in designing variants for the profiling (and other) applications described herein. Hence, the following discussion of electronic embodiments applies equally to such variants, which, naturally, will be generated and stored using a computer using known methodologies.

Accordingly, one aspect of the invention contemplates a database of at least one of the inventive sequences stored on computer readable media. Again, the individual sequences may be grouped with regard to the individual functional and structural groups mentioned above. While the individual sequences of a database may exist in printed form, they are preferably in electronic form, as in an ascii or a text file. They may also exist as word processing files or they may be stored in database applications like DB2, Sybase, Oracle, GCG and GenBank. One skilled in the art will understand the range of applications suitable for using and storing the electronic embodiments of the invention.

"Computer readable media" refers to any medium which can be read and accessed by a computer. These include: magnetic storage media, like floppy discs, hard drives and magnetic tape; optical storage media, like CD-ROM; electrical storage media, like RAM and ROM; and hybrids of these categories, like magnetic/optical

storage media. One skilled in the art will readily understand the scope of computer readable media and how to implement them.

### Biological Activities and Assays for Implementing Therapeutic and Diagnostic Applications

5 This section provides assays for biological activity that are useful in characterizing and quantifying the biological activity of the inventive molecules and their derivatives, which is relevant to the pharmacological effects of the inventive molecules. As used in this section, it will be understood that  
10 "protein" may also refer to the inventive antibodies (including fragments).

#### Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell  
15 differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve  
20 as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA16, T10, B9, B9/11, BaF3, MC9/G, M + (preB M + ), 2E8, RB5, DA1, 123,  
25 T11b5, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology,  
30 Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et  
35 al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.



Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin gamma, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6-Nordan, R. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9-Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al.,

Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### Immune Stimulating or Suppressing Activity

5 A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined  
10 immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may  
15 result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal  
20 infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of  
25 the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host  
30 disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired  
35 (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to modify immune responses, in a number of ways. Down regulation

may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated

administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

5       The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in  
10 mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental  
15 Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

      Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are  
20 the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents  
25 which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may  
30 induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include  
35 murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed.,

Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-vital immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the

patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and beta 2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol.

140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA  
 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974,  
 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et  
 al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology  
 5 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988;  
 Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown  
 et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and  
 isotype switching (which will identify, among others, proteins  
 10 that modulate T-cell dependent antibody responses and that affect  
 Th1/Th2 profiles) include, without limitation, those described  
 in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for  
 B cell function: In vitro antibody production, Mond, J. J. and  
 Brunswick, M. In Current Protocols in Immunology. J. E. e.a.  
 15 Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons,  
 Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify,  
 among others, proteins that generate predominantly Th1 and CTL  
 responses) include, without limitation, those described in:  
 20 Current Protocols in Immunology, Ed by J. E. Coligan, A. M.  
 Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub.  
 Greene Publishing Associates and Wiley-Interscience (Chapter 3,  
 In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter  
 7, Immunologic studies in Humans); Takai et al., J. Immunol.  
 25 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988;  
 Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among  
 others, proteins expressed by dendritic cells that activate naive  
 T-cells) include, without limitation, those described in: Guery  
 30 et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of  
 Experimental Medicine 173:549-559, 1991; Macatonia et al.,  
 Journal of Immunology 154:5071-5079, 1995; Porgador et al.,  
 Journal of Experimental Medicine 182:255-260, 1995; Nair et al.,  
 Journal of Virology 67:4062-4069, 1993; Huang et al., Science  
 35 264:961-965, 1994; Macatonia et al., Journal of Experimental  
 Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of  
 Clinical Investigation 94:797-807, 1994; and Inaba et al.,  
 Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in:

- 5 Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International  
10 Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood  
15 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.



Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal  
5 biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating  
10 various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful,  
15 for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in  
20 place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually  
25 treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as  
30 normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of  
35 various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995;

Keller et al., Molecular and Cellular Biology 13:473-486, 1993;  
McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-  
5 hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive  
10 hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay,  
15 Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-  
20 179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

#### Tissue Growth Activity

25 A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

30 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have  
35 prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection

induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an

appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues.

Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described

above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5        Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. W095/16035 (bone, cartilage, tendon); International Patent Publication No. W095/05846 (nerve, neuronal); International Patent Publication No. W091/07491 (skin, endothelium).

10       Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

15    Activin/Inhibin Activity

      A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their  
20    ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin alpha family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis  
25    in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- beta group, may be useful as a fertility inducing therapeutic, based upon the  
30    ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance  
35    of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing

Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors

of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

5       The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M.

10       Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 159:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

#### Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be  
20       achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by  
25       stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as  
30       septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of  
35       cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.



Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may  
5 inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing  
10 production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of  
15 the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight,  
20 hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the  
25 metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress,  
30 cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the  
35 case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability

to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

5 Particular Applications for Certain Clones

The following sets out a non-exclusive list of applications for certain embodiments of the invention. In the interest of economy, applications relevant to multiple embodiments are not duplicated in this list. Other embodiments described herein have  
10 similar characteristics, as described there. The artisan is directed, therefore, to the Description of the Sequences for similar descriptions of the functions of other embodiment.

Testes

- 15 htes3\_10i1b: The new protein can find application in diagnosis/therapy in leukemia predisposition/disease in the modulation of DNA repair.
- htes3\_10n10: The new protein can find application in  
20 studying the expression profile of testis-specific genes.
- htes3\_11a17: The new protein can find application in studying the expression profile of testis-specific genes and as a new marker for testicular cells.
- 25 htes3\_11c22: The new protein can find application in modulating/blocking of regulatory pathways.
- htes3\_11d21: The new protein can find application in  
30 diagnosis of diseases due to unnormal protein degradation like muscular dystrophy or multiple sclerosis as well as in modulating the half life of specific proteins and in expression profiling.

35 Kidney

hfkd2\_3k1 The new protein can find application in modulation of endocytosis.strong similarity to testicular dynamin (Rattus norvegicus).

Amygdala:

5 hamy2\_10h17: The new protein can find application in  
modulating protein-protein-interaction and in studying the  
expression profile of amygdala-specific genes.

10 hamy2\_10p7: The new protein can find application in  
modulation of  $Na^+/Ca^{2+}$ -exchange and voltage-dependend  
processes.

15 hamy2\_11d2: The new protein can find application in studying  
the expression profile of amygdala-specific genes and as a  
new marker for amygdala cells.

hamy2\_11n4: The new protein can find application in  
modulation of DNA-repair and a as a new tool for  
manipulation of nucleic acids.

20 hamy2\_121f19: The new protein can find application  
modulation of cyto skeleton-membrane interactions.

Fetal Brain:

25 hfbr2\_78cl2: The new protein can find application in the  
modulation of translational pathways.

hfbr2\_78dl8: The new protein can find application in  
studying the expression profile of brain-specific genes.

30 hfbr2\_78d4: The new protein can find application in studying  
the expression profile of brain-specific genes and as a new  
marker for amygdala cells.

35 hfbr2\_78el8: The new protein can find application in  
studying the expression profile of brain-specific genes.

40 hfbr2\_78i21: The new protein can find application in  
diagnosis/modulation of protein damage and age-related  
degenerative processes.

Melanoma:

hmel2\_12j1: The new protein can find application in studying the expression profile of melanoma-specific genes.

5 hmel2\_7g14: The new protein can find application in modulation of the sorting of proteins into different compartments.

10 hmel2\_7k19: The new protein can find application in studying the expression profile of melanoma-specific genes.

## VARIANTS OF THE INVENTIVE DNA MOLECULES

### *Variants in General*

15 "Variants," according to the invention, include DNA and/or protein molecules that resemble, structurally and/or functionally, those set forth herein. Variants may be isolated from natural sources ("homologs"), may be entirely synthetic or may be based in part on both natural and synthetic approaches.

20 The section set forth below presents various structural and functional characteristics of molecules within the invention. Preferred molecules are characterized by a combination of one or more of these characteristics. For instance, some preferred molecules are described with reference to at least two structural characteristics, while others may be described with reference to  
25 at least one structural and at least one functional characteristic.

It will be recognized by the skilled artisan that structure ultimately defines function, i.e. the functions of the molecules described herein derives from the structures of those molecules.  
30 Accordingly, the structural variants described below that bear the closest structural relationship (as variously defined below) to the inventive molecules are the variants that most likely will preserve biological function. This relationship between structure and function will guide the skilled artisan in identifying the  
35 preferred embodiments of the invention.

### Splicing Variants

It is well-known that eukaryotic structural genes are comprised of both protein coding and non-coding portions. When the messenger RNA is transcribed from the DNA template, it contains introns, which are non-coding, and exons, which are coding. In order to form a translation competent mRNA, the introns must be "spliced" out of this initial pre mRNA.

Specific sequences within the pre mRNA represent "splice junctions" that direct the cellular splicing machinery to the appropriate position. The splice junctions are loosely conserved sequence regions of the pre mRNA, which almost invariably begin with GT and end with AG (DNA perspective). The 5' end of the splice junction typically contains about nine somewhat conserved residues, for example, C/AAGT/A/GAGT. The 3' end usually contains a pyrimidine rich stretch of at least about 11 nucleotides, followed by NC/TAGG. Splicing occurs before the GT and after the AG. Mount, *Nucleic Acids Res.* 10:459-72 (1982).

Interestingly, exons often correspond to discrete functional domains of the protein product. The intron/exon arrangement thus creates a linear array of nucleotides which can be correlated to discrete, and often interchangeable, functional protein fragments. Go, *Nature* 291:90-92 (1981); Branden et al., *EMBO J.* 3:1307-10 (1984). This linear arrangement creates the possibility of generating multiple different full length proteins by rearranging the order of the different functional portions in the array. For example, if a set of exons are arranged 1-2-3-4, where (-) represents the introns separating the exons, a splicing event need not simply produce 1234, but may produce 123, 134, 124 and so on. Production of different mRNA products in this way is commonly called "alternative splicing." Andreadis et al., *Ann. Rev. Cell Biol.* 3:207-42 (1987).

Some of the present DNA molecules can be represented in modular fashion in terms of their coding regions. Essentially, these modules are exons (though each "exon" may in fact be made up of several exons), which may be combined in different ways to form a variety of different DNA molecules, each encoding a different functional protein. Splicing variants are indicated in the Description of the Sequences.

*Degenerate Variants*

One aspect of the present invention provides "degenerate variants" of the nucleic acid fragments of the present invention. A "degenerate variant" is a nucleotide fragment which differs from  
5 those of inventive molecules by nucleotide sequence, but due to the degeneracy of the genetic code, encodes an identical polypeptide sequence.

Given the known relationship between DNA sequences and the proteins they encode, degenerate variants typically are described  
10 by reference to this relationship. It is well known that the degeneracy of the genetic code results in many possible DNA sequences which encode a particular protein. Indeed, of the three bases which comprise an amino acid-encoding triplet, the third position, and often the second, almost always may vary. This fact  
15 alone allows for a class of variant DNA molecules which encode protein sequences identical to those disclosed herein, yet have about 30% sequence variation. In other words, the variant DNA molecules are about 70% identical to the inventive DNAs, having no additional or deleted sequences. Thus, one aspect of the  
20 invention provides degenerate variant DNA molecules encoding the inventive protein sequences.

In one embodiment, these variants have at least about 70% sequence identity with the DNA molecules described herein. In a preferred embodiment, these variants have at least about 80%  
25 sequence identity to the inventive molecules. In a more preferred embodiment these variants have at least about 90% sequence identity with the inventive molecules.

*Conservative Amino Acid Variants*

Variants according to the invention also may be made that  
30 conserve the overall molecular structure of the encoded proteins. Given the properties of the individual amino acids comprising the disclosed protein products, some rational substitutions will be recognized by the skilled worker. Amino acid substitutions, i.e. "conservative substitutions," may be made, for instance, on the  
35 basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved.

For example: (a) nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; (b) polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; (c) positively charged (basic) amino acids include arginine, lysine, and histidine; and (d) negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Substitutions typically may be made within groups (a)-(d). In addition, glycine and proline may be substituted for one another based on their ability to disrupt  $\alpha$ -helices. Similarly, certain amino acids, such as alanine, cysteine, leucine, methionine, glutamic acid, glutamine, histidine and lysine are more commonly found in  $\alpha$ -helices, while valine, isoleucine, phenylalanine, tyrosine, tryptophan and threonine are more commonly found in  $\beta$ -pleated sheets. Glycine, serine, aspartic acid, asparagine, and proline are commonly found in turns. Some preferred substitutions may be made among the following groups: (i) S and T; (ii) P and G; and (iii) A, V, L and I. Given the known genetic code, and recombinant and synthetic DNA techniques, the skilled scientist readily can construct DNAs encoding the conservative amino acid variants.

As used herein, "sequence identity" between two polypeptide sequences indicates the percentage of amino acids that are identical between the sequences. "Sequence similarity" indicates the percentage of amino acids that either are identical or that represent conservative amino acid substitutions.

#### *Functionally Equivalent Variants*

Yet another class of DNA variants within the scope of the invention may be described with reference to the product they encode. As shown in the Description of the Sequences, some of the inventive DNA molecules encode a protein having a degree of homology with known proteins, or protein domains. It is expected, therefore, that they will have some or all of the requisite functional features of such molecules. These "functionally equivalent variants" products are characterized by the fact that they are functionally equivalent, with respect to biological activity, to certain known molecules.

Also provided herein is information on common structural motifs, including consensus sequences that will guide the artisan in constructing functionally equivalent variants. It will be understood that the motifs, identified in the Description of the Sequences for each inventive protein, may be modified within the identified consensus sequences. Thus, the invention contemplates the proteins in the Description of the Sequences that contain variability in the consensus sequences identified, and the invention further contemplates the full range of nucleic acids encoding them, and the complements of those nucleic acids.

#### *Hybridizing Variants*

DNA variants within the invention also may be described by reference to their physical properties in hybridization. One skilled in the field will recognize that DNA can be used to identify its complement and, since DNA is double stranded, its equivalent or homolog, using nucleic acid hybridization techniques. It will also be recognized that hybridization can occur with less than 100% complementarity. However, given appropriate choice of conditions, hybridization techniques can be used to differentiate among DNA sequences based on their structural relatedness to a particular probe. For guidance regarding such conditions see, for example, Sambrook et al., 1989, MOLECULAR CLONING, A LABORATORY MANUAL, Cold Spring Harbor Press, N.Y.; and Ausubel et al., 1989, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Green Publishing Associates and Wiley Interscience, N.Y.

Structural relatedness between two polynucleotide sequences can be expressed as a function of "stringency" of the conditions under which the two sequences will hybridize with one another. As used herein, the term "stringency" refers to the extent that the conditions disfavor hybridization. Stringent conditions strongly disfavor hybridization, and only the most structurally related molecules will hybridize to one another under such conditions. Conversely, non-stringent conditions favor hybridization of molecules displaying a lesser degree of structural relatedness. Hybridization stringency, therefore, directly correlates with the structural relationships of two nucleic acid sequences. The following relationships are useful in correlating hybridization



and relatedness (where  $T_m$  is the melting temperature of a nucleic acid duplex):

- 5           a.  $T_m = 69.3 + 0.41(G+C)\%$
- b. The  $T_m$  of a duplex DNA decreases by  $1^\circ\text{C}$  with every increase of 1% in the number of mismatched base pairs.
- 10          c.  $(T_m)_{\mu_2} - (T_m)_{\mu_1} = 16.5 \log_{10} \mu_2 / \mu_1$   
          where  $\mu_1$  and  $\mu_2$  are the ionic strengths of two solutions.

Hybridization stringency is a function of many factors, including overall DNA concentration, ionic strength, temperature, 15 probe size and the presence of agents which disrupt hydrogen bonding. Factors promoting hybridization include high DNA concentrations, high ionic strengths, low temperatures, longer probe size and the absence of agents that disrupt hydrogen bonding.

20          Hybridization usually is done in two stages. First, in the "binding" stage, the probe is bound to the target under conditions favoring hybridization. Stringency is usually controlled at this stage by altering the temperature. For high stringency, the temperature is usually between  $65^\circ\text{C}$  and  $70^\circ\text{C}$ , unless short (<20 25 nt) oligonucleotide probes are used. A representative hybridization solution comprises 6X SSC, 0.5% SDS, 5X Denhardt's solution and 100 $\mu\text{g}$  of non-specific carrier DNA. See Ausubel et al., *supra*, section 2.9, supplement 27 (1994). Of course many different, yet functionally equivalent, buffer conditions are 30 known. Where the degree of relatedness is lower, a lower temperature may be chosen. Low stringency binding temperatures are between about  $25^\circ\text{C}$  and  $40^\circ\text{C}$ . Medium stringency is between at least about  $40^\circ\text{C}$  to less than about  $65^\circ\text{C}$ . High stringency is at least about  $65^\circ\text{C}$ .

35          Second, the excess probe is removed by washing. It is at this stage that more stringent conditions usually are applied. Hence, it is this "washing" stage that is most important in determining relatedness via hybridization. Washing solutions typically contain lower salt concentrations. One exemplary medium 40 stringency solution contains 2X SSC and 0.1% SDS. A high stringency wash solution contains the equivalent (in ionic

strength) of less than about 0.2X SSC, with a preferred stringent solution containing about 0.1X SSC. The temperatures associated with various stringencies are the same as discussed above for "binding." The washing solution also typically is replaced a  
5 number of times during washing. For example, typical high stringency washing conditions comprise washing twice for 30 minutes at 55° C. and three times for 15 minutes at 60° C.

The present invention includes nucleic acid molecules that hybridize to the inventive molecules under high stringency binding  
10 and washing conditions. More preferred molecules (from an mRNA perspective) are those that are at least 50 % of the length of any one of those depicted in the Description of the Sequences. Particularly preferred molecules are at least 75 % of the length of those molecules.

#### 15 *Substitutions, Insertions, Additions and Deletions*

In a general sense, the preferred DNA variants of the invention are those that retain the closest relationship, as described by "sequence identity" to the inventive DNA molecules. According to another aspect of the invention, therefore,  
20 substitutions, insertions, additions and deletions of defined properties are contemplated. It will be recognized that sequence identity between two polynucleotide sequences, as defined herein, generally is determined with reference to the protein coding region of the sequences. Thus, this definition does not at all  
25 limit the amount of DNA, such as vector DNA, that may be attached to the molecules described herein. Preferred DNA sequence variants include molecules encoding proteins sharing some or all of any relevant biological activity of the native molecule.

In creating these variants, the skilled worker will be guided  
30 by reference to the protein structure. First, insertions and deletions in any recognized functional domain above generally should be avoided, except as noted below in the section entitled "Proteins," where this domain is discussed in detail. Alterations in such domains usually will be limited to conservative amino acid  
35 substitutions. In addition, where insertions and deletions are desired, this may be accomplished at the N- and/or C-terminus of the protein molecule (or the corresponding coding regions of the DNA). If insertions or deletions are made within the protein,

deletions of major structural features usually should be avoided. Thus, a preferred place to make insertion or deletion variants is in non-structural regions, such as linker regions between two alpha helices.

5 "Substitutions" generally refer to alterations in the DNA sequence which do not change its overall length, but only alter one or more nucleotide positions, substituting one for another in the common sense of the word. One class of preferred substitutions, "degenerate substitutions," are those that do not  
10 alter the encoded amino acid sequence. Some substitutions retain 50%, 55%, 60% or 65% identity. Preferred substitutions retain at least about 70% identity, more preferably at least 70% or 75% identity, with the inventive DNAs. Some more preferred molecules have at least about 80% identity, more preferably at least 80% or  
15 85% identity. Particularly preferred DNAs share at least about 90% identity, more preferably at least 90% or 95% identity.

"Insertions," unlike substitutions, alter the overall length of the DNA molecule, and thus sometimes the encoded protein. Insertions add extra nucleotides to the interior (not the 5' or 3'  
20 ends) of the subject DNAs. Preferred insertions are made with reference to the protein sequence encoded by the DNA. Thus, it is most preferred to provide an insertion in the DNA at a location that corresponds to an area of the encoded protein which lacks structure. For instance, it typically would not be beneficial, if  
25 the preservation of biological activity is desired, to provide an insertion within an alpha-helical region or a beta-pleated sheet. Accordingly, non-structural areas, such as those containing helix-breaking glycines and proline residues, are most preferred sites of insertion. Other preferred sites of insertion are the splice  
30 sites, which are indicated above in the description of the inventive DNA molecules.

While the optimal size of insertions will vary depending upon the site of insertion and its effect on the overall conformation of the encoded protein, some general guides are useful.  
35 Generally, the total insertions (irrespective of their number) should not add more than about 30% (or preferably not more than 30%) to the overall size of the encoded protein. More preferably, the insertion adds less than about 10-20% (yet more preferably 10-20%) in size, with less than about 10% being most preferred. The

number of insertions is limited only by the number of suitable insertions sites, and secondarily by the foregoing size preferences.

"Additions," like insertions, also add to the overall size of the DNA molecule, and usually the encoded protein. However, instead of being made within the molecule, they are made on the 5' or 3' end, usually corresponding to the N- or C- terminus of the encoded protein. Unlike deletions, additions are not very size-dependent. Indeed, additions may be of virtually any size. Preferred additions, however, do not exceed about 100% of the size of the native molecule. More preferably, they add less than about 60 to 30% to the overall size, with less than about 30% being most preferred.

"Deletions" diminish the overall size of the DNA and, therefore, also reduce the size of the protein encoded by that DNA. Deletions may be made from either end of the molecule or internal to it. Typical preferred deletions remove discrete structural features of the encoded protein. For example, some deletions will comprise the deletion of one or more exons which may define a structural feature. Preferred deletions remove less than about 30% of the size of the subject molecule. More preferred deletions remove less than about 20% and most preferred deletions remove less than about 10%.

#### *Computer-Defined Variants and Definition of "Sequence Identity"*

In general, both the DNA and protein molecules of the invention can be defined with reference to "sequence identity." As used herein, "sequence identity" refers to a comparison made between two molecules using, for example, the standard Smith-Waterman algorithm that is well known in the art.

Some molecules have at least about 50%, 55% or 60% identity. Preferred molecules are those having at least about 65% sequence identity, more preferably at least 65% or 70% sequence identity. Other preferred molecules have at least about 80%, more preferably at least 80% or 85%, sequence identity. Particularly preferred molecules have at least about 90% sequence identity, more preferably at least 90% sequence identity. Most preferred molecules have at least about 95%, more preferably at least 95%, sequence identity. As used herein, two nucleic acid molecules or

proteins are said to "share significant sequence identity" if the two contain regions which possess greater than 85% sequence (amino acid or nucleic acid) identity.

- "Sequence identity" is defined herein with reference the
- 5 Blast 2 algorithm, which is available at the NCBI  
(<http://www.ncbi.nlm.nih.gov/BLAST>), using default parameters.  
References pertaining to this algorithm include: those found at  
[http://www.ncbi.nlm.nih.gov/BLAST/blast\\_references.html](http://www.ncbi.nlm.nih.gov/BLAST/blast_references.html);  
Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J.  
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15 141; Altschul, S.F., Madden, T.L., Schäffer, A.A., Zhang, J.,  
Zhang, Z., Miller, W. & Lipman, D.J. (1997) "Gapped BLAST and  
PSI-BLAST: a new generation of protein database search programs."  
Nucleic Acids Res. 25:3389-3402; and Zhang, J. & Madden, T.L.  
(1997) "PowerBLAST: A new network BLAST application for  
20 interactive or automated sequence analysis and annotation."  
Genome Res. 7:649-656.

#### METHODS OF MAKING VARIANTS

- It will be recognized that variants of the inventive  
molecules can be constructed in several different ways. For  
25 example, they may be constructed as completely synthetic DNAs.  
Methods of efficiently synthesizing oligonucleotides in the range  
of 20 to about 150 nucleotides are widely available. See Ausubel  
*et al.*, *supra*, section 2.11, Supplement 21 (1993). Overlapping  
oligonucleotides may be synthesized and assembled in a fashion  
30 first reported by Khorana *et al.*, J. Mol. Biol. 72:209-217 (1971);  
see also Ausubel *et al.*, Section 8.2. The synthetic DNAs are  
designed with convenient restriction sites engineered at the 5'  
and 3' ends of the gene to facilitate cloning into an appropriate  
vector.

- 35 An alternative method of generating variants is to start with  
one of the inventive DNAs and then to conduct site-directed  
mutagenesis. See Ausubel *et al.*, *supra*, chapter 8, Supplement 37

(1997). In a typical method, a target DNA is cloned into a single-stranded DNA bacteriophage vehicle. Single-stranded DNA is isolated and hybridized with a oligonucleotide containing the desired nucleotide alteration(s). The complementary strand is synthesized and the double stranded phage is introduced into a host. Some of the resulting progeny will contain the desired mutant, which can be confirmed using DNA sequencing. In addition, various methods are available that increase the probability that the progeny phage will be the desired mutant. These methods are well known to those in the field and kits are commercially available for generating such mutants.

### ISOLATING HOMOLOGS

#### *Methods*

By using the sequences disclosed herein as probes or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs. "Homologs" are essentially naturally-occurring variants and include allelic, species-specific and tissue-specific variants.

Region-specific primers or probes derived from the nucleotide sequence(s) provided can be used to prime DNA synthesis and PCR amplification, as well as to identify colonies containing cloned DNA encoding a homolog using known methods (Innis et al., *PCR Protocols*, Academic Press, San Diego, CA (1990)). Such an application is useful in diagnostic methods, as described in more detail below, as well as in preparing full-length DNAs from various sources. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. As a general guide, the formula  $3(G+C) + 2(A+T) = ^\circ C$ , is useful.

When using primers derived from the inventive sequences, one skilled in the art will recognize that by employing high stringency conditions (e.g., annealing at 50-60°C), only sequences with greater than 75% sequence identity to the primer will be amplified. By employing lower stringency conditions (e.g.,

annealing at 35-37°C), sequences which have greater than 40-50% sequence identity to the primer also will be amplified.

The PCR product may be subcloned and sequenced to confirm that it indeed displays the expected sequence identity. The PCR fragment may then be used to isolate a full length cDNA clone by a variety of methods. For example, the amplified fragment may be labeled and used to screen a bacteriophage cDNA library. Alternatively, the labeled fragment may be used to screen a genomic library.

PCR technology may also be utilized to isolate full length cDNA sequences. For example, RNA may be isolated, following standard procedures, from an appropriate cellular or tissue source. A reverse transcription reaction may be performed on the RNA using an oligonucleotide primer specific for the most 5' end of the amplified fragment for the priming of first strand synthesis. The resulting RNA/DNA hybrid may then be "tailed" with guanines using a standard terminal transferase reaction, the hybrid may be digested with RNAase H, and second strand synthesis may then be primed with a poly-C primer. Thus, cDNA sequences upstream of the amplified fragment may easily be isolated. For a review of cloning strategies which may be used, see e.g., Sambrook et al., 1989, *supra*.

When using DNA probes derived from the inventive sequences for colony/plaque hybridization, one skilled in the art will recognize that by employing medium to high stringency conditions (e.g., hybridizing at 50-65°C in 5X SSPC and 50% formamide, and washing at 50-65°C in 0.5X SSPC), sequences having regions with greater than 90% sequence identity to the probe can be obtained, and that by employing lower stringency conditions (e.g., hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in SSPC), sequences having regions with greater than 35-45% sequence identity to the probe will be obtained.

Suitably, genomic or cDNA libraries can be constructed and screened in accord with the previous paragraph. The libraries should be derived from a tissue or organism that is known to express the gene of interest, or that is suspected of expressing the gene. The clone containing the homolog may then be purified

through methods routinely practiced in the art, and subjected to sequence analysis.

Additionally, an expression library can be constructed utilizing DNA isolated from or cDNA synthesized from a tissue or organism that is known to express the gene of interest, or that is suspected of expressing the gene. In this manner, clones may be induced and screened using standard antibody screening techniques in conjunction with antibodies raised against the normal gene product, as described herein. (For screening techniques, see, for example, Harlow, E. and Lane, eds., 1988, ANTIBODIES: A LABORATORY MANUAL, Cold Spring Harbor Press, Cold Spring Harbor Press.)

#### *Human Homologs*

Any organism or tissue can be used as the source for homologs of the present invention so long as the organism or tissue naturally expresses such a protein or contains genes encoding the same. The most preferred organism for isolating homologs is human.

#### PROTEINS OF THE INVENTION

One class of proteins included within the invention is encoded by the inventive DNA molecules presented. Other proteins according to the invention are those encoded by the DNA variants described above. As noted, these variants are designed with the encoded proteins in mind.

A preferred class of protein fragments includes those fragments which retain any biological activity. These molecules share functional features common the family of proteins, although these characteristics may vary in degree.

According to one aspect of the invention fragments of the inventive proteins are contemplated. Some preferred fragments are those which are capable of eliciting an immune response. Generally these "antigenic" fragments will be from about five amino acids in length to about fifty amino acids in length. Some preferred antigenic fragments are from five to about twenty amino acids long. "Antigenic" response may refer to a T cell response, a B cell response or a response by cells of the macrophage/monocyte lineages. In most cases, however, it will



refer to the immune response involved in the generation of antibodies. In other words, the relevant immune response is that of helper T cells and/or B cells. These preferred molecules comprise one or more T cell and /or B cell epitopes.

## 5 ANTIBODIES OF THE INVENTION

Antibodies raised against the proteins and protein fragments of the invention also are contemplated by the invention. Described below are antibody products and methods for producing antibodies capable of specifically recognizing one or more  
10 epitopes of the presently described proteins and their derivatives.

Antibodies include, but are not limited to polyclonal antibodies, monoclonal antibodies (mAbs), humanized or chimeric antibodies, single chain antibodies including single chain Fv  
15 (scFv) fragments, Fab fragments, F(ab')<sub>2</sub> fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, epitope-binding fragments, and humanized forms of any of the above.

As known to one in the art, these antibodies may be used, for  
20 example, in the detection of a target protein in a biological sample. They also may be utilized as part of treatment methods, and/or may be used as part of diagnostic techniques whereby patients may be tested for abnormal levels or for the presence of abnormal forms of the such proteins.

In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A.M., *Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers,  
30 Amsterdam, The Netherlands (1984); St. Groth et al., *J. Immunol. Methods* 35:1-21 (1980); Kohler and Milstein, *Nature* 256:495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., *Immunology Today* 4:72 (1983); Cole et al., in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. (1985), pp. 77-96). Antibodies may also be generated by the  
35 known techniques of phage display and *in vitro* immunization.

### *Polyclonal Antibodies*

Polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of animals immunized with an antigen, such as an inventive protein or an antigenic derivative thereof.

Polyclonal antiserum, containing antibodies to heterogeneous epitopes of a single protein, can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified, as known in the art, to enhance immunogenicity. Immunization methods include subcutaneous or intraperitoneal injection of the polypeptide.

Effective polyclonal antibody production is affected by many factors related both to the antigen and to the host species. For example, small molecules tend to be less immunogenic than other and may require the use of carriers and/or adjuvant. In addition, host animal response may vary with site of inoculation. Both inadequate or excessive doses of antigen may result in low titer antisera. In general, however, small doses (high ng to low  $\mu$ g levels) of antigen administered at multiple intradermal sites appears to be most reliable. Host animals may include but are not limited to rabbits, mice, chickens and rats, to name but a few. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. et al., *J. Clin. Endocrinol. Metab.* 33:988-991 (1971).

The protein immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to coupling the antigen with a heterologous protein (such as globulin  $\beta$ -galactosidase) or through the inclusion of an adjuvant during immunization. Adjuvants include Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *Corynebacterium parvum*.

Booster injections can be given at regular intervals, with at least one usually being required for optimal antibody production.

The antiserum may be harvested when the antibody titer begins to fall. Titer may be determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen. See, for example, Ouchterlony et al., Chap. 19 in:  
5 *Handbook of Experimental Immunology*, Wier, ed, Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12  $\mu$ M). The antiserum may be purified by affinity chromatography using the immobilized immunogen carried on a solid support. Such methods of affinity  
10 chromatography are well known in the art.

Affinity of the antisera for the antigen may be determined by preparing competitive binding curves, as described, for example, by Fisher, Chap. 42 in: *Manual of Clinical Immunology*, second edition, Rose and Friedman, eds., Amer. Soc. For Microbiology,  
15 Washington, D.C. (1980).

In addition to using protein as the immunogen, DNA molecules may be used directly. In this manner, a DNA encoding the protein immunogen is administered. Boosting and harvesting is done in a manner analogous to that detailed above. Yet another method of  
20 producing antibodies entails immunizing chickens and harvesting the antibodies from their eggs.

#### ***Monoclonal Antibodies***

Monoclonal antibodies (MAbs), are homogeneous populations of antibodies to a particular antigen. They may be obtained by any  
25 technique which provides for the production of antibody molecules by continuous cell lines in culture or *in vivo*. MAbs may be produced by making hybridomas which are immortalized cells capable of secreting a specific monoclonal antibody.

Monoclonal antibodies to any of the proteins, peptides and epitopes thereof described herein can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* 256:495-497 (1975) (and U.S. Patent No. 4,376,110) or modifications of the methods thereof, such as the human B-cell hybridoma technique (Kosbor et al., 1983, *Immunology Today* 4:72; Cole et al., 1983, *Proc. Natl. Acad. Sci. USA* 80:2026-2030), and the EBV-hybridoma technique (Cole et al., 1985, *MONOCLONAL ANTIBODIES AND CANCER THERAPY*, Alan R. Liss, Inc., pp. 77-96).

In one method a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen are isolated.

The spleen cells are fused, typically using polyethylene glycol, with mouse myeloma cells, such as SP2/O-Ag14 myeloma cells. The excess, unfused cells are destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted, and aliquots are plated to microliter plates where growth is continued. Antibody--producing clones (hybridomas) are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures. These include ELISA, as originally described by Engvall, *Meth. Enzymol.* 70:419 (1980), western blot analysis, radioimmunoassay (Lutz et al., *Exp. Cell Res.* 175:109-124 (1988)) and modified methods thereof.

Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. et al. *BASIC METHODS IN MOLECULAR BIOLOGY*, Elsevier, New York. Section 21-2 (1989). The hybridoma clones may be cultivated *in vitro* or *in vivo*, for instance as ascites. Production of high titers of mAbs *in vivo* makes this the presently preferred method of production. Alternatively, hybridoma culture in hollow fiber bioreactors provides a continuous high yield source of monoclonal antibodies.

The antibody class and subclass may be determined using procedures known in the art (Campbell, A.M., *Monoclonal Antibody*

Technology: *Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)). MAbs may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof. Methods of purifying  
5 monoclonal antibodies are well known in the art.

#### *Antibody Derivatives and Fragments*

Fragments or derivatives of antibodies include any portion of the antibody which is capable of binding the target antigen, or a specific portion thereof. Antibody derivatives include poly-  
10 specific (e.g., bi-specific) antibodies, which contain binding sites specific for two or more different epitopes. These epitopes may be from the same or different inventive molecules or one or more epitope may be from a molecule not specifically disclosed here.

15 Antibody fragments specifically include  $F(ab')_2$ , Fab, Fab' and Fv fragments. These can be generated from any class of antibody, but typically are made from IgG or IgM. They may be made by conventional recombinant DNA techniques or, using the classical method, by proteolytic digestion with papain or pepsin.  
20 See CURRENT PROTOCOLS IN IMMUNOLOGY, chapter 2, Coligan et al., eds., (John Wiley & Sons 1991-92).

$F(ab')_2$  fragments are typically about 110 kDa (IgG) or about 150 kDa (IgM) and contain two antigen-binding regions, joined at the hinge by disulfide bond(s). Virtually all, if not all, of the  
25 Fc is absent in these fragments. Fab' fragments are typically about 55 kDa (IgG) or about 75 kDa (IgM) and can be formed, for example, by reducing the disulfide bond(s) of an  $F(ab')_2$  fragment. The resulting free sulfhydryl group(s) may be used to conveniently conjugate Fab' fragments to other molecules, such as detection  
30 reagents (e.g., enzymes).

Fab fragments are monovalent and usually are about 50 kDa (from any source). Fab fragments include the light (L) and heavy (H) chain, variable ( $V_L$  and  $V_H$ , respectively) and constant ( $C_L$   $C_H$ , respectively) regions of the antigen-binding portion of the  
35 antibody. The H and L portions are linked by an intramolecular disulfide bridge.

Fv fragments are typically about 25 kDa (regardless of source) and contain the variable regions of both the light and

heavy chains ( $V_L$  and  $V_H$ , respectively). Usually, the  $V_L$  and  $V_H$  chains are held together only by non-covalent interactions and, thus, they readily dissociate. They do, however, have the advantage of small size and they retain the same binding properties of the larger Fab fragments. Accordingly, methods have been developed to crosslink the  $V_L$  and  $V_H$  chains, using, for example, glutaraldehyde (or other chemical crosslinkers), intermolecular disulfide bonds (by incorporation of cysteines) and peptide linkers. The resulting Fv is now a single chain (i.e., SCFv).

Other antibody derivatives include single chain antibodies (U.S. Patent 4,946,778; Bird, Science 242:423-426 (1988); Huston et al., Proc. Natl. Acad. Sci. USA 85:5879-5883 (1988); and Ward et al., Nature 334:544-546 (1989)). Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain FV (SCFv).

One preferred method involves the generation of scFvs by recombinant methods, which allows the generation of Fvs with new specificities by mixing and matching variable chains from different antibody sources. In a typical method, a recombinant vector would be provided which comprises the appropriate regulatory elements driving expression of a cassette region. The cassette region would contain a DNA encoding a peptide linker, with convenient sites at both the 5' and 3' ends of the linker for generating fusion proteins. The DNA encoding a variable region(s) of interest may be cloned in the vector to form fusion proteins with the linker, thus generating an scFv.

In an exemplary alternative approach, DNAs encoding two Fvs may be ligated to the DNA encoding the linker, and the resulting tripartite fusion may be ligated directly into a conventional expression vector. The scFv DNAs generated any of these methods may be expressed in prokaryotic or eukaryotic cells, depending on the vector chosen.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, such fragments include but are not limited to: the  $F(ab')_2$  fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges

of the F(ab)<sub>2</sub> fragments. Alternatively, Fab expression libraries may be constructed (Huse et al., 1989, *Science*, 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

5        Derivatives also include "chimeric antibodies" (Morrison et al., *Proc. Natl. Acad. Sci.*, 81:6851-6855 (1984); Neuberger et al., *Nature*, 312:604-608 (1984); Takeda et al., *Nature*, 314:452-454 (1985)). These chimeras are made by splicing the DNA encoding a mouse antibody molecule of appropriate specificity with, for instance, DNA encoding a human antibody molecule of appropriate  
10        specificity. Thus, a chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. These are also known  
15        sometimes as "humanized" antibodies and they offer the added advantage of at least partial shielding from the human immune system. They are, therefore, particularly useful in therapeutic *in vivo* applications.

#### *Labeled Antibodies*

20        The present invention further provides the above-described antibodies in detectably labeled form. Antibodies can be detectably labelled through the use of radioisotopes, affinity labels (such as biotin, avidin, etc.), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, etc.) fluorescent  
25        labels (such as FITC or rhodamine, etc.), paramagnetic atoms, etc. Procedures for accomplishing such labeling are well-known in the art, for example see (Sternberger et al., *J. Histochem. Cytochem.* 18:315 (1970); Bayer et al., *Meth. Enzym.* 62:308 (1979); Engval et al., *Immunol.* 109:129 (1972); Goding, *J. Immunol. Meth.* 13:215  
30        (1976)). The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* diagnostic assays.

#### *Immobilized Antibodies*

35        The foregoing antibodies also may be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports

are well known in the art (Weir et al., "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby et al., *Meth. Enzym.* 34 Academic Press, N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as for immunoaffinity purification of the proteins of the present invention.

#### THERAPEUTIC AND DIAGNOSTIC COMPOSITIONS

The proteins, antibodies and polynucleotides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in admixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, e.g., human serum albumin, are described, for example, in *Remington's Pharmaceutical Sciences* (16th ed., Osol, A., Ed., Mack, Easton PA (1980)). In order to form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of one or more of the agents of the present invention, together with a suitable amount of carrier vehicle.

Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients. Thus, the compounds and their physiologically acceptable salts and solvate may be formulated for administration by inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral or rectal administration.

For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (e.g., lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (e.g., magnesium stearate, talc or silica); disintegrants (e.g., potato starch or sodium starch glycolate); or



wetting agents (e.g., sodium lauryl sulphate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they maybe presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (e.g., sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (e.g., lecithin or acacia); non-aqueous vehicles (e.g., almond oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (e.g., methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate.

Preparations for oral administration may be suitably formulated to give controlled release of the active compound. For buccal administration the composition may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas.

In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g. gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient

may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing  
5 conventional suppository bases such as cocoa butter or other glycerides.

In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for  
10 example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble  
15 salt.

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may for example  
20 comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

#### RECOMBINANT CONSTRUCTS AND EXPRESSION

The present invention further provides recombinant DNA constructs comprising one or more of the nucleotide sequences of  
25 the present invention. The recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a DNA or DNA fragment, typically bearing an open reading frame, is inserted, in either orientation. The gene products encoded by the subject DNAs may be produced by  
30 recombinant DNA technology using techniques well known in the art. See, for example, the techniques described in Sambrook et al., 1989, *supra*, and Ausubel et al., 1989, *supra*. Alternatively, the DNA sequences may be chemically synthesized using, for example, synthesizers. See, for example, the techniques described in  
35 OLIGONUCLEOTIDE SYNTHESIS, 1984, Gait, ed., IRL Press, Oxford, which is incorporated by reference herein in its entirety. They may be assembled from fragments and short oligonucleotide linkers,

or from a series of oligonucleotides. They are preferably made by RT-PCR methods. The resulting synthetic gene is capable of being expressed in a recombinant vector.

5 In some cases the recombinant constructs will be expression vectors, which are capable of expressing the RNA and/or protein products of the encoded DNA(s). Thus, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the open reading frame (ORF). The vector may further comprise a selectable marker sequence.

10 Specific initiation signals may also be required for efficient translation of inserted target gene coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where a target DNA includes its own initiation codon and adjacent sequences is inserted into the  
15 appropriate expression vector, no additional translation control signals may be needed. However, in cases where only a portion of an ORF is used, exogenous translational control signals, including, perhaps, the ATG initiation codon, must be provided. Furthermore, the initiation codon must be in phase with the  
20 reading frame of the desired coding sequence to ensure translation of the entire target. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer  
25 elements, transcription terminators, etc. (see Bittner et al., *Methods in Enzymol.* 153:516-544 (1987)). Some appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York  
30 (1989), the disclosure of which is hereby incorporated by reference.

If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism,  
35 as explained by Hatfield et al., U.S. Patent No. 5,082,767.

The present invention further provides host cells containing at least one of the DNAs of the present invention. The host cell can be virtually any cell for which expression vectors are

available. It may be, for example, a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into  
5 the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis et al., *Basic Methods in Molecular Biology* (1986)).

A wide variety of expression systems are available, such as: yeast (e.g. *Saccharomyces*, *Pichia*) transformed with recombinant  
10 yeast expression vectors containing the target DNA; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing the target DNA sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or  
15 transformed with recombinant plasmid expression vectors (e.g. Ti plasmid) containing target DNA coding sequences; or mammalian cell systems (e.g. COS, CHO, BHK, 293, 3T3) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from  
20 mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter).

Depending on the system chosen, the resulting product may differ. For example, proteins expressed in most bacterial cultures, e.g., *E. coli*, will be free of glycosylation  
25 modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern different from that expressed in mammalian cells.

#### Vectors

Generally, recombinant expression vectors will include  
30 origins of replication and selectable markers permitting selection of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding  
35 glycolytic enzymes such as 3-phosphoglycerate kinase (PGK),  $\alpha$ -factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate

phase with translation initiation and termination sequence, and in one aspect of the invention, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal or C-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

### ***Bacterial Expression***

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, if desirable, to provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may, also be employed as a matter of choice.

Bacterial vectors may be, for example, bacteriophage-, plasmid- or cosmid-based. These vectors can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids typically containing elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, GEM 1 (Promega Biotec, Madison, WI, USA), pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pKK232-8, pDR540, and pRIT5 (Pharmacia).

These "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Bacterial promoters include lac, T3, T7, lambda P<sub>R</sub> or P<sub>L</sub>, trp, and ara.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is derepressed/induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by

centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the protein being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of antibodies or to screen peptide libraries, for example, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., 1983, *EMBO J.* 2:1791), in which the coding sequence may be ligated into the vector in frame with the *lac Z* coding region so that a fusion protein is produced; pIN vectors (Inouye et al., 1985, *Nucleic Acids Res.* 13:3101-3109; Van Heeke et al., 1989, *J. Biol. Chem.* 264:5503-5509); pET vectors, Studier et al., *Methods in Enzymology* 185: 60-89 (Academic Press 1990); and the like.

Moreover, pGEX vectors may be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and easily can be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene protein can be released from the GST moiety.

In a one embodiment, full length cDNA sequences are appended with in-frame *Bam*HI sites at the amino terminus and *Eco*RI sites at the carboxyl terminus using standard PCR methodologies (Innis et al., 1990, *supra*) and ligated into the pGEX-2TK vector (Pharmacia, Uppsala, Sweden). The resulting cDNA construct contains a kinase recognition site at the amino terminus for radioactive labeling and glutathione S-transferase sequences at the carboxyl terminus for affinity purification (Nilsson, et al. 1985, *EMBO J.* 4: 1075; Zabeau and Stanley, 1982, *EMBO J.* 1:1217.

#### ***Eukaryotic Expression***

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts,

described by Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Mammalian promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Exemplary mammalian vectors include pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia). Selectable markers include CAT (chloramphenicol transferase).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by *in vitro* or *in vivo* recombination. Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing a target protein in infected hosts. (E.g., See Logan et al., 1984, *Proc. Natl. Acad. Sci. USA* 81:3655-3659).

In one embodiment, cDNA sequences encoding the full-length open reading frames are ligated into pCMVB replacing the  $\beta$ -galactosidase gene such that cDNA expression is driven by the CMV promoter (Alam, 1990, *Anal. Biochem.* 188: 245-254; MacGregor et al., 1989, *Nucl. Acids Res.* 17: 2365; Norton et al. 1985, *Mol. Cell. Biol.* 5: 281).

In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g.,

cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins.

5       Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene  
10       product may be used. Such mammalian host cells include but are not limited to CHO, VERO, BHK, HeLa, COS, MDCK, 293, 3T3, WI38, etc.

15       For long-term, high-yield production of recombinant proteins in eukaryotic cells, stable expression is preferred. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker.

20       Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their  
25       chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the target protein. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that affect the endogenous activity of the  
30       protein.

35       A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler, et al., *Cell* 11:223 (1977)), hypoxanthine-guanine phosphoribosyltransferase (Szybalska et al., *Proc. Natl. Acad. Sci. USA* 48:2026 (1962)), and adenine phosphoribosyltransferase (Lowy, et al., *Cell* 22:817 (1980)) genes can be employed in tk<sup>-</sup>, hgp<sup>rt</sup> or ap<sup>rt</sup> cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for dhfr, which



confers resistance to methotrexate (Wigler, et al., *Proc. Natl. Acad. Sci. USA* 77:3567 (1980)); O'Hare, et al., 1981, *Proc. Natl. Acad. Sci. USA* 78:1527); gpt, which confers resistance to mycophenolic acid (Mulligan et al., *Proc. Natl. Acad. Sci. USA* 5 78:2072 (1981)); neo, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin, et al., 1981, *J. Mol. Biol.* 150:1); and hydro, which confers resistance to hygromycin (Santerre, et al., 1984, *Gene* 30:147) genes.

An alternative fusion protein system allows for the ready 10 purification of non-denatured fusion proteins expressed in human cell lines (Janknecht, et al., *Proc. Natl. Acad. Sci. USA* 88: 8972-8976 (1991)). In this system, the gene of interest is subcloned into a vaccinia-based plasmid such that the gene's open reading frame is translationally fused to an amino-terminal tag 15 consisting of six histidine residues. Extracts from cells infected with recombinant vaccinia virus are loaded onto Ni<sup>2+</sup> nitriloacetic acid-agarose columns and histidine-tagged proteins are selectively eluted with imidazole-containing buffers.

In an insect system, *Autographa californica* nuclear 20 polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The target coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the 25 polyhedrin promoter). Successful insertion of a target gene coding sequence will result in inactivation of the polyhedrin gene and production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat coded for by the polyhedrin gene). These recombinant viruses are then used to infect *Spodoptera* 30 *frugiperda* cells in which the inserted gene is expressed. (E.g., see Smith et al., 1983, *J. Virol.* 46: 584; Smith, U.S. Patent No. 4,215,051).

While the present proteins can be expressed in recombinant systems, as described above, cell-free translation systems can 35 also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention.

### *Purification of Recombinant Proteins*

Recombinant proteins produced may be isolated by host cell lysis. This may be followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, like lysozyme and chelators.

If inclusion bodies are formed in bacterial systems, they may be extracted from cell pellets using, for example, detergents, reducing agents, salts, urea, guanidinium chloride and extremes of pH (e.g. <4 or >10). If denaturation occurs, protein refolding steps (e.g., dialysis) can be used, as necessary, in completing configuration of the mature protein. If disulfide bridges are present in the native protein, they may be reoxidized using known methods.

By way of specific non-limiting example, the recombinant bacterial cells, for example *E. coli*, are grown in any of a number of suitable media, for example LB, and the expression of the recombinant protein induced by adding IPTG (e.g., lac operator-promoter) to the media or switching incubation to a higher temperature (e.g.,  $\lambda$  cI<sup>857</sup>). After culturing the bacteria for a further period of between 2 and 24 hours, the cells are collected by centrifugation and washed to remove residual media. The bacterial cells are then lysed, for example, by disruption in a cell homogenizer and centrifuged to separate the cell membranes from the soluble cell components. If the protein aggregates into inclusion bodies, this centrifugation can be performed under conditions whereby the dense inclusion bodies are selectively enriched by incorporation of sugars such as sucrose into the buffer and centrifugation at a selective speed. The inclusion bodies can then be washed in any of several solutions to remove some of the contaminating host proteins, then solubilized in solutions containing high concentrations of urea (e.g. 8M) or chaotropic agents such as guanidinium hydrochloride in the presence of reducing agents such as  $\beta$ -mercaptoethanol or DTT (dithiothreitol).

At this stage it may be advantageous to incubate the protein for several hours under conditions suitable for the protein to undergo a refolding process into a conformation which more closely resembles that of the native protein. Such conditions generally include low protein concentrations less than 500 µg/ml), low levels of reducing agent, concentrations of urea less than 2 M and often the presence of reagents such as a mixture of reduced and oxidized glutathione which facilitate the interchange of disulphide bonds within the protein molecule. The refolding process can be monitored, for example, by SDS-PAGE or with antibodies which are specific for the native molecule. Following refolding, the protein can then be purified further and separated from the refolding mixture by chromatography on any of several supports including ion exchange resins, gel permeation resins or on a variety of affinity columns.

#### *Labeling Proteins*

When used as a component in assay systems such as those described, below, the target protein may be labeled, either directly or indirectly, to facilitate detection of the present res-like molecules either *in vitro* or *in vivo*. Any of a variety of suitable labeling systems may be used including but not limited to radioisotopes such as <sup>125</sup>I; enzyme labeling systems that generate a detectable colorimetric signal or light when exposed to substrate; and fluorescent labels.

Where recombinant DNA technology is used for protein production then it may be advantageous to engineer fusion proteins that can facilitate labeling, immobilization and/or detection. These fusion proteins may, for example, add amino acids which facilitate further chemical modification. They also may add a functional moiety, such as an enzyme, which directly facilitates detection.

## TRANSGENIC ANIMALS

The invention further contemplates animal models for studying the function of the present molecules and for overproducing the protein products. The disclosed DNA sequences may be used in conjunction with techniques for producing transgenic animals that are well known to those of skill in the art.

To prepare transgenic animals, target gene sequences may for example be introduced into, and overexpressed in, the genome of the animal of interest, or, if endogenous target gene sequences are present, they may either be overexpressed or, alternatively, be disrupted in order to underexpress or inactivate target gene expression, such as described for the disruption of apoE in mice (Plum et al., Cell 71: 343-353 (1992)).

In order to overexpress a target gene sequence, the coding portion of the target gene sequence may be ligated to a regulatory sequence which is capable of driving gene expression in the animal and cell type of interest. Such regulatory regions will be well known to those of skill in the art, and may be utilized in the absence of undue experimentation.

For underexpression of an endogenous target gene sequence, such a sequence may be isolated and engineered such that when reintroduced into the genome of the animal of interest, the endogenous target gene alleles will be inactivated. Preferably, the engineered target gene sequence is introduced via gene targeting such that the endogenous target sequence is disrupted upon integration of the engineered target gene sequence into the animal's genome. Animals of any species, including, but not limited to, mice, rats, rabbits, guinea pigs, pigs, micro-pigs, goats, and non-human primates, e.g., baboons, monkeys, and chimpanzees may be used to generate cardiovascular disease animal models. Goats, cows and sheep are particularly preferred for producing protein *in vivo*.

Any technique known in the art may be used to introduce a target gene transgene into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to pronuclear microinjection (Hoppe et al., U.S. Pat. No. 4,873,191 (1989)); retrovirus mediated gene transfer into germ lines (Van der Putten et al., Proc. Natl. Acad. Sci., USA 82:6148-

6152 (1985)); gene targeting in embryonic stem cells (Thompson et al., *Cell* 56:313-321 (1989)); electroporation of embryos (Lo, *Mol. Cell. Biol.* 3:1803-1814 (1983)); and sperm-mediated gene transfer (Lavitrano et al., *Cell* 57:717-723 (1989)); etc. For a review of such techniques, see Gordon, *Transgenic Animals*, *Intl. Rev. Cytol.* 115:171-229 (1989).

The present invention provides for transgenic animals that carry the transgene in all their cells, as well as animals which carry the transgene in some, but not all their cells, i.e., mosaic animals. The transgene may be integrated as a single transgene or in concatamers, e.g., head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching of Lasko et al. (Lasko et al., *Proc. Natl. Acad. Sci. USA* 89:3232-6236 (1992)). The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. When it is desired that the target gene be integrated into the chromosomal site of the endogenous target gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous target gene of interest are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleotide sequence of the endogenous target gene.

The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous gene of interest in only that cell type, by following, for example, the teaching of Gu et al. *Science* 265: 103-106 (1994)). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art.

Once transgenic animals have been generated, the expression of the recombinant target gene and protein may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to analyze animal tissues to assay whether integration of the transgene has taken place. The level of mRNA expression of the

transgene in the tissues of the transgenic animals may also be assessed using techniques which include but are not limited to Northern blot analysis of tissue samples obtained from the animal, in situ hybridization analysis, and RT-PCR. Samples of target gene-expressing tissue, may also be evaluated immunocytochemically using antibodies specific for the target gene transgene gene product of interest.

The transgenic animals that express target gene mRNA or target gene transgene peptide (detected immunocytochemically, using antibodies directed against the target gene product's epitopes) at easily detectable levels should then be further evaluated to identify those animals which display characteristic increased susceptibility to carcinogenesis. Additionally, specific cell types within the transgenic animals may be analyzed and assayed *in vitro* for cellular phenotypes characteristic of mutant phenotype.

Once target gene transgenic founder animals are produced, they may be bred, inbred, outbred, or crossbred to produce colonies of the particular animal. Examples of such breeding strategies include but are not limited to: outbreeding of founder animals with more than one integration site in order to establish separate lines; inbreeding of separate lines in order to produce compound target gene transgenics that express the target gene transgene of interest at higher levels because of the effects of additive expression of each target gene transgene; crossing of heterozygous transgenic animals to produce animals homozygous for a given integration site in order both to augment expression and eliminate the possible need for screening of animals by DNA analysis; crossing of separate homozygous lines to produce compound heterozygous or homozygous lines; breeding animals to different inbred genetic backgrounds so as to examine effects of modifying alleles on expression of the target gene transgene and the possible development of carcinogenesis. One such approach is to cross the target gene transgenic founder animals with a wild type strain to produce an F1 generation that exhibits increased susceptibility to carcinogenesis. The F1 generation may then be inbred in order to develop a homozygous line, if it is found that homozygous target gene transgenic animals are viable.

Methods of generating "knockout" mice using homologous recombination in embryonic stem cells are well known in the art. Suitable methods are described, for example, in Mansour et al., *Nature*, 336:348 (1988); Zijlstra et al., *Nature*, 342:435 (1989) and 344:742 (1990); and Hasty et al., *Nature*, 350:243 (1991). This genomic DNA can be obtained by conventional methods using the cDNA sequence as a probe in a commercially-available genomic DNA library.

Briefly, a genomic fragment is cleaved with a restriction endonuclease and a heterologous cassette containing a neomycin-resistance gene is inserted at the cleavage site. A suitable cassette is the GTI-II neo cassette described by Lufkin et al., *Cell* 66:1105 (1991). The modified genomic fragment is cloned into a suitable targeting vector that is introduced into murine embryonic stem cells by electroporation. Cells that have undergone homologous recombination (and hence disruption of the gene) are selected by resistance to G418, and used to generate chimeric mice using well known methods. See Lufkin et al., *supra*. Traditional breeding methods then can be used to generate mice that are homozygous for the disrupted gene.

The phenotype of mice that are homozygous for the mutation then can be studied to provide insights into the role of the protein in, for example, carcinogenesis. These mice also can be used as models for developing new treatments for cancers. If this mutation is lethal in homozygous mice (for example during embryogenesis) heterozygous mice, which express only half the amount of the protein can also be studied.

#### GENE THERAPY APPLICATIONS

When mutations in the inventive protein, or in the elements controlling expression of that protein, are found to be associated with a malignant phenotype, control of cellular proliferation can be restored by gene therapy methods. For example, overexpression of the protein can be counteracted by concurrent expression of an antisense molecule that binds to and inhibits expression of the mRNA encoding the protein. Alternatively, overexpression can be inhibited in an analogous manner using a ribozyme that cleaves the mRNA. In another embodiment, where expression of a mutated

protein induces the malignant phenotype, concomitant expression of the non-mutated molecule via introduction of an exogenous gene may be used. Methods of using antisense and ribozyme technology to control gene expression, or of gene therapy methods for expression  
5 of an exogenous gene in this manner are well known in the art.

Each of these methods requires a system for introducing a vector into the cells containing the mutated gene. The vector encodes either an antisense or ribozyme transcript of the inventive protein. The construction of a suitable vector can be  
10 achieved by any of the methods well-known in the art for the insertion of exogenous DNA into a vector. See, e.g., Sambrook et al., *Molecular Cloning* (Cold Spring Harbor Press 2d ed. 1989), which is incorporated herein by reference. In addition, the prior art teaches various methods of introducing exogenous genes into  
15 cells *in vivo*. See Rosenberg et al., *Science* 242:1575-1578 (1988) and Wolff et al., *PNAS* 86:9011-9014 (1989), which are incorporated herein by reference. The routes of delivery include systemic administration and administration *in situ*. Well-known techniques include systemic administration with cationic liposomes, and  
20 administration *in situ* with viral vectors. Any one of the gene delivery methodologies described in the prior art is suitable for the introduction of a recombinant vector containing an inventive gene according to the invention into a MTX-resistant, transport-deficient cancer cell. A listing of present-day vectors suitable  
25 for the purpose of this invention is set forth in Hodgson, *Bio/Technology* 13: 222 (1995), which is incorporated by reference.

For example, liposome-mediated gene transfer is a suitable method for the introduction of a recombinant vector containing an inventive gene according to the invention into a MTX-resistant,  
30 transport-deficient cancer cell. The use of a cationic liposome, such as DC-Chol/DOPE liposome, has been widely documented as an appropriate vehicle to deliver DNA to a wide range of tissues through intravenous injection of DNA/cationic liposome complexes. See Caplen et al., *Nature Med.* 1:39-46 (1995) and Zhu et al.,  
35 *Science* 261:209-211 (1993), which are herein incorporated by reference. Liposomes transfer genes to the target cells by fusing with the plasma membrane. The entry process is relatively efficient, but once inside the cell, the liposome-DNA complex has



no inherent mechanism to deliver the DNA to the nucleus. As such, the most of the lipid and DNA gets shunted to cytoplasmic waste systems and destroyed. The obvious advantage of liposomes as a gene therapy vector is that liposomes contain no proteins, which thus minimizes the potential of host immune responses.

As another example, viral vector-mediated gene transfer is also a suitable method for the introduction of the vector into a target cell. Appropriate viral vectors include adenovirus vectors and adeno-associated virus vectors, retrovirus vectors and herpesvirus vectors.

Adenoviruses are linear, double stranded DNA viruses complexed with core proteins and surrounded by capsid proteins. The common serotypes 2 and 5, which are not associated with any human malignancies, are typically the base vectors. By deleting parts of the virus genome and inserting the desired gene under the control of a constitutive viral promoter, the virus becomes a replication deficient vector capable of transferring the exogenous DNA to differentiated, non-proliferating cells. To enter cells, the adenovirus fibre interacts with specific receptors on the cell surface, and the adenovirus surface proteins interact with the cell surface integrins. The virus penton-cell integrin interaction provides the signal that brings the exogenous gene-containing virus into a cytoplasmic endosome. The adenovirus breaks out of the endosome and moves to the nucleus, the viral capsid falls apart, and the exogenous DNA enters the cell nucleus where it functions, in an epichromosomal fashion, to express the exogenous gene. Detailed discussions of the use of adenoviral vectors for gene therapy can be found in Berkner, *Biotechniques* 6:616-629 (1988) and Trapnell, *Advanced Drug Delivery Rev.* 12:185-199 (1993), which are herein incorporated by reference. Adenovirus-derived vectors, particularly non-replicative adenovirus vectors, are characterized by their ability to accommodate exogenous DNA of 7.5 kB, relative stability, wide host range, low pathogenicity in man, and high titers ( $10^4$  to  $10^5$  plaque forming units per cell). See Stratford-Perricaudet et al., *PNAS* 89:2581 (1992).

Adeno-associated virus (AAV) vectors also can be used for the present invention. AAV is a linear single-stranded DNA parvovirus

that is endogenous to many mammalian species. AAV has a broad host range despite the limitation that AAV is a defective parvovirus which is dependent totally on either adenovirus or herpesvirus for its reproduction *in vivo*. The use of AAV as a vector for the introduction into target cells of exogenous DNA is well-known in the art. See, e.g., Lebkowski et al., *Mole. & Cell. Biol.* 8:3988 (1988), which is incorporated herein by reference. In these vectors, the capsid gene of AAV is replaced by a desired DNA fragment, and transcomplementation of the deleted capsid function is used to create a recombinant virus stock. Upon infection the recombinant virus uncoats in the nucleus and integrates into the host genome.

Another suitable virus-based gene delivery mechanism is retroviral vector-mediated gene transfer. In general, retroviral vectors are well-known in the art. See Breakfield et al., *Mole. Neuro. Biol.* 1:339 (1987) and Shih et al., in *Vaccines* 85: 177 (Cold Spring Harbor Press 1985). A variety of retroviral vectors and retroviral vector-producing cell lines can be used for the present invention. Appropriate retroviral vectors include Moloney Murine Leukemia Virus, spleen necrosis virus, and vectors derived from retroviruses such as Rous Sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, human immunodeficiency virus, myeloproliferative sarcoma virus, and mammary tumor virus. These vectors include replication-competent and replication-defective retroviral vectors. In addition, amphotropic and xenotropic retroviral vectors can be used. In carrying out the invention, retroviral vectors can be introduced to a tumor directly or in the form of free retroviral vector producing-cell lines. Suitable producer cells include fibroblasts, neurons, glial cells, keratinocytes, hepatocytes, connective tissue cells, ependymal cells, chromaffin cells. See Wolff et al., *PNAS* 84:3344 (1989).

Retroviral vectors generally are constructed such that the majority of its structural genes are deleted or replaced by exogenous DNA of interest, and such that the likelihood is reduced that viral proteins will be expressed. See Bender et al., *J. Virol.* 61:1639 (1987) and Armento et al., *J. Virol.* 61:1647 (1987), which are herein incorporated by reference. To facilitate expression of the antisense or ribozyme molecule, of the inventive

protein, a retroviral vector employed in the present invention must integrate into the genome of the host cell genome, an event which occurs only in mitotically active cells. The necessity for host cell replication effectively limits retroviral gene  
5 expression to tumor cells, which are highly replicative, and to a few normal tissues. The normal tissue cells theoretically most likely to be transduced by a retroviral vector, therefore, are the endothelial cells that line the blood vessels that supply blood to the tumor. In addition, it is also possible that a retroviral  
10 vector would integrate into white blood cells both in the tumor or in the blood circulating through the tumor.

The spread of retroviral vector to normal tissues, however, is limited. The local administration to a tumor of a retroviral vector or retroviral vector producing cells will restrict vector  
15 propagation to the local region of the tumor, minimizing transduction, integration, expression and subsequent cytotoxic effect on surrounding cells that are mitotically active.

Both replicatively deficient and replicatively competent retroviral vectors can be used in the invention, subject to their  
20 respective advantages and disadvantages. For instance, for tumors that have spread regionally, such as lung cancers, the direct injection of cell lines that produce replication-deficient vectors may not deliver the vector to a large enough area to completely eradicate the tumor, since the vector will be released only from  
25 the original producer cells and their progeny, and diffusion is limited. Similar constraints apply to the application of replication deficient vectors to tumors that grow slowly, such as human breast cancers which typically have doubling times of 30 days versus the 24 hours common among human gliomas. The much  
30 shortened survival-time of the producer cells, probably no more than 7-14 days in the absence of immunosuppression, limits to only a portion of their replicative cycle the exposure of the tumor cells to the retroviral vector.

The use of replication-defective retroviruses for treating  
35 tumors requires producer cells and is limited because each replication-defective retrovirus particle can enter only a single cell and cannot productively infect others thereafter. Because these replication-defective retroviruses cannot spread to other tumor cells, they would be unable to completely penetrate a deep,

multilayered tumor *in vivo*. See Markert et al., *Neurosurg.* 77: 590 (1992). The injection of replication-competent retroviral vector particles or a cell line that produces a replication-competent retroviral vector virus may prove to be a more effective therapeutic because a replication competent retroviral vector will establish a productive infection that will transduce cells as long as it persists. Moreover, replicatively competent retroviral vectors may follow the tumor as it metastasizes, carried along and propagated by transduced tumor cells. The risks for complications are greater, with replicatively competent vectors, however. Such vectors may pose a greater risk than replicatively deficient vectors of transducing normal tissues, for instance. The risks of undesired vector propagation for each type of cancer and affected body area can be weighed against the advantages in the situation of replicatively competent versus replicatively deficient retroviral vector to determine an optimum treatment.

Both amphotropic and xenotropic retroviral vectors may be used in the invention. Amphotropic viruses have a very broad host range that includes most or all mammalian cells, as is well known to the art. Xenotropic viruses can infect all mammalian cell cells except mouse cells. Thus, amphotropic and xenotropic retroviruses from many species, including cows, sheep, pigs, dogs, cats, rats, and mice, *inter alia* can be used to provide retroviral vectors in accordance with the invention, provided the vectors can transfer genes into proliferating human cells *in vivo*.

Clinical trials employing retroviral vector therapy treatment of cancer have been approved in the United States. See Culver, *Clin. Chem.* 40: 510 (1994). Retroviral vector-containing cells have been implanted into brain tumors growing in human patients. See Oldfield et al., *Hum. Gene Ther.* 4: 39 (1993). These retroviral vectors carried the HSV-1 thymidine kinase (HSV-tk) gene into the surrounding brain tumor cells, which conferred sensitivity of the tumor cells to the antiviral drug ganciclovir. Some of the limitations of current retroviral based cancer therapy, as described by Oldfield are: (1) the low titer of virus produced, (2) virus spread is limited to the region surrounding the producer cell implant, (3) possible immune response to the producer cell line, (4) possible insertional mutagenesis and

transformation of retroviral infected cells, (5) only a single treatment regimen of pro-drug, ganciclovir, is possible because the "suicide" product kills retrovirally infected cells and producer cells and (6) the bystander effect is limited to cells in direct contact with retrovirally transformed cells. See Bi et al., *Human Gene Therapy* 4: 725 (1993).

Yet another suitable virus-based gene delivery mechanism is herpesvirus vector-mediated gene transfer. While much less is known about the use of herpesvirus vectors, replication-competent HSV-1 viral vectors have been described in the context of antitumor therapy. See Martuza et al., *Science* 252: 854 (1991), which is incorporated herein by reference.

#### DIAGNOSTIC METHODS

The present invention also contemplates, for certain molecules described below, methods for diagnosis of human disease. In particular, patients can be screened for the occurrence of cancers, or likelihood of occurrence of cancers, associated with mutations in the encoded protein. DNA from tumor tissue obtained from patients suffering from cancer can be isolated and the gene encoding the protein can be sequenced. By examining a number of patients in this manner, mutations in the gene that are associated with a malignant cellular phenotype can be identified. In addition, correlation of the nature of the observed mutations with subsequent observed clinical outcomes allows development of prognostic model for the predicted outcome in a particular patient.

Screening for mutations conveniently can be carried out at the DNA level by use of PCR, although the skilled artisan will be aware that many other well known methods are available for the screening. PCR primers can be selected that flank known mutation sites, and the PCR products can be sequenced to detect the occurrence of the mutation. Alternatively, the 3' residue of one PCR primer can be selected to be a match only for the residue found in the unmutated gene. If the gene is mutated, there will be a mismatch at the 3' end of the primer, and primer extension cannot occur, and no PCR product will be obtained. Alternatively, primer mixtures can be used where the 3' residue of one primer is

any nucleotide other than the nonmutated residue. Observation of a PCR product then indicates that a mutation has occurred. Other methods of using, for example, oligonucleotide probes to screen for mutations are described, for example, in U.S. Patent No. 4,871,838, which is herein incorporated by reference in its entirety.

Alternatively, antibodies can be generated that selectively bind either mutated or non-mutated protein. The antibodies then can be used to screen tissue samples for occurrence of mutations in a manner analogous to the DNA-based methods described *supra*.

The diagnostic methods described above can be used not only for diagnosis and for prognosis of existing disease, but may also be used to predict the likelihood of the future occurrence of disease. For example, clinically healthy patients can be screened for mutations in the inventive molecule that correlate with later disease onset. Such mutations may be observed in the heterozygous state in healthy individuals. In such cases a single mutation event can effectively disable proper functioning of the gene and induce a transformed or malignant phenotype. This screening also may be carried out prenatally or neonatally.

DNA molecules according to the invention also are well suited for use in so-called "gene chip" diagnostic applications. Such applications have been developed by, *inter alia*, Synteni and Affymetrix. Briefly, all or part of the DNA molecules of the invention can be used either as a probe to screen a polynucleotide array on a "gene chip," or they may be immobilized on the chip itself and used to identify other polynucleotides via hybridization to the surface of the chip. In this manner, for example, related genes can be identified, or expression patterns of the gene in various tissues can be simultaneously studied. Such gene chips have particular application for diagnosis of disease, or in forensic analysis to detect the presence or absence of an analyte. Suitable chip technology is described for example, in Wodicka *et al.*, *Nature Biotechnology*, 15:1359 (1997) which is hereby incorporated by reference in its entirety, and references cited therein.

#### PROTEIN-PROTEIN INTERACTIONS

Due to their similarity to certain known proteins, it is anticipated that some of the inventive protein molecules will interact with another class of cellular proteins. This is particularly true of those molecule containing leucine zipper motifs.

Any method suitable for detecting protein-protein interactions can be employed for identifying interacting targets. Among the traditional methods which can be employed are co-immunoprecipitation, crosslinking and co-purification through gradients or chromatographic columns. Utilizing procedures such as these allows for the identification of GAP gene products. Once identified, a GAP protein can be used, in conjunction with standard techniques, to identify its corresponding pathway gene. For example, at least a portion of the amino acid sequence of the pathway gene product can be ascertained using techniques well known to those of skill in the art, such as via the Edman degradation technique (see, e.g., Creighton, 1983, PROTEINS: STRUCTURES AND MOLECULAR PRINCIPLES, W.H. Freeman & Co., N.Y., pp.34-49). The amino acid sequence obtained can be used as a guide for the generation of oligonucleotide mixtures that can be used to screen for pathway gene sequences. Screening can be accomplished, for example, by standard hybridization or PCR techniques. Techniques for the generation of oligonucleotide mixtures and for screening are well-known. (See e.g., Ausubel, *supra*, and PCR PROTOCOLS: A GUIDE TO METHODS AND APPLICATIONS, 1990, Innis et al., eds. Academic Press, Inc., New York).

Additionally, methods can be employed which result in the simultaneous identification of interacting target genes. One method which detects protein interactions *in vivo*, the two-hybrid system, is described in detail for illustration purposes only and not by way of limitation. One version of this system has been described (Chien et al., *Proc. Natl. Acad. Sci. USA*, 88: 9578-9582 (1991)) and is commercially available from Clontech (Palo Alto, CA).

Briefly, utilizing such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to a known protein, in this case an inventive protein, and the other contains

the activator protein's activation domain fused to an unknown protein (a putative GAP, for instance) that is encoded by a cDNA which has been recombined into this plasmid as part of a cDNA library. The plasmids are transformed into a strain of the yeast  
5 *Saccharomyces cerevisiae* that contains a reporter gene (e.g., *lacZ*) whose regulatory region contains the transcription activator's binding sites. Either hybrid protein alone cannot activate transcription of the reporter gene, the DNA-binding domain hybrid cannot because it does not provide activation  
10 function, and the activation domain hybrid cannot because it cannot localize to the activator's binding sites. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product.

15 The two-hybrid system or related methodology can be used to screen activation domain libraries for proteins that interact with a known "bait" gene product. By way of example, and not by way of limitation, gene products known to be involved in TH cell subpopulation-related disorders and/or differentiation,  
20 maintenance, and/or effector function of the subpopulations can be used as the bait gene products. Total genomic or cDNA sequences are fused to the DNA encoding on activation domain. This library and a plasmid encoding a hybrid of the bait gene product fused to the DNA-binding domain are cotransformed into a yeast reporter  
25 strain, and the resulting transformants are screened for those that express the reporter gene. For example, and not by way of limitation, the bait gene can be cloned into a vector such that it is translationally fused to the DNA encoding the DNA-binding domain of the GAL4 protein. These colonies are purified and the  
30 library plasmids responsible for reporter gene expression are isolated. DNA sequencing is then used to identify the proteins encoded by the library plasmids.

35 The present invention, thus generally described, will be understood more readily by reference to the following examples, which are provided by way of illustration and are not intended to be limiting of the present invention.



The examples below are provided to illustrate the subject invention. These examples are provided by way of illustration and are not included for the purpose of limiting the invention.

#### EXAMPLES

##### 5 EXAMPLE I: cDNA Library Construction

cDNA library plates and clones originated from five cDNA libraries that were constructed by directional cloning. These are available through the Resource Center (<http://www.rzpd.de>) of the  
10 German Genome Project. In particular, the hfbr2 (human fetal brain; RZPD number DKFZp564) and hfkd2 (human fetal kidney; DKFZp566) libraries were generated using the Smart kit (Clontech), except that PCR was carried out with primers that contained uracil residues to permit directional cloning without  
15 restriction digestion and ligation, and were complementary with the pAMPL (LifeTechnologies) cloning sites for directional cloning. The htes3 (human testes; DKFZp434), hute1 (human uterus; DKFZp586) and hmcfl (human mammary carcinoma; DKFZp727) libraries are conventional (Gubler, U., Hoffman, B.J., (1983), A simple and  
20 very efficient method for generating cDNA libraries. Gene 25, 263-269), size-selected cDNA libraries. They are cloned into pSPORT1 (LifeTechnologies) via a NotI site which is introduced during reverse transcription downstream of the oligo dT primer and a SalI site that is introduced by the ligation of a adapters.  
25 The human mammary carcinoma library was constructed from MCF7 cells.

In a similar fashion, the hamy2 (human amygdala nucleus (inside the brain); RZPD number DKFZp761) and hmel2 (human melanoma; RZPD number DKFZp762) libraries have been generated  
30 using conventional approaches, employing a NotI -dT V primer for first strand synthesis (GAGCGGCCGC(T)19V). After second strand synthesis, SalI adapters were ligated to the blunted cDNA. Then the cDNA was cut with NotI to generate SalI-NotI compatible ends at the 5' and 3' ends of the cDNA, respectively, to allow  
35 directional cloning. The cDNAs were then size selected on agarose gels in two dimensions and cloned into the pSPORT1 plasmid vector which had been pre-cut with SalI and NotI (LifeTechnologies). The

DNA was transformed into the DH10B bacterial strain and single colonies were picked into 384well microtiter plates from the non-amplified library. The human melanoma library was constructed from MeWo cells, published by Kern, M.A., Helmbach, H., Artuc, M., Karmann, D., Jurgovsky, K. and Schadendorf, D. (1997) Human melanoma cell lines selected in vitro displaying various levels of drug resistance against cisplatin, fotemustine, vindesine or etoposide: modulation of proto-oncogene expression. Anticancer Res. 17, 4359-4370.

The cDNA sequences of this application were first identified among the sequences comprising various libraries. Technology has advanced considerably since the first cDNA libraries were made. Many small variations in both chemicals and machinery have been instituted over time, and these have improved both the efficiency and safety of the process. Although the cDNAs could be obtained using an older procedure, the procedure presented in this application is exemplary of one currently being used by persons skilled in the art. For the purpose of providing an exemplary method, the mRNA isolation and cDNA library construction described here is for the MCF-7 library (DKFZp727) from which the clones named DKFZphmcf1\_xxyyxx were obtained.

The human cell line MCF-7 was grown in DMEM supplemented with 10% fetal calf serum until confluency.  $3 \times 10^8$  cells were harvested with a cell scraper in PBS. Cells were lysed in buffer containing 0.5 % NP-40 to leave the nuclei intact. The debris was pelleted by centrifugation at 15 000 x g for 10 minutes at 4 degrees Celsius. Proteins in the supernatant were degraded in presence of SDS and Proteinase K (30 minutes at 56 degrees Celsius). Precipitation of proteins was done in a Phenol/Chloroform extraction, RNA was precipitated from the aqueous phase with Na-acetate and Ethanol. Polyadenylated messages were isolated using Qiagen Oligotex (QIAGEN, Hilden Germany).

First strand cDNA synthesis was accomplished using an oligo (dT) primer which also contained an NotI restriction site. Second strand synthesis was performed using a combination of DNA polymerase I, *E. coli* ligase and RNase H, followed by the

addition of a SalI adaptor to the blunt ended cDNA. The SalI adapted, double-stranded cDNA was then digested with NotI restriction enzyme, and fractionated by size on an agarose gel. DNA of the appropriate size was cut from the gel and cast into a second gel in a 90° angle. After electrophoresis in the second dimension, cDNA of the appropriate size was cut from the gel. The agarose block was broken down with help of gelase. The cDNA was purified with help of two phenol extractions and an ethanol precipitation. The cDNA was ligated into SalI/NotI pre-digested pSport1 vector (LifeTechnologies) and transformed into DH10B bacteria.

The libraries were arrayed into 384-well microtiter plates and spotted on high density nylon membranes for hybridization analysis. All libraries have been arrayed into 384well microtiter plates and spotted on high density nylon membranes for hybridization analysis.

The hamy2 Library consists of 121 384well plates comprising 46464 clones. The hmel2 library consists of 72 384well plates comprising 27648 clones. Filters and clones are available through the Resource Center of German Genome Project (<http://www.RZPD.de>). Whole library plates were distributed to the sequencing partners of the consortium for systematic sequencing.

## 25 EXAMPLE II: Sequencing of cDNA Clones

All clones in the 384-well microtiter plates were sequenced from the 5' end. Sequencing was done preferentially using dye terminator chemistry (ABD or Amersham) on ABI automated DNA sequencers (ABI 377, Applied Biosystems), one partner used EMBL prototype instruments (Arakis) mainly with dye primer chemistry.

The resulting expressed sequence tag (EST) sequences ("r1 ESTs" = sequenced from 5'-end) were analysed for:

a) the lack of identical matches with known genes.

For this, the EST-sequence was blasted against the cDNA consortiums own database and after that against public databases

and (with BLASTn and BLASTx against EMBL/EMBLNEW and assembled ESTs, please refer to EXAMPLE III: Bioinformatics analysis of full length cDNAs, for description and parameter settings). ESTs which were identical to known genes in more than 100 bp, with  
5 less than 2 mismatches, were excluded from further analysis.

b) the presence of an open reading frame

Open reading frames (ORFs) were detected with an tool developed by Munich Information Center for Protein Sequences (MIPS) called ORF-map. ORF-map visualises potential start and  
10 stop-codons. If an ORF without a stop codon was detected in a rl-EST, the sequence was processed further.

c) the presence of GC rich sequences

A script developed by MIPS computed the GC-content of the rl-sequence, which should be >40%. Writing similar scripts is  
15 within the ordinary skill of one in bioinformatics.

d) the lack of repeat structures

Repeats such as Alu, Line or CA-repeats were detected by blasting (BLASTn and BLASTx, please refer to EXAMPLE III: Bioinformatics analysis of full length cDNAs, for description and  
20 parameter settings) against a repeat-database compiled by MIPS. If a repeat was present within the rl-sequence, the sequence were not processed further.

Novel clones that met all criteria were identified to the sequencers, who then performed 3'-end sequencing of these clones.  
25 The resulting 3' ESTs ("s1 ESTs" = sequenced from 3'-end) were checked for

a) the lack of matches with known genes in public databases, and sequences already generated by us.

This was done by blasting against EMBL/EMBLNEW and assembled EST (BLASTn and BLASTx, please refer to EXAMPLE III: Bioinformatics analysis of full length cDNAs, for description and  
30 parameter settings).

b) the presence of polyadenylation signals.

Again only clones matching the selection criteria were chosen to be sequenced completely by the sequencers. Clones were selected after the following criteria:

5        A very good ORF had at least one BLASTx match to other proteins. A "good ORF" should extend to the 3' end and be longer than ~40 codons. If the ORF started in the r1 sequence, in front of the potential start codon, there should not exist too many competing start codons in frame with the ORF start codon and the  
10       start should match the Kozak consensus ATG. If the EST sequence was too short to decide according to the potential ORF, and there were only a few or no start codons in the sequence the GC content of the Sequence should be greater than 40%. The r1 sequences  
15       needed not contain an polyA-tail at the 3' end. In addition, the results of the blasting against the assembled human ESTs could help in questionable cases to decide whether to stop or to continue. A hit against these ESTs was an indication to go further.

Clones passing the above-described screening were sequenced  
20       in full. Sequencing was done preferentially using dye terminator chemistry (ABD or Amersham) on ABI automated DNA sequencers (ABI 377, Applied Biosystems), one partner used EMBL prototype instruments (Arakis) mainly with dye primer chemistry. Primer walking (Strauss et al., 1986, Specific-primer-directed DNA  
25       sequencing. Anal Biochem. 154, 353-360) was the preferred sequencing strategy because of the lower redundancy possible compared to random shotgun (Messing, J., Crea, R., Seeburg, H.P. (1981) A system for shotgun DNA sequencing. Nucleic Acids Res. 9, 32-39) methods. Walking primers were generally designed using  
30       software (e.g. Haas, S., Vingron, M., Poustka, A., Wiemann, S. (1998) Primer design in large-scale sequencing. Nucleic Acids Res. 26, 3006-3012, Schwager, C., Wiemann, S., Ansorge, W. (1995) GeneSkipper: integrated software environment for DNA sequence assembly and alignment. HUGO Genome Digest 2, 8-9) that permitted  
35       complete automation of this usually time consuming process and helped in the parallel processing of large numbers of clones.

**EXAMPLE III: Bioinformatics analysis of full length cDNAs**

Each sequence obtained was compared on nucleotide level in a stepwise manner to sequences in EMBL/EMBLNEW, EMBL-EST, EMBL-STS using the BLASTn algorithm. Basic Local Alignment Search Tool (BLAST, Altschul S. F. (1993) J Mol Evol 36:290-300; Altschul, S. F. et al (1990) J Mol Biol 215:403-10) is used to search for local sequence alignments. BLAST produces alignments of both nucleotide (BLASTn) and amino acid sequences (BLASTp or BLASTx) to determine sequence similarity. BLAST is especially useful in determining exact matches or in identifying homologs, because of the local nature of the alignments. While it is useful for matches which do not contain gaps, it is inappropriate for performing motif-style searching. The fundamental unit of BLAST algorithm output is the High-scoring Segment Pair (HSP).

An HSP consists of two sequence fragments of arbitrary but equal lengths whose alignment is locally maximal and for which the alignment BLAST approach is to look threshold or cut off score set by the user. BLAST looks for HSPs between a query sequence and a database sequence, to evaluate the statistical significance of any matches found, and to report only those matches which satisfy the user-selected threshold of significance. The parameter E establishes the statistically significant threshold for reporting database sequence matches. E is interpreted as the upper bound of the expected frequency of chance occurrence of an HSP (or set of HSPs) within the context of the entire database search. Any database sequence whose match satisfies E is reported in the program output. Parameter settings for the BLAST-operations (BLASTN 2.0a19MP-WashU) described were: EMBL-EMBLNEW: H=0 V=5 B=5 -filter seg; EMBL-EST: H=0 E=1e-10 B=500 V=500 -filter seg; EMBL-STS: H=0 V=5 B=5.

Search against EMBL/EMBLNEW was done to determine whether the cDNAs are already known, and also to find out whether the cDNAs are encoded by genomic sequences already sequenced and published/submitted to these databases.

Search against EMBL-EST was performed to get a first impression how abundant a particular cDNA would be and to get

information on tissue specificity (so-called "electronic Northern-Blot", e.g. some of the cDNAs derived of the testis library show only hits to ESTs also derived of testis libraries).

5 The cDNA-sequences were blasted against EMBL-STS to determine STS-sequence-match to the cDNA, thus providing a mapping information to the new cDNA.

10 The potential protein-sequences were generated automatically by a script searching for the longest open reading frame (ORF) in each of the three forward frames with a minimum length of 90 codons. Next, the automatically generated ORFs were translated into protein sequences. These protein sequences were searched against the non redundant protein data set of PIR/SwissProt/Trembel/Tremblnew (BLASTP 2.0a19MP-WashU, parameter setting: V=7 B=7 H=0 -filter seg). If the script generated more  
15 than one ORF, one ORF was chosen manually by the annotater according to the degree of similarity to known proteins, the location of the ORF in the cDNA, the length, the amino acid composition and the content of Prosite-Motifs.

20 Additionally there was a BLASTx (BLASTX 2.0a19MP-WashU against non redundant protein database comprising PIR/SWISSPROT/TREMBL/TREMBLNEW; parameter-settings were: matrix/home/data/blast/matrix/aa/BL0SUM62 H=0 V=5 B=5 -filter seg) search to find potential frame shift in the complementary cds of the cDNAs and to identify unspliced or partly spliced  
25 cDNAs. The protein sequence was then transferred to the PEDANT system, in order to generate additional information on the new proteins. PEDANT (Protein Extraction, Description, and Analysis Tool, Frishman, D. & Mewes, H.-W. (1997) PEDANTic genome analysis. Trends in Genetics , 13, 415-416) is a platform  
30 developed at the Munich Information Center for Protein Sequences (MIPS, Munich, Germany), which incorporates practically all bioinformatics methods important for the functional and structural characterisation of protein sequences. Computational methods used by PEDANT are:

## FASTA

Very sensitive protein sequence database searches with estimates of statistical significance. Pearson W.R. (1990) Rapid and sensitive sequence comparison with FASTP and FASTA. Methods  
5 Enzymol. 183, 63-98.

## BLAST2

Very sensitive protein sequence database searches with estimates of statistical significance. Altschul S.F., Gish W., Miller W., Myers E.W., and Lipman D.J. Basic local alignment  
10 search tool. Journal of Molecular Biology 215, 403-10.

## PREDATOR

High-accuracy secondary structure prediction from single and multiple sequences. Frishman, D. and Argos, P. (1997) 75% accuracy in protein secondary structure prediction. Proteins, 27,  
15 329-335. Frishman, D. and Argos, P. (1996) Incorporation of long-distance interactions in a secondary structure prediction algorithm. Prot. Eng. 9, 133-142.

## STRIDE

Secondary structure assignment from atomic coordinates. Frishman, D. and Argos, P. (1995) Knowledge-based secondary  
20 structure assignment. Proteins 23, 566-579.

## CLUSTALW

Multiple sequence alignment. Thompson, J.D., Higgins, D.G. and Gibson, T.J. (1994) CLUSTAL W: improving the sensitivity of  
25 progressive multiple sequence alignment through sequence weighting, positions-specific gap penalties and weight matrix choice. Nucleic Acids Research, 22:4673-4680.

## TMAP

Transmembrane region prediction from multiply aligned sequences. Persson, B. and Argos, P. (1994) Prediction of  
30 transmembrane segments in proteins utilising multiple sequence alignments. J. Mol. Biol. 237, 182-192.



## ALOM2

Transmembrane region prediction from single sequences.

Klein, P., Kanehisa, M., and Delisi, C. Prediction of protein  
function from sequence properties: A discriminant analysis of a  
5 database. Biochim. Biophys. Acta 787, 221-226 (1984). Version 2  
by Dr. K. Nakai.

## SIGNALP

Signal peptide prediction Nielsen, H., Engelbrecht, J.,  
Brunak, S., and von Heijne, G (1997). Identification of  
10 prokaryotic and eukaryotic signal peptides and prediction of  
their cleavage sites. Protein Engineering 10, 1-6.

## SEG

Detection of low complexity regions in protein sequences.  
Wootton, J.C., Federhen, S. (1993) Statistics of local complexity  
15 in amino acid sequences and sequence databases. Computers &  
Chemistry 17, 149-163.

## COILS

Detection of coiled coils. Lupas, A., M. Van Dyke, and J.  
Stock, "Predicting Coiled Coils from Protein Sequences." Science  
20 (1991) 252, 1162-1164.

## PROSEARCH

Detection of PROSITE protein sequence patterns. Kolakowski  
L.F. Jr., Leunissen J.A.M., Smith J.E. (1992) ProSearch: fast  
searching of protein sequences with regular expression patterns  
25 related to protein structure and function. Biotechniques 13, 919-  
921.

## BLIMPS

Similarity searches against a database of ungapped blocks.  
J.C. Wallace and Henikoff S., (1992) PATMAT: a searching and  
30 extraction program for sequence, pattern and block queries and  
databases, CABIOS 8, 249-254. Written by Bill Alford.

## HMMER

Hidden Markov model software . Sonnhammer E.L.L., Eddy S.R., Durbin R. (1997) Pfam: A Comprehensive Database of Protein Families Based on Seed Alignments. Proteins 28, 405-420.

## 5 pI

Perl script that returns the amino acid composition, molecular weight, theoretical pI, and expected extinction coefficient of an amino acid sequence. By Fred Lindberg. The parameter-settings were as follows: known3d: score > 100; BLAST: E-value < 10; SCOP: 10 <= 50 Alignments, E-Value < 0.0001; signalp: Y=0.7; untersucht vom N-Terminus her: 50 aa; funcat: E-value < 0.001; BLOCKS: <= 10 hits; BLIMPS: threshold 1100.0; COILS: threshold 0.95; SEG: threshold 20.0; BLAST in report: E-value < 0.001; PIR-KW, superfamilies, EC-Nummern in report: E-value < 0.00001; known3d 15 in report: score > 120

The results of PEDANT analysis together with the results of the similarity searches constitute the basis for the structural and functional annotation of the cDNAs and the encoded proteins, as specified herein.

We claim:

1. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: amy2\_12g7; amy2\_12il; amy2\_13gl9; amy2\_1bel4;  
 5 amy2\_24kl5; amy2\_2al3; amy2\_2il7; fbr2\_78dl8; fbr2\_78el8; amy2\_12lm2; amy2\_24b4; amy2\_12lfl9; tes3\_1bb5; amy2\_1i24; amy2\_1jl9; amy2\_2bl9; amy2\_7j5; amy2\_14b5; amy2\_2ol3; fkd2\_3kl; mel2\_7gl4; mel2\_12jl ; mel2\_7kl9; amy2\_2c22; fbr2\_78i2l;  
 amy2\_1ln4; amy2\_1cl2; amy2\_1il; amy2\_2f22; amy2\_2gl2; fbr2\_78cl2;  
 10 tes3\_10ilb; tes3\_3la10; amy2\_10hl7; amy2\_10p7; amy2\_12d7; amy2\_2fl8; tes3\_1lc22; tes3\_1ld2l; tes3\_29f24; tes3\_3lj20; tes3\_5k22; Tes3\_10nl0; Tes3\_1lel7; Tes3\_12dl8 ; Tes3\_14l7; Tes3\_15nl4; Tes3\_1bp3; Tes3\_19pl2; Tes3\_2lk14; Tes3\_22il1; Tes3\_22l24; tes3\_2bg3; tes3\_30pb; amy2\_1ld2; amy2\_12lol7;  
 15 amy2\_1il4; amy2\_24c8; fbr2\_78d4; tes3\_1la17; tes3\_17i2l; tes3\_20hl2; tes3\_7nl2; tes3\_9elb; amy2\_14mlb; tes3\_18nl4; their complements; and variants thereof.

2. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: amy2\_12g7; amy2\_12il; amy2\_13gl9; amy2\_1bel4;  
 amy2\_24kl5; amy2\_2al3; amy2\_2il7; amy2\_12lm2; amy2\_24b4;  
 amy2\_12lfl9; amy2\_1i24; amy2\_1jl9; amy2\_2bl9; amy2\_7j5;  
 amy2\_14b5; amy2\_2ol3; amy2\_2c22; amy2\_1ln4; amy2\_1cl2; amy2\_1il;  
 25 amy2\_2f22; amy2\_2gl2; amy2\_10hl7; amy2\_10p7; amy2\_12d7; amy2\_2fl8; amy2\_1ld2; amy2\_12lol7; amy2\_1il4; amy2\_24c8; their complements; and variants thereof.

3. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: fbr2\_78dl8; fbr2\_78el8; fbr2\_78i2l; fbr2\_78cl2;  
 30 fbr2\_78d4; their complements; and variants thereof.

4. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: amy2\_12lm2; amy2\_24b4; their complements; and  
 35 variants thereof.

5. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: amy2\_121f19; tes3\_1bb5; their complements; and variants thereof.

5        6. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: amy2\_1i24; amy2\_1j19; amy2\_2b19; amy2\_7j5; their complements; and variants thereof.

7. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: amy2\_14b5; amy2\_2o13; fkd2\_3k1; mel2\_7g14; their complements; and variants thereof.

8. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of mel2\_7g14; mel2\_12j1 ; mel2\_7k19; their complements; and variants thereof.

9. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: amy2\_2c22; fbr2\_78i21; their complements; and variants thereof.

10. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: amy2\_1ln4; amy2\_1il; amy2\_2g12; fbr2\_78cl2; tes3\_10ilb; tes3\_3la10; their complements; and variants thereof.

11. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: amy2\_10h17; amy2\_10p7; amy2\_12d7; amy2\_2f18; tes3\_1lc22; tes3\_1ld21; tes3\_29f24; tes3\_3lj20; tes3\_5k22; their complements; and variants thereof.

12. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: tes3\_1bb5; tes3\_10ilb; tes3\_3la10; tes3\_1lc22; tes3\_1ld21; tes3\_29f24; tes3\_3lj20; tes3\_5k22; Tes3\_10n10; Tes3\_1le17; Tes3\_12d18 ; Tes3\_1417; Tes3\_15n14; Tes3\_1bp3;

Tes3\_19p12; Tes3\_21k14; Tes3\_22i11; Tes3\_22l24; tes3\_2bg3;  
 tes3\_30pb; tes3\_11a17; tes3\_17i21; tes3\_20h12; tes3\_7n12;  
 tes3\_9e1b; their complements; and variants thereof.

5        13. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: amy2\_11d2; amy2\_12l017; amy2\_1i14; amy2\_24c8; fbr2\_78d4; tes3\_11a17; tes3\_17i21; tes3\_20h12; tes3\_7n12; tes3\_9e1b; their complements; and variants thereof.

10       14. An assemblage, comprising at least one nucleic acid molecule having the sequence of a clone selected from the group consisting of: amy2\_14m1b; tes3\_18n14; amy2\_1c12; amy2\_2f22; their complements; and variants thereof.

15       15. A nucleic acid molecule comprising a nucleotide sequence of the clone fkd2\_3k1.

16. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: amy2\_12g7; amy2\_12i1; amy2\_13g19; amy2\_1be14; amy2\_24k15; amy2\_2a13; amy2\_2i17; fbr2\_78d18; fbr2\_78e18; amy2\_12l2m2; amy2\_24b4; amy2\_12l1f19; tes3\_1bb5; amy2\_1i24; amy2\_1j19; amy2\_2b19; amy2\_7j5; amy2\_14b5; amy2\_2o13; fkd2\_3k1; mel2\_7g14; mel2\_12j1; mel2\_7k19; amy2\_2c22; fbr2\_78i21; amy2\_1ln4; amy2\_1c12; amy2\_1i1; amy2\_2f22; amy2\_2g12; fbr2\_78c12; tes3\_10i1b; tes3\_31a10; amy2\_10h17; amy2\_10p7; amy2\_12d7; amy2\_2f18; tes3\_11c22; tes3\_11d21; tes3\_29f24; tes3\_31j20; tes3\_5k22; Tes3\_10n10; Tes3\_11e17; Tes3\_12d18; Tes3\_1417; Tes3\_15n14; Tes3\_16p3; Tes3\_19p12; Tes3\_21k14; Tes3\_22i11; Tes3\_22l24; tes3\_2bg3; tes3\_30pb; amy2\_11d2; amy2\_12l017; amy2\_1i14; amy2\_24c8; fbr2\_78d4; tes3\_11a17; tes3\_17i21; tes3\_20h12; tes3\_7n12; tes3\_9e1b; amy2\_14m1b; tes3\_18n14; their complements; and variants thereof.

17. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: amy2\_12g7; amy2\_12i1; amy2\_13g19; amy2\_1be14; amy2\_24k15; amy2\_2a13; amy2\_2i17;

amy2\_121m2; amy2\_24b4; amy2\_121f19; amy2\_1i24; amy2\_1j19;  
amy2\_2b19; amy2\_7j5; amy2\_14b5; amy2\_2o13; amy2\_2c22; amy2\_11n4;  
amy2\_1c12; amy2\_1i1; amy2\_2f22; amy2\_2g12; amy2\_10h17; amy2\_10p7;  
amy2\_12d7; amy2\_2f18; amy2\_11d2; amy2\_121o17; amy2\_1i14;  
5 amy2\_24c8; their complements; and variants thereof.

18. A computer readable medium, comprising in electronic  
form at least one nucleic acid or protein sequence of a clone  
selected from the group consisting of: fbr2\_78d18; fbr2\_78e18;  
fbr2\_78i21; fbr2\_78c12; fbr2\_78d4; their complements; and  
10 variants thereof.

19. A computer readable medium, comprising in electronic  
form at least one nucleic acid or protein sequence of a clone  
selected from the group consisting of: amy2\_121m2; amy2\_24b4;  
their complements; and variants thereof.

15 20. A computer readable medium, comprising in electronic  
form at least one nucleic acid or protein sequence of a clone  
selected from the group consisting of: amy2\_121f19; tes3\_1bb5;  
their complements; and variants thereof.

21. A computer readable medium, comprising in electronic  
20 form at least one nucleic acid or protein sequence of a clone  
selected from the group consisting of: amy2\_1i24; amy2\_1j19;  
amy2\_2b19; amy2\_7j5; their complements; and variants thereof.

22. A computer readable medium, comprising in electronic  
form at least one nucleic acid or protein sequence of a clone  
25 selected from the group consisting of: amy2\_14b5; amy2\_2o13;  
fkd2\_3k1; mel2\_7g14; their complements; and variants thereof.

23. A computer readable medium, comprising in electronic  
form at least one nucleic acid or protein sequence of a clone  
selected from the group consisting of: mel2\_12j1; mel2\_7k19;  
30 their complements; and variants thereof.

24. A computer readable medium, comprising in electronic  
form at least one nucleic acid or protein sequence of a clone  
selected from the group consisting of: amy2\_2c22; fbr2\_78i21;  
their complements; and variants thereof.

25. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: amy2\_11n4; amy2\_1i1; amy2\_2gl2; fbr2\_78cl2; tes3\_10ilb; tes3\_3la10; their complements; and variants thereof.

26. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: amy2\_10hl7; amy2\_10p7; amy2\_12d7; amy2\_2fl8; tes3\_11c22; tes3\_11d21; tes3\_29f24; tes3\_3lj20; tes3\_5k22; their complements; and variants thereof.

27. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: tes3\_1bb5; tes3\_10ilb; tes3\_3la10; tes3\_11c22; tes3\_11d21; tes3\_29f24; tes3\_3lj20; tes3\_5k22; Tes3\_10n10; Tes3\_11el7; Tes3\_12dl8 ; Tes3\_14l7; Tes3\_15n14; Tes3\_1bp3; Tes3\_19pl2; Tes3\_21k14; Tes3\_22il1; Tes3\_22l24; tes3\_2bg3; tes3\_30pb; tes3\_11al7; tes3\_17i21; tes3\_20hl2; tes3\_7nl2; tes3\_9elb; their complements; and variants thereof.

28. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: amy2\_11d2; amy2\_12lo17; amy2\_1il4; amy2\_24c8; fbr2\_78d4; tes3\_11al7; tes3\_17i21; tes3\_20hl2; tes3\_7nl2; tes3\_9elb; their complements; and variants thereof.

29. A computer readable medium, comprising in electronic form at least one nucleic acid or protein sequence of a clone selected from the group consisting of: amy2\_14mlb; tes3\_18n14; amy2\_1cl2; amy2\_2f22; their complements; and variants thereof.

30. A computer readable medium, comprising in electronic form a nucleic acid or protein sequence of the clone fkd2\_3kl.

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